

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 1843.35 seconds
(without alignments)
10908.879 Million cell updates/sec

Title: US-09-674-716B-1

Perfect score: 415
Sequence: 1 aagctttacagttactcagc.....tggggccaaggacactagt 415

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_on:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_ey:*

13: gb_un:*

14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	415	100.0	415	6	BD232417
C 2	415	100.0	415	6	BD232449
3	415	100.0	415	6	AX010600 Sequence
C 4	415	100.0	415	6	AX010643 Sequence
5	310.6	74.8	1658	10	BC031470
6	310.4	74.8	453	6	AR302238 Sequence
7	310.4	74.8	453	6	AR560594
8	310.4	74.8	453	6	AX080317 Sequence
9	301.4	72.6	1774	6	BD137123
10	295.6	71.2	405	10	MMU05819
11	295.2	70.1	477	10	AB050074
12	292.6	70.5	399	10	MUSIGHFZX
13	289.8	69.8	396	10	MMU223543
14	289	69.6	314	10	MUSIGHRT
15	288	69.4	314	10	MUSIGHRU
16	287.4	69.3	314	10	MUSIGHRW
C 17	286.4	69.0	204107	10	AC073590
18	286.2	69.0	1589	10	BC049143
19	284.4	68.5	313	10	MUSIGHRY

20	284.2	68.5	314	10	MUSIGHRX	M32048 Mouse Ig ac
21	283.8	68.4	345	10	MMIGM18	X76014 Mus musculu
22	283.2	68.2	306	10	MUSIGHRV	M32046 Mouse Ig ac
23	281	67.7	314	10	MUSIGHRZ	M32050 Mouse Ig ac
24	278.6	67.1	414	10	MUSIGHAA2	M59222 Mouse Ig he
25	278.6	67.1	417	10	MUSIGHAA1	M59921 Mus musculu
26	278.4	67.1	305	10	MUSIGHSA	M32051 Mouse Ig ac
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28	274.2	66.1	1581	10	AB097849	AB097849 Mus muscu
29	273.6	65.9	375	10	AY090914	AY090914 Mus muscu
30	273.4	65.9	417	10	MUSIGHBMA	M98041 Mouse Ig re
31	272.4	65.6	300	10	MMIGVH22	X03398 Mouse gene
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C 33	271.6	65.4	856	6	AR452612	AR452612 Sequence
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35	271.2	65.3	345	10	AF132844	AF132844 Mus muscu
36	270.4	65.2	363	10	MUSIGKCLI	M15232 Mouse IgM r
37	270.2	65.1	408	6	CQ867384	CQ867384 Sequence
38	269.4	64.9	403	6	AR022572	AR022572 Sequence
39	269.4	64.9	403	6	AR037587	AR037587 Sequence
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41	269	64.8	351	10	AY090913	AY090913 Mus muscu
42	268.8	64.8	351	10	MMU73591	U73591 Mus musculu
43	268.8	64.8	351	10	S73907	S73907 Ig V kappa
44	268.6	64.7	427	10	MUSIGHRT	M17167 Mouse Ig mu
45	268.4	64.7	351	10	AF242213	AF242213 Mus muscu

ALIGNMENTS

RESULT 1
BD232417
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD232417 415 bp DNA linear PAT 17-JUL-2003
Antibodies against CD23, derivatives thereof and therapeutic utilization of the same.

BD232417
JP 2002514421-A/1
Mus musculus (house mouse)
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Bonney, J.Y.M.P., Crowe, S.J., Ellis, J.H., Rapson, N.T. and Shearin, J.

Antibodies against CD23, derivatives thereof and therapeutic utilization of the same
Patent: JP 2002514421-A 1 21-MAY-2002;

GLAXO GROUP LTD
OS Mus musculus (mouse)
PN JP 2002514421-A/1
PD 21-MAY-2002

PF 07-MAY-1999 JP 2000548470
PI 09-MAY-1998 GB 9809839.5
PI JEAN YVES MARCEL PAUL BONNEFOY, SCOTT JAMES CROWE, JONATHAN PI HENRY ELLIS,

PI NICHOLAS TIMOTHY RAPSON JEAN SHEARIN
PC C12N15/02.A61K39/395.C07K16/28.C12N15/00
CC Antibodies against CD23, derivatives thereof and therapeutic utilization

CC of the same
PH Key Location/Qualifiers
FT CDS (3) (413).

FEATURES
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/db_xref="taxon:10090"

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Best Local Similarity 100.0%; Pred. No. 4.6e-112;

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61	TT	GTTCCTTTTAAAGGGGTCAGAGTGAAGCTTGAAGAGCTTCGAGAGAGGCTTGG	120						
61	TT	GTTCCTTTTAAAGGGGTCAGAGTGAAGCTTGAAGAGCTTCGAGAGAGGCTTGG	120						
121	TG	CAACCTGGAGGATCCATGAAACTCTCCTGTGTAGCCTCTGGATTACTTTCAGTGGCT	180						
121	TG	CAACCTGGAGGATCCATGAAACTCTCCTGTGTAGCCTCTGGATTACTTTCAGTGGCT	180						
181	ACT	GGATGCTTGGGTCGCGAGTCTCCAGAGAAGGGGCTTGAGTGGGTGCTGAAATTA	240						
181	ACT	GGATGCTTGGGTCGCGAGTCTCCAGAGAAGGGGCTTGAGTGGGTGCTGAAATTA	240						
241	GAT	GAAATCTGATAATATGCAACACATATGCGGAGTCTGTGAAAGGGAAGTTCACCA	300						
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301	TCT	CAAGAGATGATTCCTGCAAAATGAACTGCTCTACCTGCAAAATGAACTTAAAGCTGAAG	360						
361	AC	AGTGGAGTTTATTACTGTACAGATTTTATAGACTGGGGCCCAAGGGACACTAGT	415						
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RESULT 2	415 bp	DNA	linear	PAT 17-JUL-2003
BD232449/c	Antibodies against CD23, derivatives thereof and therapeutic			
LOCUS	utilization of the same.			
DEFINITION				
ACCESSION	BD232449, 1	GI:33042219		
VERSION	BD232449			
KEYWORDS	JP 2002514421-A/33.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
	1 (bases 1 to 415)			
	Bonnefoy, J.Y.M.P., Crowe, S.J., Ellis, J.H., Rapson, N.T. and			
	Shearin, J.			
TITLE	Antibodies against CD23, derivatives thereof and therapeutic			
	utilization of the same			
JOURNAL	Patent: JP 2002514421-A 33 21-MAY-2002;			
	GLAXO GROUP LTD			
COMMENT	OS Mus musculus (mouse)			
	PN JP 2002514421-A/33			
	PD 21-MAY-2002			
	PF 07-MAY-1999 JP 2000548470			
	PR 09-MAY-1998 GB 9809839.5			
	PI JEAN YVES MARCEL PAUL BONNEFOY, SCOTT JAMES CROWE, JONATHAN PI			
	HENRY ELLIS,			
	PI NICHOLAS TIMOTHY RAPSON, JEAN SHEARIN			
	PC C12N15/02, A61K39/395, C07K16/28, C12N15/00			
	CC Antibodies against CD23, derivatives thereof and therapeutic			
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	of the same			
	key			
	FT source			
	1..415			
	/organization="Mus musculus (mouse)".			
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	/db_xref="taxon:10090"			
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Query Match	100.0%	Score 415;	DB 6;	Length 415;

	Best Local Similarity	100.08;	Pred. No.	4.6e-112;	Mismatches	0;	Indels	0;	Gaps	0;
	Matches	415;	Conservative							
QY	1	AAGCTTTTACAGTTACTCAGCACACAGAGACCTTCACCATGGATTTTGGGCTGATTTTTTA	60							
Dd	415	AAGCTTTTACAGTTACTCAGCACACAGGACCTCCACATGGATTTTGGGCTGATTTTTTA	356							
QY	61	TGTCTCTTTTAAAGGGTCCAGAGTGGAAGTGAAGCTTGAAGAGTCTGGAGGAGCGTTGG	120							
Dd	355	TGTCTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAAGAGTCTGGAGGAGCGTTGG	296							
QY	121	TGCACCTGGAGGATCCATGATAA CTCTCTGTGTAGCCTCTGGATTATTTCTTCAGTGGCT	180							
Dd	295	TGCACCTGGAGGATCCATGATAA CTCTCTGTGTAGCCTCTGGATTATTTCTTCAGTGGCT	236							
QY	181	ACTGGATGCTTTGGGTCGCCAGTCTCCAGAGAGGGGCTTGTAGTGGGTCTCTCAAAATTA	240							
Dd	235	ACTGGATGCTTTGGGTCGCCAGTCTCCAGAGAGGGGCTTGTAGTGGGTCTCTCAAAATTA	176							
QY	241	GATTGGAATCTGATAATTATGCAACA CATTATGCGAGTCTGTGAAAAGGGAAGTTCACCA	300							
Dd	175	GATTGGAATCTGATAATTATGCAACA CATTATGCGAGTCTGTGAAGGGAAGTTCACCA	116							
QY	301	TCTCAAGAGATGATTTCCAAAAGTCGCTCTAC TCTGCAAATGAACAGCTTAAAGAGCTGAAG	360							
Dd	115	TCTCAAGAGATGATTTCCAAAAGTCGCTCTAC TCTGCAAATGAACAGCTTAAAGAGCTGAAG	56							
QY	361	ACAGTGGAGTTTATTATGTGACAGATTTTCATAGACTGGGGCCAGGGACACTAGT	415							
Dd	55	ACAGTGGAGTTTATTACTGTGACAGATTTTCATAGACTGGGGCCAGGGACACTAGT	1							

RESULT 3

AX010600 LOCUS AX010600 linear PAT 06-SEP-2000
DEFINITION Sequence 1 from Patent WO9958679.
ACCESSION AX010600
VERSION AX010600.1 GI:9997411

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 Bonney, J.Y., Crowe, S.J., Rapson, N.T., Ellis, J.H. and Shearman, J.
Antibodies to cd23, derivatives thereof, and their therapeutic uses
Patent: WO 9958679-A 18-NOV-1999;
BONNEY JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON
NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY
(GB); SHEARMAN JEAN (US)

FEATURES source
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"
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CDS

ORIGIN

Query Match 100.0%; Score 415; DB 6; Length 415;
Best Local Similarity 100.0%; Pred No. 4.6e-112;
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| | | | |
Db 1 AAGCTTTACAGTTACTCAGCACACAGGACCTACCATGGATTTTGCGCTATTITTITA 60
| | | | |

QY 61 TTGTTCTTTTAAAGGGGTCAGAGTGAAGTGAAGCTTGAAGAGTCTGGAGGAGGCTTGG 120
 Db 61 TTGTTCTTTTAAAGGGGTCAGAGTGAAGTGAAGCTTGAAGAGTCTGGAGGAGGCTTGG 120
 QY 121 TGCACCTGGAGGATCCATGAAGTCTCCCTGTGTAGGCTCTGGATTACTTTTTCAGTGGCT 180
 Db 121 TGCACCTGGAGGATCCATGAAGTCTCCCTGTGTAGGCTCTGGATTACTTTTTCAGTGGCT 180
 QY 181 ACTGGATGTCTTGGGTCGGGTCCTCCAGAGAGGGGCTTGAAGTGGTGTCTGGAATTA 240
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 Db 301 TCTCAAGAGATGATCCAAAGTCTCTTACCTGCAAGTGAAGTGAAGTGAAGTGAAG 360
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 Db 361 ACAGTGGAGTTTATTACTGTACAGATTTTATAGACTGGGCGCAAGGACACTAGT 415

RESULT 4
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 LOCUS 415 bp DNA linear PAT 06-SEP-2000
 DEFINITION Sequence 46 from Patent WO9958679.
 ACCESSION AX010643
 VERSION AX010643.1 GI:9997452
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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 REFERENCES
 AUTHORS Bonney, J.Y., Crowe, S.J., Rapson, N.T., Ellis, J.H. and Shearin, J.
 TITLE Antibodies to cd23, derivatives thereof, and their therapeutic uses
 JOURNAL Patent: WO 9958679-A 46 18-NOV-1999;
 BONNEY JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON
 NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY
 (GB); SHEARIN JEAN (US)
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 source Location/Qualifiers
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 /mol_type="unassigned DNA"
 /db_xref="taxon:10090"

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 Best Local Similarity 100.0%; Pred. NO. 4.6e-112;
 Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 415 AAGCTTTTACAGTTACTCAGCACAGGACCTCACCAGTATTTGGGCTGATTTTTTTA 356
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 QY 121 TGCACCTGGAGGATCCATGAAGTCTCCCTGTGTAGGCTCTGGATTACTTTTCAGTGGCT 180
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 QY 181 ACTGGATGTCTTGGGTCGGGTCCTCCAGAGAGGGGCTTGAAGTGGTGTCTGGAATTA 240
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 QY 241 GATTGAAATCTGATAATTATGCAACATTTATGCGAGTCTGTGAAGAGGAAAGTTCACCA 300
 Db 175 GATTGAAATCTGATAATTATGCAACATTTATGCGAGTCTGTGAAGAGGAAAGTTCACCA 116

QY 301 TCTCAAGAGATGATCCAAAGTCTCTTACCTGCAAGTGAAGTGAAGTGAAGTGAAG 360
 Db 115 TCTCAAGAGATGATCCAAAGTCTCTTACCTGCAAGTGAAGTGAAGTGAAGTGAAG 56
 QY 361 ACAGTGGAGTTTATTACTGTACAGATTTTATAGACTGGGCGCAAGGACACTAGT 415
 Db 55 ACAGTGGAGTTTATTACTGTACAGATTTTATAGACTGGGCGCAAGGACACTAGT 1

RESULT 5
 BC031470
 LOCUS 1658 bp mRNA linear ROD 19-NOV-2003
 DEFINITION Mus musculus cDNA clone MGC:25748 IMAGE:3991558, complete cds.
 ACCESSION BC031470
 VERSION BC031470.1 GI:21594582
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1658)
 REFERENCES
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Donaldson, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Loquellano, N.A., Peters, G.J.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S.S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalys, D.E.,
 Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 22388257
 JOURNAL MEDLINE
 PUBMED 12477932
 2 (bases 1 to 1658)
 REFERENCES
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 1A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lousheed, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LMNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 30 Row: h Column: 18
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis, Similarity but not identity to protein.

FEATURES
source

Location/Qualifiers
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Query Match 74.8%; Score 310.6; DB 10; Length 1658;
Best Local Similarity 87.4%; Pred. No. 4.9e-81;
Matches 340; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 8 ACAGTTTACTCAGCACACAGGACCTCACCATTGGATTGTTGGCTGATTTTATTCTTCT 67
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QY 68 TTTAAAGGGGTCAGAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGTCGCAACC 127
DB 92 TTTAAAGGGGTCAGAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGTCGCAACC 151

QY 128 TGAGAGATCCATGAACCTCTCTGTGTAGCTCTGGATTATCTTCAGTGGCTTCTGGAT 187
DB 152 TGAGAGATCCATGAACCTCTCTGTGTAGCTCTGGATTATCTTCAGTGGCTTCTGGAT 211

QY 188 GTCTTGGGTCGCGAGCTCCACAGAGGGGCTTGAGTGGTTCGTAATAGATTGAA 247
DB 212 GAATGGGTCGCGAGCTCCACAGAGGGGCTTGAGTGGTTCGTAATAGATTGAG 271

QY 248 ATCTGATAATTATGCAACATTCATTCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAG 307
DB 272 ATCTGATAATTATGCAACATTCATTCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAG 331

QY 308 AGATGATTCGAAAGTCTCTTACCTGCAATGAAACAGCTTAAGAGCTGAAGACAGTGG 367
DB 332 AGATGATTCGAAAGTCTCTTACCTGCAATGAAACAGCTTAAGAGCTGAAGACAGTGG 391

QY 368 AGTTTATTACTGTACAGATTTTCATAGACT 396
DB 392 AATTATTACTGCACAAATGCTATGACT 420

RESULT 6

AR302238
LOCUS AR302238 453 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 14 from patent US 6541212.
ACCESSION AR302238
VERSION AR302238.1 GI:31690457
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 453)
AUTHORS Reiter,R.E. and Witte,O.N.
TITLE Methods for detecting prostate stem cell antigen protein
JOURNAL Patent: US 6541212-A 14 01-APR-2003;
FEATURES Location/Qualifiers
1. .453
/organism="unknown"
/mol_type="genomic DNA"

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Query Match 74.8%; Score 310.4; DB 6; Length 453;
Best Local Similarity 92.6%; Pred. No. 5.4e-81;
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 35 CATGATTTTGGGCTGATTTTATTTGTTCTTTTAAAGGGTCCAGAGTGAAGTAA 94
DB 6 CTTGGGTTGAGCTGGGTTTTTATTATTGTTCTTTTAAAGGGTCCGAGTGAAGTGA 65

QY 95 GCTTGAAGATCTGAGGAGGCTTGTCGCAACTGAGGATCCATGAACCTCTCTGTGT 154
DB 68 GCTTGAAGATCTGAGGAGGCTTGTCGCAACTGAGGATCCATGAACCTCTCTGTGT 125

QY 155 ACCTCTGTGATTTACTTTTCAGTGGCTTCTGGATGCTCTGGGTCGCGAGTCTCCAGAGAA 214
DB 126 ACCTCTGTGATTTACTTTTCAGTGAATTAATCTGGATGCTTGGGTCGCGAGTCTCCAGAGAA 185

QY 215 GGGGCTTGAGTGGTGTCTGAAATTAGATTTGAAATCTGATAATATGCAACATTAATGC 274
DB 186 GGGGCTTGAGTGGTGTCTGAAATTCGATTTGAGATCTGAAATTTATGCAACATTAATGC 245

QY 275 GGAGTCTGTGAAGGGAAGTTCAACATCTCAGAGATGATTCGAAAGTCTCTTACCT 334
DB 246 GGAGTCTGTGAAGGGAAGTTCAACATCTCAGAGATGATTCGAAAGTCTCTTACCT 305

QY 335 GCAAAATGAACAGCTTAAGAGCTGAAGAGCAGTGGAGTTTATTACTGTACAGAT 386
DB 306 GCAAAATGAACAGCTTAAGAGCTGAAGAGCAGTGGAGTTTATTACTGTACAGAT 357

RESULT 7

AR560594
LOCUS AR560594 453 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 14 from patent US 6756036.
ACCESSION AR560594
VERSION AR560594.1 GI:53972904
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 453)
AUTHORS Reiter,R.E. and Witte,O.N.
TITLE Methods for treating cancer using PSA antibodies and fragments thereof
JOURNAL Patent: US 6756036-A 14 29-JUN-2004;
FEATURES Location/Qualifiers
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QY      352 GAGCTGAAGACAGCTGGAGTTTATTACTGTACAGATTTCAATAG---ACTGGGGCCAAAGGGA 408
Db      323 GAGCTGAAGACACTGGCATTTATTACTGTACGATTACGATGCTTACTGGGGCCAAAGGGA 382
QY      409 CACTAGT 415
Db      383 CTCTGGT 389

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RESULT 10
MMU05819
LOCUS   Mus musculus BALB/c Ig mu heavy chain V-JH2 region mRNA, partial
DEFINITION
ACCESSION U05819
VERSION   U05819.1
KEYWORDS  405 bp mRNA linear ROD 22-FEB-1994
SOURCE    cds.
ORGANISM  Mus musculus (house mouse)
REFERENCE 1.
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL   1 (bases 1 to 405)
AUTHORS   Yong, I.J., Chan, S. and Ren, E.
TITLE     Identification of a new VH J606 family member utilized in the
JOURNAL   murine immune response to Hepatitis B surface antigen
REFERENCE 2 (bases 1 to 405)
AUTHORS   Ren, E.
TITLE     Direct Submission
JOURNAL   Submitted (27-JAN-1994) Be-Chee Ren, Microbiology and W.H.O.
IMMUNOLOGY Center, National University of Singapore, Faculty of
Medicine, Singapore, 0511, Republic of Singapore

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ORIGIN
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Best Local Similarity 92.8%; Pred. No. 1.3e-76;
Matches 310; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 53 TTTTATTATGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGAGTCTGGAGG 112
Db 24 TTTTATTATGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGTCTTGAGAGTCTGGAGG 83

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QY      113 AGGCTTGGTGCACCTGGAGGATCCATGAACCTCTCTCTGTAGCCTCTGGATTTACTTT 172
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QY      173 CAGTGGCTACTGATGTCTTGGGTCCGCCAGTCTCCAGAGAAGGGCTTGAGTGGGTTGC 232
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Db      204 TGAATTTAGATTGAATCTGATAATTTTGCACATATTATGCGAGTCTCTGAAAGGGA 263
QY      293 GTTCACCATCTCAAGAGATGATTCCAAAAGTCGTCTTACCTGCAAAATGAACAGCTTAA 352
Db      264 GTTCACCATCTCAAGAGATGATTCCAAAAGTCGTCTTACCTGCAAAATGAACAGCTTAA 323
QY      353 AGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
Db      324 AACTGAAGACACTGGAAATTTATTACTGTACGGCT 357

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RESULT 11
AB050074
LOCUS   Mus musculus VH10G1 mRNA for anti-dsRNA (RDV-RNA) antibody, partial
DEFINITION
ACCESSION AB050074
VERSION   AB050074.1
KEYWORDS  477 bp mRNA linear ROD 02-APR-2002
SOURCE    cds.
ORGANISM  Mus musculus (house mouse)
REFERENCE 1.
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL   1 (bases 1 to 477)
AUTHORS   Kitagawa, Y., Matsumoto, T., Okuhara, E. and Shikata, E.
TITLE     Immunogenicity of rice dwarf virus ribonucleic acid
JOURNAL   Tohoku J. Exp. Med. 122 (4), 337-343 (1977)
MEDLINE   78034786
PUBMED    918970

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REFERENCE 2
AUTHORS   Kitagawa, Y.
TITLE     anti-dsRNA (RDV-RNA) Ab VH region-VH10G1
JOURNAL   Published Only in Database (2002)
REFERENCE 3 (bases 1 to 477)
AUTHORS   Kitagawa, Y.
TITLE     Direct Submission
JOURNAL   Submitted (17-OCT-2000) Yoshichika Kitagawa, Akita Prefectural
University, Biotechnology Institute; minami 2-2, Ogata, Akita
010-0444, Japan (E-mail:kitagawa@agri.akita-pu.ac.jp,
URL:www.akita-pu.ac.jp/, Tel:81-185-45-2026(ex.400),
Fax:81-185-45-2678)

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ORIGIN
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Matches 306; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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 QY 113 AGCTTGGTGCAACCTCGAGGATCCATGAACCTCTCTGTGTAGCCCTCTGGATTTACTTT 172
 Db |||||
 84 AGCTTGGTGCAACCTCGAGGATCCATGAACCTCTCTGTGTAGCCCTCTGGATTTACTTT 143
 QY 173 CAGTGGCTACTGATGTCTTGGTGCCGCCAGTCTCCAGAGAAGGGCTTCAGTGGGTTC 232
 Db |||||
 144 CAGTAACTACTGATGAACCTGGGTCCGCCAGTCTCCAGAAAAGGGCTTCAGTGGGTTC 203
 QY 233 TGAATTAGTGAATCTGAATTAATTCACACACATTAATTCGGAGTCTGTGAAGGGA 292
 Db |||||
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 QY 293 GTTCACCATCTCAAGAGATGATTCCAAAGTCTCTCTACCTGCAATGAACAGCTTAAG 352
 Db |||||
 264 GTTCACCATCTCAAGAGATGATTCCAAAGTCTCTCTACCTGCAATGAACAGCTTAAG 323
 QY 353 AGCTGAAGCAGTGGAGTTTATTACTGTACAGA 385
 Db |||||
 324 GGCTGAAGCAGTGGAGTTTATTACTGTCTCAGA 356

RESULT 14
 MUSIGHRT
 LOCUS
 DEFINITION
 Mouse Ig active H-chain (GAC1) mRNA linear ROD 27-APR-1993
 68.2D8, partial cds.

ACCESSION M32044.1 GI:195969
 VERSION V-region; immunoglobulin heavy chain; processed gene.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 314)
 AUTHORS Jarvis,C.D., Cannon,L.E. and Stavnezer,J.
 TITLE Mouse antibody response to group A streptococcal carbohydrate
 JOURNAL J. Immunol. 143 (12), 4213-4220 (1989)
 MEDLINE 90079033
 PUBMED 2512352
 COMMENT Original source text: Mouse (strain A/J), cDNA to mRNA, anti-GAC
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 /db_xref="taxon:10090"
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 Best Local Similarity 95.2%; Pred. No. 1.2e-74;
 Matches 298; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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 2 GGGTCAGAGTGAAGTCAAGCTTCGAGGAGCTTGGTGCACCTCGAGGAT 61
 QY 136 CCATGAACCTCTCTGTGTAGCCCTCTGGATTTACTTTTCAGTGGCTACTGGATCTTTGGG 195
 Db |||||
 62 CCATGAACCTCTCTGTGTAGCCCTCTGGATTTACTTTTCAGTGGCTACTGGATCTTTGGG 121
 QY 196 TCGGCCAGTCTCCAGAGAAGGGCTTCAGTGGGTTCGTAATTAAGTGAATCTGATA 255
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QY 76 GGGTCAGAGTGAAGTCAAGCTTCGAGGCTCGAGGAGCTTGGTGCACCTCGAGGAT 135
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 QY 196 TCGGCCAGTCTCCAGAGAAGGGCTTCAGTGGGTTCGTAATTAAGTGAATCTGATA 255
 Db |||||
 122 TCGGCCAGTCTCCAGAGAAGGGCTTCAGTGGGTTCGTAATTAAGTGAATCTGATA 181

QY 256 ATTATGCAACACATTATTCGGAGTCTGTGAAGGGAAGTTCCACCATCTCAAGAGATGATT 315
 Db |||||
 182 ATTATGCAACACATTATTCGGAGTCTGTGAAGGGAAGTTCCACCATCTCAAGAGATGATT 241
 QY 316 CCAAAAGTCTCTTACCTGCAAAATGAACAGCTTAAGAGCTGAACAGAGTGGAGTTATT 375
 Db |||||
 242 CCAAAAGTCTCTTACCTGCAAAATGAACAGCTTAAGAGCTGAACAGAGTGGAGTTATT 301
 QY 376 ACTGTACAGATTT 388
 Db |||||
 302 ACTGCACAGATCT 314

MUSIGHRU
 LOCUS
 DEFINITION
 Mouse Ig active H-chain (GAC1) mRNA linear ROD 27-APR-1993
 68.3D3, partial cds.

ACCESSION M32045
 VERSION M32045.1 GI:195970
 KEYWORDS V-region; immunoglobulin heavy chain; processed gene.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 314)
 AUTHORS Jarvis,C.D., Cannon,L.E. and Stavnezer,J.
 TITLE Mouse antibody response to group A streptococcal carbohydrate
 JOURNAL J. Immunol. 143 (12), 4213-4220 (1989)
 MEDLINE 90079033
 PUBMED 2512352
 COMMENT Original source text: Mouse (strain A/J), cDNA to mRNA, anti-GAC
 hybridoma 68.3D3.

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 ORIGIN Chromosome 12.

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 Best Local Similarity 94.9%; Pred. No. 2.4e-74;
 Matches 237; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 76 GGGTCAGAGTGAAGTCAAGCTTCGAGGAGCTTGGAGGAGCTTGGTGCACCTCGAGGAT 135
 Db |||||
 2 GGGTCAGAGTGAAGTCAAGCTTCGAGGAGCTTGGAGGAGCTTGGTGCACCTCGAGGAT 61
 QY 136 CCATGAACCTCTCTGTGTAGCCCTCTGGATTTACTTTTCAGTGGCTACTGGATCTTTGGG 195
 Db |||||
 62 CCATGAACCTCTCTGTGTAGCCCTCTGGATTTACTTTTCAGTGGCTACTGGATCTTTGGG 121
 QY 196 TCGGCCAGTCTCCAGAGAAGGGCTTCAGTGGGTTCGTAATTAAGTGAATCTGATA 255
 Db |||||
 122 TCGGCCAGTCTCCAGAGAAGGGCTTCAGTGGGTTCGTAATTAAGTGAATCTGATA 181

QY 256 ATTATGCAACACATTATTCGGAGTCTGTGAAGGGAAGTTCCACCATCTCAAGAGATGATT 315
 Db |||||
 182 ATTATGCAACACATTATTCGGAGTCTGTGAAGGGAAGTTCCACCATCTCAAGAGATGATT 241
 QY 316 CCAAAAGTCTCTTACCTGCAAAATGAACAGCTTAAGAGCTGAACAGAGTGGAGTTATT 375
 Db |||||
 242 CCAAAAGTCTCTTACCTGCAAAATGAACAGCTTAAGAGCTGAACAGAGTGGAGTTATT 301
 QY 376 ACTGTACAGATTT 388
 Db |||||
 302 ACTGCACAGATCT 314

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 34239544 seqs, 19032134700 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	284	68.4	1526	3	BC011342
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7	277.2	66.8	531	6	CA571287
8	276.2	66.6	560	2	BF581663
9	273.4	65.9	597	1	AA472093
10	269.2	64.9	955	5	BUS24174
11	266	64.1	625	8	BH021344
12	247.4	59.6	615	2	BE288134
13	244.4	58.9	713	4	BG967386
14	236	56.9	642	7	CF110127
15	223	53.7	904	2	BF133700
16	221.4	53.3	352	5	BY219846
17	220	53.0	832	7	CO567572
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25 207.4 50.0 398 5 BQ711108
26 205 49.4 355 2 BF116408
27 204.6 49.3 422 5 BX439233
28 202.6 48.8 565 5 BQ711793
29 202.4 48.8 966 4 BG686641
30 202 48.7 429 5 BX360630
31 201 48.4 636 6 CD684919
32 200.2 48.2 900 5 BQ952498
33 199.6 48.1 934 2 BF181593
34 199.4 48.0 527 6 CD699968
35 199.4 48.0 830 4 BG756192
36 198.8 47.9 948 2 BF663384
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38 197.6 47.6 430 2 AW402433
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41 196.2 47.3 476 2 AW404015
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43 195.6 47.1 636 7 CK430742
44 195.2 47.0 516 2 AW402430
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ALIGNMENTS

RESULT 1
LOCUS BF163883
DEFINITION 601772396F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3991558 5', mRNA linear EST 30-OCT-2000
ACCESSION BF163883
VERSION BF163883.1 GI:11044161
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 914)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Plate: L1AM9204 row: p column: 23
High quality sequence stop: 679.

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Stem cell origin.
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu29"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 71.5%; Score 296.8; DB 2; Length 914;
Best Local Similarity 90.8%; Pred. No. 5.4e-76;
Matches 327; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

found through the I.M.A.G.E. Consortium/LLNL at:
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FEATURES
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providing samples: Lohman,
NTH"

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84	GAGGCTTTGGTACAACTGGAGGATCCATGAACCTCTCCTGTGTGCTCTGGATTCACITT	143		
172	TCAGTGCTACTGGATGTCTTTGGGTCCGCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTG	231		
144	TCACAACTACTACATGAACCTGGGTCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTG	203		
232	CTGAAATTAGATTGAATCTGATAATTATTCACACACATTATCGGAGTCTGTGAAAGGGA	291		
204	CTGAAATTAGATTGAATCTAATAATTATTCACACACATTATCGGAGTCTGTGAAAGGGA	263		
292	AGTTTCACCATCTCAAGAGATGATTCCAAAGTGGTCTCTACCTGTGCAAAATGAACAGCTTAA	351		
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601758583F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3992829 5',
mRNA sequence.

RESULT 5	
BC011342	
LOCUS	
DEFINITION	

BC011342 1526 bp mRNA linear HTC 13-FEB-2004
Mus musculus cDNA clone IMAGE:3992829, with apparent retained intron.

BC011342
BC011342.1 GI:15030173
HTC.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1526)

Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, P. S., Wagner, L., Shenmen, C. M., Schuler, G. D., Alschul, S. F., Zeeberg, B. B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, F.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schermer, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1526)

Direct Submission

Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: angbcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegged, H., Kowals, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 23 Row: n Column: 19

This clone has the following problem: retained intron.

FEATURES

source

1..1526

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/clone="IMAGE:3992829"

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/notes="Vector: pCMV-SPORT6"

ORIGIN

Query Match 68.4%; Score 284; DB 3; Length 1526;

Best Local Similarity 87.6%; Pred. No. 3.6e-72;

Matches 324; Conservative 0; Mismatches 40; Indels 6; Gaps 1;

QY 52 TTTTCTTTTATGTTCTTTTAAAGGGGTCCAGAGTGAAGCTTGAGGAGTCTGGAG 111

DB 35 TATTCATAGTTTCTTTTAAAGGTGTCAGAGTGAAGTGAAGTTTGATGAGTCTGGAG 94

QY 112 GAGGCTTGTGCAACTGGAGGATCCATGAACCTCTCTGTGTGAGCTCTGGATTACTT 171

DB 95 GAGGCTTGTGCAACCTGGAGGATCCATGAACCTCTCTGTGTGAGCTCTGGATTACTT 154

QY 172 TCAGTGGCTACTGGATGTTCTTGGTCCGCGAGTCTCCAGAGAGGGGCTTGAGTGGTTG 231

DB 155 TCACCTAACTACTACATGAACCTGGTCCGCGAGTCTCCAGAGAGGGGCTTGAGTGGTTG 214

QY 232 CTGAATAGTAGTTGAATCTGATTAATTATGCAACACATTATTCGCGAGTCTGTGAAGGGA 291

DB 215 CTGAATAGTAGTTGAATCTGATTAATTATGCAACACATTATTCGCGAGTCTGTGAAGGGA 274

QY 292 AGTTTCAACCTCTCAAGAGATGATTCCTCAAAAGTCGTCCTTACCTGCAAAATGAACAGCTTAA 351

DB 275 GGTTCACCATCTCAAGAGATGATTCCTCAAAAGTAGTGTCTTACCTGCAAAATGAACACTTAA 334

QY 352 GAGCTGAGACAGTGGAGTGTATTACTGTGTA-----CAGATTTCTAGACTGGGGCCAAAG 405

DB 335 GAGTTGGAAGACACTGGCATTATTACTGTACCAGGGCTGGGTTTCTTACTTGGGGCCAAAG 394

QY 406 GGACACTAGT 415

DB 395 GGACTCTGT 404

RESULT 6

BB842247

LOCUS

DEFINITION

BB842247 RIKEN full-length enriched, 6 days neonate spleen Mus musculus cDNA clone F430004H07 5', mRNA sequence.

ACCESSION

BB842247

VERSION

BB842247.1 GI:17042978

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 367)

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Soabe, Y., Suzuki, H., Tagawa, A., Takahashi, P., Takaku-Akahita, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)

Unpublished (2001)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Muramatsu, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

Location/Qualifiers

1..367

/organism="Mus musculus"

FEATURES

source

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/db_xref="taxon:10090"
/clone="F430004H07"
/tissue_type="spleen"
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Query Match 67.0%; Score 278.2; DB 2; Length 367;
Best Local Similarity 87.7%; Pred. No. 1.2e-70;
Matches 315; Conservative 0; Mismatches 43; Indels 1; Gaps 1;

QY 8 ACAGTTACTCAGCACACAGGACCTCACCTGGATTTTGGGCTGATTTTTTTTATTGTTCT 67
DB 10 ACACGGACAAGAACAATTCACCTGGACTTGAGACTGAGCTGTGCTTTATTATTGTTCT 69
QY 68 TTTAAAGGGGTCAGAGTGGAAGCTTGAGGAGCTCTGGAGGAGCTTGGTGCAACC 127
DB 70 TTTAAAGGGGTCAGAGTGGAAGCTTGAGGAGCTCTGGAGGAGCTTGGTGCAACC 129
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QY 248 ATCTGATTAATTGCAACACATTATGCGGAGTCTGTGAAGGAGGATTCACCATCTCAAG 307
DB 249 ATCTGATTAATTGCAACACATTATGCGGAGTCTGTGAAGGAGGATTCACCATCTCAAG 308
QY 308 AGATGATTCCAAAGTCTCTACCTGCAAAATGAACAGCTTAAGAGCTGAACAGTG 366
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RESULT 7
CA571287 531 bp mRNA linear EST 19-NOV-2002
LOCUS K0518C07-5N NIA Mouse Hematopoietic Stem Cell (lin-/c-kit+/Sca-1+)
DEFINITION cDNA Library (Long) Mus musculus cDNA clone NIA:K0518C07
IMAGE:30065598 5', mRNA sequence.
CA571287
CA571287.1 GI:25115988
EST.
Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 531)
AUTHORS Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G., Taub,D., Longo,D.L., Keller,J. and Ko,M.S.H.
TITLE Systematic Analyses of NIA Mouse Hematopoietic Stem Cell (lin-/c-kit+/Sca-1+) cDNA Library (Long)
JOURNAL Unpublished (2001)
COMMENT Other_ESTs: K0518C07-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0518 row: C column: 07
Seq primer: M13 Reverse
High quality sequence stop: 531
POLYA=No.
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/clone="F430004H07"
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/dev_stage="6 days neonate"
/clone_lib="RIKEN full-length enriched, 6 days neonate spleen"

ORIGIN
Query Match 67.0%; Score 278.2; DB 2; Length 367;
Best Local Similarity 87.7%; Pred. No. 1.2e-70;
Matches 315; Conservative 0; Mismatches 43; Indels 1; Gaps 1;

QY 8 ACAGTTACTCAGCACACAGGACCTCACCTGGATTTTGGGCTGATTTTTTTTATTGTTCT 67
DB 10 ACACGGACAAGAACAATTCACCTGGACTTGAGACTGAGCTGTGCTTTATTATTGTTCT 69
QY 68 TTTAAAGGGGTCAGAGTGGAAGCTTGAGGAGCTCTGGAGGAGCTTGGTGCAACC 127
DB 70 TTTAAAGGGGTCAGAGTGGAAGCTTGAGGAGCTCTGGAGGAGCTTGGTGCAACC 129
QY 128 TGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTTACTTTCAGTGGCTACTGGAT 187
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QY 188 GTCTTGGGTCGGCAGCTCTCAGAGAGGGGCTTGAGTGGTGTGCTGAAATTTAGATTGAA 247
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QY 248 ATCTGATTAATTGCAACACATTATGCGGAGTCTGTGAAGGAGGATTCACCATCTCAAG 307
DB 249 ATCTGATTAATTGCAACACATTATGCGGAGTCTGTGAAGGAGGATTCACCATCTCAAG 308
QY 308 AGATGATTCCAAAGTCTCTACCTGCAAAATGAACAGCTTAAGAGCTGAACAGTG 366
DB 309 AGATGATTCCAAAGTCTCTACCTGCAAAATGAACAGCTTAAGAGCTGAACAGTG 367

RESULT 7
CA571287 531 bp mRNA linear EST 19-NOV-2002
LOCUS K0518C07-5N NIA Mouse Hematopoietic Stem Cell (lin-/c-kit+/Sca-1+)
DEFINITION cDNA Library (Long) Mus musculus cDNA clone NIA:K0518C07
IMAGE:30065598 5', mRNA sequence.
CA571287
CA571287.1 GI:25115988
EST.
Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 531)
AUTHORS Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G., Taub,D., Longo,D.L., Keller,J. and Ko,M.S.H.
TITLE Systematic Analyses of NIA Mouse Hematopoietic Stem Cell (lin-/c-kit+/Sca-1+) cDNA Library (Long)
JOURNAL Unpublished (2001)
COMMENT Other_ESTs: K0518C07-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0518 row: C column: 07
Seq primer: M13 Reverse
High quality sequence stop: 531
POLYA=No.
Location/Qualifiers
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/tissue_type="Hematopoietic Stem Cell (lin-/c-kit+/Sca-1+)"
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/clone_lib="NIA Mouse Hematopoietic Stem Cell (lin-/c-kit+/Sca-1+) cDNA Library (Long)"
/notes="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Drs. Dennis Taub, Dan Longo (National Institute on Aging, USA), Jonathan Keller (National Cancer Institute, USA). Double-stranded cDNAs were synthesized with an oligo(dt) primer [Invitrogen]: 5'-pGACTAGTTCTAGATCGGAGCGCGCCCTTTTTTTTTTT-3' from 4.8 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.7 kb. The library was constructed by Yulan Piao (NIA)."
```

ORIGIN

Query Match 66.8%; Score 277.2; DB 6; Length 531;
Best Local Similarity 88.8%; Pred. No. 2.7e-70;
Matches 300; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 52 TTTTCTTTTATTGTTCTTTTAAAGGGTCCAGAGTCAAGTGAAGCTTGAGAGCTCTGGAG 111
DB 52 TATTCATAGTTTCTCTTAAAGGGTGTCCAGAGTGAAGTGAAGCTTGAGAGCTGGAG 111
QY 112 GAGGCTTGGTGCACACCTGGAGGATCCATGAACTCTCTGTGTAGCTCTGGATTACTT 171
DB 112 GAGGCTTGGTGCACACCTGGAGGATCCATGAACTCTCTGTGTAGCTCTGGATTACTT 171
QY 172 TCAGTGGCTACTGGATGTCTTGGGTCGGCAGTCTCCAGAGAGGGGCTTGAAGGTTG 231
DB 172 TTAGTCAGCGCTGGAGTGGTCCGCCAGTCTCCAGAGAGGGGCTTGAAGGTTG 231
QY 232 CTGAAATTAGATTGAATCTGATTAATGCAACATATGCGGAGTCTGTGAAGGGA 291
DB 232 CTGAAATTAGAACAAAGCTAATAATCATGCAACATATGCTGATGCTGTGAAGGGA 291
QY 292 AGTTCAACCTCTCAAGAGATGATTCACAAAGTCTCTACCTGCAAAATGAACAGCTTAA 351
DB 292 GGTTCACCATCTCAAGAGATGATTCACAAAGTCTCTACCTGCAAAATGAACAGCTTAA 351
QY 352 GAGCTGAAGACACTGGAGTTTATTACTGTACAGATTTC 389
DB 352 GAGCTGAAGACACTGGCAATTTATTACTGTACTGGCTAC 389

RESULT 8

BF581663 560 bp mRNA linear EST 12-DEC-2000
LOCUS 602099628F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4219447 5',
DEFINITION mRNA sequence.
ACCESSION BF581663
VERSION BF581663.1 GI:11655375
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM	Mus musculus	ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 560)	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 597)
AUTHORS	NIH-MGC http://mgi.nci.nih.gov/	AUTHORS	Marra, M., Hillier, L., Allien, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
TITLE	CDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)	TITLE	The WashU-HMI Mouse EST Project
JOURNAL	CDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)	JOURNAL	Unpublished (1996)
COMMENT	DNA Sequencing by: Incyte Genomics, Inc. Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLN9801 row: h column: 08 High quality sequence stop: 555. Location/Qualifiers 1. .560	COMMENT	Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:514504 Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 440. Location/Qualifiers 1. .597
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ORIGIN	Query Match 66.6%; Score 276.2; DB 2; Length 560; Best Local Similarity 90.0%; Pred. No. 5.4e-70; Matches 307; Conservative 0; Mismatches 33; Indels 1; Gaps 1; Qy 52 TTTTCTTTATGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGCTCGGAG 111 Db 82 TATTCATGATTTTCTCTTAAAGGTTCCAGAGTGAAGTGAAGCTTGAGGCTCGGAG 141 Qy 112 GAGCTTGGTGCAACCTGGAGGATCCATGAATCTCTCTGTAGCTCTCGGATTTACTT 171 Db 142 GAGG-TTGGTGGCAACCTGGAGGATCCATGAATCTCTCTGTAGCTCTCGGATTTACTT 200 Qy 172 TCAGTGGCTACTGGATCTTTGGGTCCGCGAGTCCAGAGAGGGGCTTGAGTGGTTG 231 Db 201 TTGCAACTACTGGATGACCTGGGTCCGCGAGTCCAGAGAGGGGCTTGAGTGGATTG 260 Qy 232 CTGAATAGATTGAATCTGATAATTATGCAACACATTATGCGGAGTCTGTGAAGGGA 291 Db 261 CTGAATTAATTAATGACATCTGATAATTTTGGACACATTAATGCGGAGTCTGTATAGGA 320 Qy 292 AGTTCCACCATCTCAAGAGATGATTCACAAAGTCTCTCTACCTGCAATGAACAGCTTAA 351 Db 321 GTTTCACCATCTCAAGAGATGATTCACAAAGTCTCTACCTGCAATGAACAGCTTAA 380 Qy 352 GAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTCTA 392. Db 381 GAGCTGAAGACACTGGCTTTTATTACTGTACGGGTCTACTA 421	ORIGIN	Query Match 65.9%; Score 273.4; DB 1; Length 597; Best Local Similarity 80.8%; Pred. No. 3.7e-69; Matches 332; Conservative 0; Mismatches 76; Indels 3; Gaps 1; Qy 8 ACAGTTACTCAGACACAGGACCTCACCATGGATTTGGGCTGATTTTTTTTATTGTTCT 67 Db 32 ACACAGATAGAACATCCACATGACTTGGGACTGAAGTGTACTCATAGTTTCT 91 Qy 68 TTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGAGTCTGGAGGGCTTGGTGAACC 127 Db 92 CTTTAAAGGGTCCAGAGTGAAGGAAAGCTTGAGGAGTCTGGAGGGGCTTGGTGAACC 151 Qy 128 TGGAGGATCCATGAAGAACTCTCTGTGTAGCTCTGGATTTACTTTTCAGTGGCTTGGAT 187 Db 152 TGGAGGATCCATAAAACTCTCTGTGTGTCTCTGTGATTCACCTTCAGTGGCTTGGAT 211 Qy 188 GTCTTGGGTCGCGGACGCTCTCCAGAGAGGGGCTTGAGTGGGTTGCTGAATTAGATTGAA 247 Db 212 GGAAGTGGTCCGCGGACGCTCTCCAGAGAGGGGACTTGAGTGGGTTGCTGAATTAGACAA 271 Qy 248 ATCTGATAATATTGCAACACATTTATCGGAGTCTGTGAAGGGAGGTTTCCACCATCTCAAG 307 Db 272 AGCTAGTAATATTGCAACACATTTATCTGAGTGTGTGAGAGGGAGGTTTCCACCATCTCAAG 331 Qy 308 AGATGATTCACAAAGCGTCTCTCTACCTGCAATGAACAGCTTAAAGAGCTGAACAGCTGG 367

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Db	392	CATTATTACTGTACTAGTACGGACATAGACTGGGGCCAAAGGACTCTAGT	442
RESULT 10			
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LOCUS	BU5241174	955 bp mRNA linear EST 13-SEP-2002	
DEFINITION	AGENCOURT_10126522 NCI_CGAP_Co24 Mus musculus cDNA clone		
ACCESSION	IMAGE:6530936 5', mRNA sequence.		
VERSION	BU5241174		
KEYWORDS	EST.		
SOURCE	BU5241174.1 GI:22834613		
ORGANISM	Mus musculus (house mouse)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	1 (bases 1 to 955)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-re@mail.nih.gov		
	Tissue Procurement: The Cepko Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LHAM14133 row: h column: 08		
	High quality sequence stop: 561.		
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	Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.		
	Average insert size 1.6 kb. Constructed by Life		
	Technologies. Note: this is a NCI_CGAP Library."		
ORIGIN			
Query Match	64.9%	Score 269.2; DB 5; Length 955;	
Best Local Similarity	87.3%	Pred. No. 7.3e-68;	
Matches	295; Conservative	0; Mismatches 43; Indels 0; Gaps 0;	
Qy	52	TTTTTTTATTGTTCTTTTAAAAAGGGGTCCAGAGTGAAGTGAAGTCTTGAGGAGTCTCGAG	111
Db	70	TATTTCATAGTTTCTCTTAAAGAGGTCTCCAGAGTGATGTGAAGTTTGAGGAGTCTCGAG	129
Qy	112	GAGGCTTGGTGCAACCTCGGAGGATCCATGAAACTCTCTGTGTAGCTCTCGGATTTACTT	171
Db	130	GAGGCTTGGTGCAACCTCGGAGGATCCAGGAACTCTCTGTGTTCCTCTGGATTTCACTT	189
Qy	172	TCAGTGCTACTCGGATGTCCTTTGGTCCGAGTCTCCAGAGAGGGGCTTGAGTGGGTTG	231
Db	190	TCAGTAACTATTTGGTGAACCTGGGTCCGAGTCTCCAGAGAGGGGACTTGAGTGGGTTG	249
Qy	232	CTGAAATFAGATTGAAATCTGTATAATTATTCACACATTAATGCGGAGTCTGTGAAAGGGA	291
Db	250	CTGAGATTAGATTGAAATCTAATGATTATGTGAACGCAATTATGCGAGTCTGTGAAAGGGA	309
Qy	292	AGTTCCACATCTCAAGAGATGATTCCAAAAGTCGTCTCTACTGTCAAATGAACAGCTTAA	351
Db	310	GGTTTCACATTTCAAGAGATGATTCCAAAAGTAGTGGTACTCTGCAATGAACAACTTAA	369

```

Db 181 GCGAGCTCTGTGAAGGGAGGTTTACCATCTCAAGAGATGATTCACAAAAGTAGTGCTAC 240
QY 333 CTGCAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGCTGAAGAGCTTAATTAAGTAC 382
Db 241 CTGCAATGAACAACTTAAGAGCTGAAGAGCTGAAGAGCTTAATTAAGTAC 290

RESULT 12
BE288134 615 bp mRNA linear EST 26-OCT-2000
LOCUS 601095304F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3489841 5',
DEFINITION mRNA sequence.
ACCESSION BE288134
VERSION BE288134
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 615)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8531 row: h column: 02
High quality sequence stop: 583.
Location/Qualifiers
FEATURES
source
1..615
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3489841"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

ORIGIN
Query Match 59.8%; Score 247.4; DB 2; Length 615;
Best Local Similarity 78.5%; Pred. No. 1.7e-61;
Matches 296; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 8 ACAGTTACTCAGCACACAGGACCTCACCATGGATTTGGCTGATTTTATTTTATTTCT 67
Db 19 AAGTGACACAGATCAATCAATGACTTGGACCTGAGCTGTGATTAATCATGTTTTTCT 78
QY 68 TTTTAAAGGGGTCAGAGTGAAGTGAAGCTTGAGGAGCTTGAGGAGGCTTGCGCAACC 127
Db 79 CTTTAAAGGTTCCAGTGTGAGGTGAAGTGAAGCTGGATGAGCTGGAGGAGGCTTGCGCAACC 138
QY 128 TGAGGATCCATGAACACTCTCTGTAGCTCTGATTTACTTTTCACTGCTGCTTGGAT 187
Db 139 TGGGAGGCCCATGAACACTCTCTGTGTGCTCTGATTCACCTTTTGGTACTTGGAT 198
QY 188 GTCTTGGTCCGCGAGCTCCAGAGAGGGGCTTGAGTGGGTGCTGAAATTAAGATTGAA 247
Db 199 GAACCTGGTCCGCGAGCTCCAGAGAGAGGACTGGAGTGGGTATCACAATTAAGAACAA 258
QY 248 ATCTGATAATTATGCAACACATTTATCGGAGTCTGTGAAGAGGAGTTTACCACATCTCAAG 307

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Db 259 ACCTTATAATTATGAACACATATTATTCAGATTCTGTGAAGGCAGATTCCACCATCTCAAG 318
QY 308 AGATGATTCCTCAAAAGCTGCTCTTACTGCAATGAACAGCTTAAGAGCTGAAGAGCAGTGG 367
Db 319 AGATGATTCCTCAAAAGCTGCTCTTACTGCAATGAACAACTTAAGACCTGAAGACATGGG 378
QY 368 AGTTATTACTGTACAG 384
Db 379 TATCTATTATTGTACAG 395

RESULT 13
BG967386 713 bp mRNA linear EST 12-JUN-2001
LOCUS 602833514F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4988282 5',
DEFINITION mRNA sequence.
ACCESSION BG967386
VERSION BG967386
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 713)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1000 row: k column: 03
High quality sequence stop: 703.
Location/Qualifiers
FEATURES
source
1..713
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4988282"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 Kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match 58.9%; Score 244.4; DB 4; Length 713;
Best Local Similarity 85.3%; Pred. No. 1.3e-60;
Matches 285; Conservative 0; Mismatches 46; Indels 3; Gaps 1;

QY 52 TTTTATTTATTTCTTTTAAAGGGTCCAGAGTGAAGCTTGAGGAGTCTGGAG 111
Db 79 TATTCATAGTTTTTCTTTAAAGGGTCCAGAGTGAAGCTTGAGGAGTCTGGAG 138
QY 112 GAGGCTTGGTGCACACTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTTTACTT 171
Db 139 GAGGCTTGGTGCACACTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTTTACTT 198
QY 172 TCAGTGGCTACTTGGAGTCTTGGGTCCGCGAGCTCTCCAGAGAGGGGCTTGAGTGGGTG 231
Db 199 TCACTAACTACTTGGAGTGAACCTGGTCCGCGAGCTCTCCAGAGAGGGGCTTGAGTGGGTG 258
QY 232 CTGAAATAGATTGAATCTGATTAATGCAACACATTTATCGGAGTCTGTGAAAGGGA 291
Db 259 CTGAAGTTAGATTGAATCTAATTAATTTATGCCACACATTTATGCCAGTCTGTGAAAGGGA 318

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QY 292 AGTTCACCATCTCAAGAGATGATTCCTCAAAAGTCGCTCTCTACTCTCAAAAT---GAACAGCT 348
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 Db 319 GGTTCACCATCTCAAGAGATGATTCCTCAAAAGTCGCTCTCTACTCTCAAAATTTGAACCAACT 378
 |||||
 QY 349 TAAGAGCTGAGACAGTGGAGTCTTATCTACTTAC 382
 |||||
 Db 379 TAAGAACTGGAAGACACTGGGTTTATATCTGTGC 412
 |||||

RESULT 14
 LOCUS CF110127 642 bp mRNA linear EST 23-JUL-2003
 DEFINITION Shultzomicao3378 Rat lung airway and parenchyma cDNA libraries
 Rattus norvegicus cDNA clone Contig298 5', mRNA sequence.
 CF110127
 ACCESSION CF110127.1 GI:33165670
 VERSION EST.
 KEYWORDS Rattus norvegicus (Norway rat)
 SOURCE Rattus norvegicus
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 642)
 Shultz, M.A., Zhang, L., Gu, Y.-Z., Baker, G.L., Fannuchi, M.V.,
 Padua, A.M., Gurske, W.A., Morin, D., Penn, S.G., Jovanovich, S.B.,
 Plopper, C.G. and Buckpitt, A.R.
 TITLE Gene expression analysis in response to lung toxicants: I.
 Sequencing and microarray development
 JOURNAL Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
 COMMENT Contact: Shultz MA
 Dept. of Molecular Biosciences, School of Veterinary Medicine
 University of California, Davis
 1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA
 Tel: 530 752 0793
 Fax: 530 752 4698
 Email: mashultz@ucdavis.edu
 Average Phred score is 20 or better. All poor quality data (Phred <
 20) and vector/linker sequence has been removed.
 High quality sequence stop: 642.

FEATURES

source
 1..642
 Location/Qualifiers
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="Contig298"
 /sex="male"
 /tissue_type="airway or parenchyma"
 /dev_stage="adult"
 /clone_lib="Rat lung airway and parenchyma cDNA libraries"
 /note="Organ: lung; Vector: pGEM-11zf(-); Site_1: Eco RI;
 Site_2: Not I; mRNA was isolated from microdissected rat
 lung airways and parenchyma tissues."

ORIGIN

Query Match 56.9%; Score 236; DB 7; Length 642;
 Best Local Similarity 81.9%; Pred. No. 3.9e-58;
 Matches 272; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
 QY 52 TTTTATTTATGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 111
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 Db 99 TTTTATTTGTCATTTTAAAGGTGTCTTGTCTGAGGTGAACACTCGAGGATCTGGG 158
 |||||
 QY 112 GAGCTTGGTGCACCTGGAGGATCCATGAACCTCTCTGTGTGTAGCTCTGGATTTACTT 171
 |||||
 Db 159 GAGGTTTGGTACACACCTGGAGTGTCCCTGAAACTCTCTTGTGCAACCTCTGGATTTCACTT 218
 |||||
 QY 172 TCAGTGGCTACTGTATGTTCTTGGGTCCGAGTCTCCAGAGAGGGGCTTGAGTGGTTG 231
 |||||
 Db 219 TCAGTAACCTACTGTGATGAATGGGTTCGACAGTCTCCAGGAGGGGTTAGAATTTGGTTG 278
 |||||
 QY 232 CTGAATATTAGATTGAAATCTGATAATTATTAATGCAACATATTATGCGGAGTCTGTGAAGGGA 291
 |||||

Db 279 CTGAATATTAGAACCAAACTCTATAATTATGCAACATATATGGGAGTCTAGTGAAGGCA 338
 |||||
 QY 292 AGTTCCACCTCTCAAGAGATGATTCCTCAAAAGTCGCTCTACTCTGCAAAATGAACAGCTTAA 351
 |||||
 Db 339 GATTCACCATTCAGAGATGATTCCTCAAAAGTATGGTCTACCTGCGAGATGAACAGCATAA 398
 |||||
 QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTACA 383
 |||||
 Db 399 GATCTGAAGATACCTGGCATTTTATTACTGTACA 430
 |||||

RESULT 15
 LOCUS BF133700 904 bp mRNA linear EST 24-OCT-2000
 DEFINITION 601778606F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4006801 5',
 mRNA sequence.
 BF133700
 ACCESSION BF133700.1 GI:10972740
 VERSION EST.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@email.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1AM9238 row: 1 column: 02
 High quality sequence stop: 680.

FEATURES

source
 1..904
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CZECH II"
 /db_xref="taxon:10090"
 /clone="IMAGE:4006801"
 /tissue_type="tumor, metastatic to mammary"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Lu30"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; transgenic model WNT-1, expression driven by
 MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
 dt. Library constructed by Life Technologies.
 Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 53.7%; Score 223; DB 2; Length 904;
 Best Local Similarity 79.0%; Pred. No. 2.8e-54;
 Matches 290; Conservative 0; Mismatches 75; Indels 2; Gaps 2;
 QY 10 AGTTACTCAGCACACAGGACCTCACCATGGATTTTGGGCTGATTTTTTTTATTGTTCTTT 69
 |||||
 Db 2 AGTGACACAGACCATTCACCATGTACTTGGGACTGAGCTGTGATTATCATGGTTTTCTCT 61
 |||||
 QY 70 TAAAGGGTCCAGAGTGAAGTGAAGCTTGAGAGGCTTGAGAGGCTTGGTGCACACCTG 129
 |||||
 Db 62 TAAAGGTGTCCAGTGTGAGGTGAAGCTGAGTCTGCTGAGGCTTGGTGCACACCTG 121
 |||||
 QY 130 GAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTTTTCAGTGGCTACTGGATGT 189
 |||||
 Db 122 GGAGGTCCATGAACCTCTCTGTGT -GCCTCTGGATTCACTTTTAGTGACTA-TGGATGA 179
 |||||
 QY 190 CTTGGGTCCGCCAGTCTCCAGAGAGGGGCTTGAGTGGGTGCTGAAATTAGATTGAAT 249
 |||||

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 233.448 Seconds
(without alignments)
10523.523 Million cell updates/sec

Title: US-09-674-716B-1

Perfect score: 415
Sequence: 1 agcgttacgtactcagc.....tgggcgcaaggacactagt 415

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	415	100.0	415	3	Aaz34745
2	310.4	74.8	453	3	ABK09984
3	310.4	74.8	453	5	AAF27975
4	301.4	72.6	1774	2	Aaz20419
5	293.6	70.7	496	2	AAV71155
6	293.6	70.7	497	2	AAQ08605
7	293.6	70.7	497	2	AAV22331
8	293.6	70.7	497	8	ABX79231
9	289.4	69.7	480	2	AAQ85388
10	282.2	68.0	469	2	AAQ12060
11	282.2	68.0	469	2	AAQ12016
12	272	65.5	357	2	AAV22331
13	271.6	65.4	856	5	AAC90472
14	270.2	65.1	408	13	ADR59058
15	269.8	65.0	1979	2	AAQ85386
16	269.4	64.9	403	2	AAQ62750
17	269.4	64.9	403	2	AAQ62775
18	269.2	64.9	445	10	ADF53232
19	268.6	64.7	498	2	AAQ11969
20	267.8	64.5	360	2	AAV58263

21	267.2	64.4	366	3	AAA38896
22	267.2	64.4	374	13	ADR59064
23	265.4	64.0	765	6	AAQ97143
24	265.2	63.9	809	2	AAQ34841
25	265	63.9	350	2	AAQ31971
26	263.6	63.5	899	5	AAC90471
27	263	63.4	403	2	AAQ62791
28	262.4	63.2	768	6	AAQ97139
29	262.4	63.2	1509	6	AAQ97147
30	260.6	62.8	5227	2	AAV79537
31	260.2	62.7	789	12	ADG16988
32	259.2	62.5	348	8	ACD17061
33	259.2	62.5	348	8	ACD17060
34	259.2	62.5	348	8	ACC69834
35	259.2	62.5	348	8	ACC69835
36	259.2	62.5	348	12	ADQ90876
37	259.2	62.5	348	12	ADQ90877
38	259	62.4	342	3	AAA38900
39	258.2	62.2	351	12	ADG16990
40	256.6	61.8	357	2	AAV58262
41	256.6	61.8	810	8	ACD17048
42	256.6	61.8	810	8	ACD17049
43	256.6	61.8	810	8	ACC69823
44	256.6	61.8	810	8	ACC69822
45	256.6	61.8	810	12	ADQ90804

ALIGNMENTS

RESULT 1

AAZ34745

ID AAZ34745 standard; cDNA; 415 BP.

XX

AC AAZ34745;

XX

DT 15-FEB-2000 (first entry)

XX

DE Mouse anti-CD23 MAb C11 heavy chain variable region cDNA.

XX

KW CD23; FCER1I; IGE receptor; monoclonal antibody; C11; mouse;

KW monoclonal antibody; chimeric antibody; humanised antibody;

KW complementarity determining region; CDR; autoimmune disease;

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;

KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

KW urticaria; nephrotic syndrome; glomerulonephritis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;

KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;

KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;

XX therapy; ds.

OS Mus musculus.

XX

FH Key Location/Qualifiers

CDS 3..413

FT /*tag= a

XX

PN WO9958679-A1.

XX

PD 18-NOV-1999.

XX

PF Abx79231 DNA encod

XX

PP Aaq85388 MAB.4197X

XX

PR Aaq12060 Sequence

XX

PR Aav22331 Nucleic a

XX

PA Aac90472 Antibody

XX

PI Aar59058 Anti-K88

XX

PI Aaq85386 Anti-cata

XX

PI Aaq62750 Murine Br

XX

PI Aaq62775 Murine Br

XX

PI Aaf53232 HAb18 rel

XX

PI Aaf11969 Sequence

XX

PI Aat58263 Lead bind

PT

Cell receptor specific antibodies useful for treating e.g. arthritis,

Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

WPI; 2000-053101/04.

F-PSDB; AAY32260.

PT diabetes, multiple sclerosis and psoriasis.

XX Claim 16; Fig 1; 81pp; English.

XX This DNA sequence encodes the heavy chain variable region (VH) of murine
PS anti-CD23 (FCERII) monoclonal antibody C11. The invention provides
CC altered antibodies, such as chimeric or humanised antibodies (see
CC AAZ34747 and AAZ34748), which comprise sufficient of the amino acid
CC sequences of the C11 light and heavy chain complementarity determining
CC regions (see AAZ32254-59) to render them capable of binding to the CD23
CC type II molecule expressed on haematopoietic cells. The antibodies are
CC used to block soluble CD23 formation in human therapy, for the treatment
CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
CC malignancies (claimed). They are also useful for studying interactions
CC between CD23 and various ligands and determining the binding agents

XX Sequence 415 BP; 111 A; 76 C; 110 G; 118 T; 0 U; 0 Other;

Query Match 100.0%; Score 415; DB 3; Length 415;

Best Local Similarity 100.0%; Pred. No. 1.3e-114; Indels 0; Gaps 0;
Matches 415; Conservative 0; Mismatches 0;

QY 1 AAGCTTTTACAGTTTACTCAGCACAGACCTCACCATGATTTTGGGCTGATTTTAAAA 60
DB 1 AAGCTTTTACAGTTTACTCAGCACAGACCTCACCATGATTTTGGGCTGATTTTAAAA 60
QY 61 TTGTTCTTTTAAAGGGGTCACAGTGAAGTGAAGTCTGAGGAGTCTGGAGGAGGCTGG 120
DB 61 TTGTTCTTTTAAAGGGGTCACAGTGAAGTGAAGTCTGAGGAGTCTGGAGGAGGCTGG 120
QY 121 TGCACCTGGAGGATCATGAATCTCCTGCTGAGCTGAGCTGATTTTCAAGTGGCT 180
DB 121 TGCACCTGGAGGATCATGAATCTCCTGCTGAGCTGAGCTGATTTTCAAGTGGCT 180
QY 181 ACTGGATGTTCTGGGTCGGCAGTCTCCAGAGAGGGGCTTGGTGGTGTGCTGAATTA 240
DB 181 ACTGGATGTTCTGGGTCGGCAGTCTCCAGAGAGGGGCTTGGTGGTGTGCTGAATTA 240
QY 241 GATTGAATCTGATAATATGCAACACATTTATGCGGAGTCTGTGAAGGGAAGTTACCA 300
DB 241 GATTGAATCTGATAATATGCAACACATTTATGCGGAGTCTGTGAAGGGAAGTTACCA 300
QY 301 TCTCAAGAGATGATTCACAAAGTCTCTACCTGCAATGAACAGCTTAAGAGCTGAAG 360
DB 301 TCTCAAGAGATGATTCACAAAGTCTCTACCTGCAATGAACAGCTTAAGAGCTGAAG 360
QY 361 ACAGTGGAGTTTATTACTGTACAGATTTTATAGACTGGGCCCAAGGACACTAGT 415
DB 361 ACAGTGGAGTTTATTACTGTACAGATTTTATAGACTGGGCCCAAGGACACTAGT 415

RESULT 2

ABK09984

ID ABK09984 standard; DNA; 453 BP.

XX AC ABK09984;

XX 21-MAY-2002 (first entry)

DE Mouse heavy chain variable domain region of PSCA antibody 2H9 gene.

XX Mouse; prostate stem cell antigen; PSCA; gene; antibody; immunogen;
KW prostate cancer; bladder cancer; pancreatic cancer; immunoconjugate;
KW PSCA-associated cancer; heavy chain variable domain region; PSCA antigen;
KW PSCA antibody 2H9; db.

XX Mus sp.

OS

XX FH Location/Qualifiers
FT 1. .453
FT /*tag= a
FT /partial
FT /product= "Mouse PSCA antibody 2H9"
FT /note= "This sequence lacks both a start and stop codon"
FT misc_feature 133. .162
FT /*tag= b
FT /note= "Complementarity determining region 1 (CDR1)"
FT misc_feature 205. .261
FT /*tag= c
FT /note= "Complementarity determining region 2 (CDR2)"
FT misc_feature 358. .375
FT /*tag= d
FT /note= "Complementarity determining region 3 (CDR3)"
PN US2001055751-A1.
XX 27-DEC-2001.
XX 03-MAY-2000; 2000US-00564329.
XX 10-MAR-1997; 97US-0228816P.
XX 12-JAN-1998; 98US-0071141P.
XX 13-FEB-1998; 98US-0074675P.
XX 10-MAR-1998; 98US-00038261.
XX 02-DEC-1998; 98US-00203939.
XX 21-DEC-1998; 98US-0113230P.
XX 17-FEB-1999; 99US-00251835.
XX 16-MAR-1999; 99US-0124658P.
XX 25-MAY-1999; 99US-00318503.
XX 20-JUL-1999; 99US-00359326.
XX (REIT/) REITER R E.
XX (WITT/) WITTE O N.
XX (SAFF/) SAFFRAN D C.
XX (JAKO/) JAKOBOVITS A.
XX Reiter RE, Witte ON, Saffran DC, Jakobovits A;
XX WPI; 2001-159478/16.
XX P-PSDB; AAU76696.
XX Antibodies binding to prostate stem cell antigen inhibit the growth of
XX cancer cells and are used to detect and treat prostate, pancreatic or
XX bladder cancers.

Example 21; Fig 60; 127pp; English.

The present invention relates to new antibodies that specifically bind a novel prostate stem cell antigen (PSCA), which is widely over-expressed across all stages of prostate cancer. The antibodies of the invention are useful to kill tumour cells expressing PSCA and as PSCA expression is observed in prostate tumour cells and in other human cancers, particularly bladder and pancreatic carcinomas, the antibodies are useful therapeutically to treat these diseases. In particular, monoclonal antibodies can be administered to subjects suffering from PSCA-associated cancers, e.g. prostate, bladder or pancreatic cancer, to inhibit the cancer and prolong the subject's life. The antibodies can be combined with a therapeutic agent in immunoconjugates useful to treat subjects suffering from malignant diseases, characterised by killing the cells. The antibodies and immunoconjugates may also be included with a carrier in pharmaceutical compositions useful to kill human cells expressing PSCA antigen on the cell surface. The antibodies are also useful diagnostically to detect cancers, especially prostate cancer, to isolate prostate cancer cells e.g. to enable culture growth to evaluate candidate therapeutic compounds, assist in identification of rare genes associated with prostate cancer, and to isolate and purify PSCA and PSCA homologues. The present nucleic acid sequence encodes the mouse heavy chain variable

CC	domain region of the PSCA monoclonal antibody 2H9 of the invention
XX	
SQ	Sequence 453 BP; 115 A; 93 C; 122 G; 123 T; 0 U; 0 Other;
	Query Match 74.8%; Score 310.4; DB 4; Length 453;
	Best Local Similarity 92.6%; Pred. No. 4.4e-83;
	Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0
Qy	35 CATGATTTTGGCTGATTTTTTTTATTGTCTTTTAAAAAGGGGTCACAGTGAAAGTCAA 94
Db	
Db	6 CTTCGGGTGAAGCTGGGTTTTATTATTGTCTTTTAAAAAGGGGTCGCGAGTGAAGTGAG 65
Qy	95 GCTTTGAGGAGTCTGGAGGAGCCTGGTGCACACTGGAGATCCATGAACAATCTCTCTGTGT 154
Db	66 GCTTTGAGGAGTCTGGAGGAGCCTGGGTGCACACTGGAGATCCATGAACAATCTCTCTGTGT 125
Qy	155 AGCCTCTGGATTACTTTTCAGTGGGTACTTGGATGCTTGGGTCCGCCAGTCTCCAGAGAA 214
Db	126 AGCCTCTGGATTACTTTTCAGTAATTAATCTGGATGACTTTGGGTCCGCCAGTCTCCAGAGAA 185
Qy	215 GGGGCTTGAGTGGGTGCTGAAATTAGATTGAAATCTCATTAATTATGCAACACATTATGC 274
Db	186 GGGGCTTGAGTGGGTGCTGAAATTTCGATTGAGATCTGAAAATTTATGCAACACATTATGC 245
Qy	275 GGAGTCTGTGAAAGGGAAGTTTACCATCTCAAGAGATGATTTCCAAAAGTCGTCTCTACT 334
Db	246 GGAGTCTGTGAAAGGGAATTTACCATCTCAAGAGATGATTTCCAGNAAGTCGTCTCTACT 305
Qy	335 GCAAAATGAACAGCTTAAAGCTGTAAGA CAGTGGAGTTTATTACTGTACAGAT 386
Db	306 GCAAAATGAACAACTTAAAGCCTGAAGACAGTGGAAATTTATTACTGTACAGAT 357

RESULT 3	
AAF27975	
ID	AAF27975 standard; DNA; 453 BP.
XX	
XX	
AC	
AAF27975;	
XX	
DT	08-MAY-2001 (first entry)
XX	
XX	Murine PSCA antibody 2H9 H chain V region coding sequence.
DE	
XX	
XX	Prostate stem cell antigen; PSCA; human; mouse; prostate cancer;
KW	diagnosis; treatment; chromosome 8q24.2; ds.
XX	
OS	Mus sp.
XX	
XX	
WO	2000105427-A1.
PN	
XX	
PD	25-JAN-2001.
XX	
PF	
XX	20-JUL-2000; 2000WO-US019967.
XX	
PR	20-JUL-1999; 99US-00359326.
PR	03-MAY-2000; 2000US-00564329.
XX	
XX	(REGC) UNIV CALIFORNIA.
PA	(UROG-) UROGENESYS.
PA	
XX	
PI	Reiter R, Witte O, Saffran DC, Jakobovits A;
XX	
XX	WPI; 2001-159478/16.
DR	P-PSDB; AAB35292.
XX	
XX	
FT	Antibodies binding to prostate stem cell antigen inhibit the growth of
PT	cancer cells and are used to detect and treat prostate, pancreatic or
PT	bladder cancers.
XX	
XX	
PS	Example 21; Fig 60; 229pp; English.
XX	
CC	The present invention describes a method of treating cancer associated
CC	with prostate stem cell antigen (PSCA) by administering an antibody which
CC	

CC	selectively binds to p5CA and inhibits the growth of the cancer cells.
CC	The p5CA gene is found on human chromosome 8q24.2. The invention provides
CC	the human and murine p5CA protein and coding sequences, which can be used
CC	not only in the treatment of, but also in detection and prognosis of
CC	prostate cancer
XX	
SQ	Sequence 453 BP; 115 A; 93 C; 122 G; 123 T; 0 U; 0 Other;
	Query Match 74.8%; Score 310.4; DB 5; Length 453;
	Best Local Similarity 92.6%; Pred. No. 4.4e-83;
	Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0
Qy	35 CATGGATTTTGGCTGATTTTTTTTATTGTTCCTTTAAAGGGGTCACAGTGGAAGTCAA 94
Db	6 CTTCGGGCTCGAGCTGGGCTTTTATTATTGTCTTTTAAAGGGGTCGGAGTGAAGTCAG 65
Qy	95 GCTTGGAGAGTCTGGAGAGGCTTGGTGCCAACCTGGAGGATCCATGAAACTCTCCTGTGT 154
Db	66 GCTTGGAGAGTCTGGAGAGGCTGGGTGCACAACCTGGAGGATCCATGAAACTCTCCTGTGT 125
Qy	155 AGCCTCTGGATTACTTTTTCAGTGCGCTACTCGATCTCTGGGTCGCCAGTCTCCAGAGAA 214
Db	126 AGCCTCTGGATTACTTTTCAGTAATAATTACTGGTAGCTTGGGTCGCCAGTCTCCAGAGAA 185
Qy	215 GGGGCTTTGAGTGGGTTGCTGCAAAATTAGAATTGAAAATCTGATAATTATGCAACACATATTGC 274
Db	186 GGGGCTTTGAGTGGGTTGCTGNAATTGATTGAGATCTGAAAAATTATGCACACATATTGC 245
Qy	275 GGAGTCTGTGAAAGGGAGTTTACCACATCTCAAGAGATGATTTCCAAAAGTCGTCTCTACCT 334
Db	246 GGAGTCTGTGAAAGGGAGAAATTCACCATCTCAAGAGATGATTTCCAGAAGTCGTCTCTACCT 305
Qy	335 GCMAATGAACAGCTTAAGAGCTGAAGCAGTGGAGTTTATTACTGTACAGAT 386
Db	306 GCMAATGAACAACTTAAAGACTGAAGCAGTGGAGTTTATTACTGTACAGAT 357

RESULT 4	
AAZ20419	AAZ20419 standard; cDNA; 1774 BP.
XX	
XX	AAZ20419;
XX	
XX	
DT	19-NOV-1999 (first entry)
XX	
DE	Antibody ABX-CBL heavy chain coding sequence.
XX	
XX	Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
KW	activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW	organ transplant rejection disease; lymphoma; pancreatic disease;
KW	autoimmune disease; inflammatory disease; arthritis; binding site; ss.
XX	
OS	Homo sapiens.
XX	
XX	
FH	Key
FT	CDS
FT	58..1770
FT	/*tag= a
XX	
XX	WO9945031-A2.
XX	
XX	
PD	10-SEP-1999.
XX	
XX	
PF	03-MAR-1999; 99WO-US004583.
XX	
PR	03-MAR-1998; 98US-00034607.
PR	03-FEB-1999; 99US-00244253.
XX	
XX	
PA	(ABGE-) ABGENIX INC.
XX	
PI	Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI	Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX	
DR	WPI; 1999-540816/45.

DR P-PSDB; AAY39451.
 XX New monoclonal antibody, used for treating e.g. graft versus host
 PT disease, cancers, autoimmune diseases and inflammatory diseases.
 XX
 XX
 XX Disclosure; Page 57-58; 245pp; English.
 XX
 CC This sequence encodes the heavy chain of the antibody ABX-CXL. The
 CC invention relates to a monoclonal antibody (MAB) with an isotype that
 CC fixes complement and a variable region that binds to the epitope on CD147
 CC bound by the IgM MAB ABX-CBL, providing that the antibody is not CB11.
 CC The MAB can selectively kill activated T-cells, activated B-cells or
 CC resting or activated monocytes. The products and methods can be used for
 CC treating diseases involving activated T-cells or B-cells or monocytes,
 CC e.g. graft versus host disease (GVHD), organ transplant rejection
 CC diseases (e.g. renal transplant, ocular transplant), cancers (e.g.
 CC cancers of the blood (e.g. leukaemia's and lymphomas) and pancreatic),
 CC autoimmune diseases (e.g. lupus), and inflammatory diseases (e.g.
 CC arthritis)
 XX
 XX Sequence 1774 BP; 460 A; 488 C; 420 G; 406 T; 0 U; 0 Other;

Query Match 72.6%; Score 301.4; DB 2; Length 1774;
 Best Local Similarity 90.7%; Pred. No. 3.8e-80;
 Matches 333; Conservative 0; Mismatches 31; Indels 3; Gaps 1;
 QY 52 TTTTATTTATTTCTTTTAAAGGGTCCAGAGTGAAGCTTGAGGAGTCTGGAG 111
 DB 23 TATTCATAGTTTTCTTTAAATGGTGTCCAGAGTGAAGCTTGAGGAGTCTGGAG 82
 QY 112 GAGGCTTGTGCAACCTGGAGGATCCATGAAGTCTCTCTGAGCTCTGGATTACTT 171
 DB 83 GAGGCTTGTGCAACCTGGAGGATCCATGAAGTCTCTCTGAGCTCTGGATTACTT 142
 QY 172 TCAGTGCTACTGAGTCTTGGTCCGAGTCTCCAGAGAGGGGCTTGAGTGGTTG 231
 DB 143 TCAGTAACTACTGAGTGAAGTGGTCCGAGTCTCCAGAGAGGGGCTTGAGTGGTTG 202
 QY 232 CTGAATAGTGAATCTGATAATATGCAACACATATGCGGAGTCTGTGAAGGGA 291
 DB 203 CTGAATAGTGAATCTGATAATATGCAACACATATGCGGAGTCTGTGAAGGGA 262
 QY 292 AGTTCACCTCAAGAGTGAATCCAAAGTCTCTCTACCTGCAAAATGAACAGCTTAA 351
 DB 263 GGTTCACCTCAAGAGTGAATCCAAAGTCTCTCTACCTGCAAAATGAACAGCTTAA 322
 QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTCATAG---ACTGGGGCCAAAGGA 408
 DB 323 GAGCTGAAGACAGTGGCAATTTATTACTGTACGATTACGATGCTTACTGGGGCCAAAGGA 382
 QY 409 CACTAGT 415
 DB 383 CTCTGGT 389

RESULT 5
 AAV71155
 ID AAV71155 standard; DNA; 496 BP.
 XX
 XX AAV71155;
 XX
 XX 20-MAR-2003 (revised)
 DT 16-APR-1999 (first entry)
 XX
 XX Coding strand for mouse Br-3 heavy chain variable region.
 DE
 XX Heavy chain variable region; murine antibody Br-3; antibody ING-1;
 KW chimeric immunoglobulin; human tumour antigen; chimeric antibody;
 KW treatment; human cancer; 88.
 XX
 XX Mus sp.
 OS
 XX
 XX Key Location/Qualifiers
 PH

CDS
 FT 69. .494
 FT /*tag= a
 XX /note= "Partial CDS, no termination codon"
 PN US5843685-A.
 XX
 XX 01-DEC-1998.
 XX
 XX 06-JUN-1995; 95US-00466034.
 XX
 XX 06-SEP-1988; 88US-00240624.
 XX
 XX 08-SEP-1988; 88US-00241744.
 XX
 XX 13-SEP-1988; 88US-00243739.
 XX
 XX 04-OCT-1988; 88US-00253002.
 XX
 XX 19-JUN-1989; 89US-00367641.
 XX
 XX 21-JUL-1989; 89US-00382768.
 XX
 XX 06-SEP-1989; 89WO-US003852.
 XX
 XX 06-MAY-1991; 91US-00659401.
 XX
 XX 27-DEC-1994; 94US-00364001.
 XX
 XX (XOMA) XOMA CORP.
 XX
 XX Horwitz AH, Lei S, Chang CP, Better MD, Robinson RR;
 XX
 XX WPI; 1999-044574/04.
 XX
 XX P-PSDB; AAW85059.
 XX
 XX Chimeric antibody specific for human tumour antigen - useful as
 PT immunoassay, imaging or antitumour agent.
 XX
 XX Example 3; Fig 15; 92pp; English.
 XX
 XX The present sequence encodes the heavy chain variable region of murine
 CC antibody Br-3. The sequence was used to create chimeric mouse-human
 CC immunoglobulins which recognise the human tumour antigen bound by
 CC antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The
 CC chimeric antibodies also have an antigen-binding site that competitively
 CC inhibits the binding of antibody ING-1, and mediate complement-dependent
 CC cytotoxicity of target cells or antibody-dependent cellular cytotoxicity to
 CC target cells. The chimeric antibodies can be used for therapeutic
 CC purposes in the treatment of human cancer. (Updated on 20-MAR-2003 to
 CC correct PR field.)
 XX
 XX Sequence 496 BP; 141 A; 106 C; 118 G; 131 T; 0 U; 0 Other;
 SQ
 Query Match 70.7%; Score 293.6; DB 2; Length 496;
 Best Local Similarity 92.8%; Pred. No. 5.3e-78;
 Matches 308; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 QY 52 TTTTATTTATTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGTCTGAGGAGTCTGGAG 111
 DB 91 TATTCATAGTTTTCTTTAAAGGGTCCAGAGTGAAGTGAAGTCTGAGGAGTCTGGAG 150
 QY 112 GAGGCTTGTGCAACCTGGAGGATCCATGAAGTCTCTCTGAGTACCTCTGATTACTT 171
 DB 151 GAGGCTTGTGCAACCTGGAGGATCCATGAAGTCTCTCTGAGTACCTCTGATTACAT 210
 QY 172 TCAGTGGCTACTGGATGCTCTGCGTCCGAGTCTCCAGAGAGGGGCTTGAGTGGTTG 231
 DB 211 TCAGTAACTATTGGATGAACCTGGTCCGAGTCTCCAGAGAGGGGCTTGAGTGGTTG 270
 QY 232 CTGAATAGTGAATCTGATAATATGCAACACATTTATCGGAGTCTGTGAAGGGA 291
 DB 271 CTGAATAGTGAATCTGATAATATGCAACACATTTATCGGAGTCTGTGAAGGGA 330
 QY 292 AGTTCACCTCAAGAGTGAATCCAAAGTCTCTCTACCTGCAAAATGAACAGCTTAA 351
 DB 331 GGTTCACCTCAAGAGTGAATCCAAAGTCTCTCTACCTGCAAAATGAACAGCTTAA 390
 QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTACA 383
 DB 391 GAGCTGAAGACAGTGGCATTATTACTGTACA 422


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CC correct PF field.)
XX Sequence 497 BP; 141 A; 106 C; 118 G; 132 T; 0 U; 0 Other;
SQ
Query Match 70.7%; Score 293.6; DB 2; Length 497;
Best Local Similarity 92.8%; Pred. No. 5.3e-78;
Matches 308; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 52 TTTTATTTATTTGTTCTTTTAAAGGGGTCAGAGTGAAGCTTGAGGAGTCTGGAG 111
DB 92 TATTCATAGTTTCTTTCTTTAAAGGTGTCAGAGTGAAGCTTGAGGAGTCTGGAG 151
QY 112 GAGGCTTGTGCAACTGAGGAGTCCATGAACTCTCCTGTGTAGCTCTGGATTACTT 171
DB 152 GAGGCTTGTGCAACTGAGGAGTCCATGAACTCTCCTGTGTAGCTCTGGATTACTT 211
QY 172 TCAGTGGCTACTGGATGTCTTGGGTCGCCAGCTCCAGAGAGGGGCTTGAGTGGTTG 231
DB 212 TCAGTAACTATTGGATGAAGTGGGTCGCCAGCTCCAGAGAGGGGCTTGAGTGGTTG 271
QY 232 CTGAAATTAGATTGAATCTGATAATTATGCAACACATTTATGCGGAGTCTGGAAGGGA 291
DB 272 CTGAAATTAGATTGAATCTGATAATTATGCAACACATTTATGCGGAGTCTGGAAGGGA 331
QY 292 AGTTTACCCTCTCAAGAGATGATTCCTCAAAAGTGGTCTCTACCTGCAAAATGAACAGCTTAA 351
DB 332 GGTTTACCCTCTCAAGAGATGATTCCTCAAAAGTGGTCTCTACCTGCAAAATGAACAGCTTAA 391
QY 352 GAGCTGAAGACACTGGAGTTTATTACTGTACA 383
DB 392 GAGCTGAAGACACTGGCATTATTACTGTACA 423

RESULT 8
ABX79231
ID ABX79231 standard; DNA; 497 BP.
AC ABX79231;
XX
DT 16-APR-2003 (first entry)
DE DNA encoding mouse antibody heavy chain variable region #2.
XX
KW Mouse; human tumour antigen; anti-human tumour antigen-antibody;
KW ING-1 antibody; cell line HB9812; immunoassay; imaging; tumour diagnosis;
KW tumour therapy; cytostatic; gene; ds; heavy chain variable region.
XX
OS Mus sp.
XX
PN US6461824-B1.
XX
PD 08-OCT-2002.
XX
PF 06-JUN-1995; 95US-00467142.
XX
PR 06-SEP-1988; 88US-00240624.
PR 08-SEP-1988; 88US-00241744.
PR 13-SEP-1988; 88US-00243739.
PR 04-OCT-1988; 88US-00253002.
PR 19-JUN-1989; 89US-00367641.
PR 21-JUL-1989; 89US-00382768.
PR 06-SEP-1989; 89WO-US003852.
PR 06-MAY-1991; 91US-00659401.
PR 27-DEC-1994; 94US-00364001.
XX
PA (XOMA ) XOMA TECHNOLOGY LTD.
XX
XX Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
PI
XX WPI; 2003-196707/19.
DR P-PSDB; ABUS8893.
XX
XX Antibody for detecting antigen in animal or killing cells carrying
PT

```

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PT antigen comprises human constant region and variable region having
PT specificity for human tumor antigen bound by ING-1 antibody.
XX Example 3; Fig 15; 101pp; English.
PS
XX The invention describes an antibody comprising a human constant region
CC and a variable region having specificity for the human tumour antigen
CC bound by the ING-1 antibody, where the ING-1 is produced by cell line
CC HB9812 as deposited with ATCC, and the antibody has the same affinity as
CC the ING-1 for the human tumour antigen. The antibody is useful in an
CC immunoassay method for detecting an antigen in a sample by contacting a
CC label-detectable antigen in the sample with the antibody, detecting the
CC label and relating the detected label to the presence of the antigen; for
CC use in an imaging method for revealing the presence of a label-detectable
CC antigen in an animal by contacting the antibody with a part of the animal
CC suspected of containing the antigen, detecting the label and relating the
CC detected label to the presence of the antigen; and for killing cells
CC carrying an antigen by contacting the cells with the antibody and
CC allowing the killing to occur. The antibodies are useful in tumour
CC diagnosis and therapy. The chimeric antibodies bind to the surface of
CC human tumour cells but do not bind detectably to normal cells, e.g.,
CC fibroblasts, endothelial cells or epithelial cells in the major organs.
CC The high biological activity of the chimeric antibodies against human
CC tumour cell lines combined with minimal reactivity with normal tissues
CC imply that these antibodies may mediate selective destruction of
CC malignant tissue. The presence of human rather than murine antigenic
CC determinants on the chimeric antibodies increases their resistance to
CC rapid clearance from the body relative to the original murine mAbs. This
CC resistance to clearance enhances the potential utility of these chimeric
CC antibodies, as well as their derivatives, in tumour diagnosis and
CC therapy. This sequence encodes a mouse antibody heavy chain variable
CC region used in the creation of an anti-human tumour antigen-antibody
XX
SQ Sequence 497 BP; 141 A; 106 C; 118 G; 132 T; 0 U; 0 Other;
Query Match 70.7%; Score 293.6; DB 8; Length 497;
Best Local Similarity 92.8%; Pred. No. 5.3e-78;
Matches 308; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 52 TTTTATTTATTTGTTCTTTTAAAGGGGTCAGAGTGAAGCTTGAGGAGTCTGGAG 111
DB 92 TATTCATAGTTTCTTTCTTTAAAGGTGTCAGAGTGAAGCTTGAGGAGTCTGGAG 151
QY 112 GAGGCTTGTGCAACTGAGGAGTCCATGAACTCTCCTGTGTAGCTCTGGATTACTT 171
DB 152 GAGGCTTGTGCAACTGAGGAGTCCATGAACTCTCCTGTGTAGCTCTGGATTACTT 211
QY 172 TCAGTGGCTACTGGATGTCTTGGGTCGCCAGCTCTCCAGAGAGGGGCTTGAGTGGTTG 231
DB 212 TCAGTAACTATTGGATGAAGTGGGTCGCCAGCTCTCCAGAGAGGGGCTTGAGTGGTTG 271
QY 232 CTGAAATTAGATTGAATCTGATAATTATGCAACACATTTATGCGGAGTCTGGAAGGGA 291
DB 272 CTGAAATTAGATTGAATCTGATAATTATGCAACACATTTATGCGGAGTCTGGAAGGGA 331
QY 292 AGTTTACCCTCTCAAGAGATGATTCCTCAAAAGTGGTCTCTACCTGCAAAATGAACAGCTTAA 351
DB 332 GGTTTACCCTCTCAAGAGATGATTCCTCAAAAGTGGTCTCTACCTGCAAAATGAACAGCTTAA 391
QY 352 GAGCTGAAGACACTGGAGTTTATTACTGTACA 383
DB 392 GAGCTGAAGACACTGGCATTATTACTGTACA 423

RESULT 9
AAQ85388
ID AAQ85388 standard; cDNA; 480 BP.
XX
XX AAQ85388;
XX
XX 25-MAR-2003 (revised)
DT 31-AUG-1995 (first entry)
XX

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RESULT 10
AAQ12060

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Db      269 CTGAAATTAGAACGAAAGCTAATAATCATGCAACATCTATCTGAGTCTGTGAAAGGGA 328
QY      292 AGTTACCATCTCAAGAGATGATTCCAAAGTCGTCTCTACCTGCAAAATGAAACAGCTTAA 351
Db      329 GGTTCACCATCTCAAGAGATGATTCCAAAGTAGTGTCTACCTGCAAAATGAAACAGCTTAA 388
QY      352 GAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTTCATAG---ACTGGGGCCCAAGGGA 408
Db      389 GAGCTGAAGACAGTGGCAATTATTACTGTACCGACTGGTTTCTACTTGGGGCCCAAGGGA 448
QY      409 CACTAGT 415
Db      449 CTCTGGT 455

RESULT 11
AAQ12016
ID      AAQ12016 standard; DNA; 469 BP.
XX
AC      AAQ12016;
XX
XX      25-MAR-2003 (revised)
DT      19-AUG-1991 (first entry)
XX
XX      Sequence encoding mouse MAb 1C11 H chain V region.
DE
XX      HIV-1; chimera; ds.
KW
XX      Mus sp.
OS
XX      Key Location/Qualifiers
FH      67..469
FT      CDS /*tag= a
FT
XX
XX      WO9107494-A.
XX
XX      30-MAY-1991.
XX
XX      13-NOV-1989; 89US-00433703.
XX
XX      13-NOV-1989; 89US-00433703.
XX
XX      (XOMA ) XOMA CORP.
PA      (GREG ) GREEN CROSS CORP.
PA      (ZOMA-) ZOMA CORP.
XX
XX      Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;
XX
XX      WPI; 1991-178106/24.
DR      P-PSDB; AAR12236.
XX
XX      New chimeric mouse human antibodies - used in treatment, diagnosis and
FT      prophylaxis of HIV infections.
PT
XX      Disclosure; Fig 12; 108pp; English.
PS
XX
XX      The mouse VH gene product may be used to produce chimeric mouse- human
CC      Abs against HIV-1 comprising human Ig constant regions and murine
CC      variable regions. These novel sequence are useful in treatment, diagnosis
CC      and prophylaxis of HIV infections, and may be produced by a bacterial,
CC      yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct
CC      PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
XX      Sequence 469 BP; 127 A; 96 C; 120 G; 126 T; 0 U; 0 Other;
SQ
Query Match 68.0%; Score 282.2; DB 2; Length 469;
Best Local Similarity 87.5%; Pred. No. 1.4e-74;
Matches 321; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

QY      52 TTTTATTTTATGTTCTTTTAAAGGGTCCAGATGAAGTGAAGCTTGAGGAGCTGGAG 111
Db      89 TATTATAGTTTTTCTTCTTAATGTTGTCCAGATGAAGTGAAGCTTGAGGAGCTGGAG 148

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QY      112 GAGCTTGGTGCACCTGGAGGATCCATGAACTCTCTCTGTAGCCTCTGGATTTACTT 171
Db      149 GAGCTTGGTGCACCTGGAGGATCCATGAACTCTCTCTGTAGCCTCTGGATTTACTT 208
QY      172 TCAGTGGCTACTGATGTCTTTGGGTCCGCCAGTCTCCAGAGAGAGGGCTTTGAGTGGGTTG 231
Db      209 TTAGTGAGGCTGTGATGGAGCTGGGTCCGCCAGTCTCCAGAGAGAGGGCTTTGAGTGGGTTG 268
QY      232 CTGAAATTTAGATTCGAATCTGATTAATTATGCAACACATTTATGCGGAGTCTGTGAAAGGGA 291
Db      269 CTGAAATTTAGAGCAAAAGCTAAATTAATCATGCAACATCTATGCTGAGTCTGTGAAAGGGA 328
QY      292 AGTTACCATCTCAAGAGATGATTCCAAAGTCGTCTCTACCTGCAAAATGAAACAGCTTAA 351
Db      329 GGTTCACCATCTCAAGAGATGATTCCAAAGTAGTGTCTACCTGCAAAATGAAACAGCTTAA 388
QY      352 GAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTTCATAG---ACTGGGGCCCAAGGGA 408
Db      389 GAGCTGAAGACAGTGGCAATTATTACTGTACCGACTGGTTTCTACTTGGGGCCCAAGGGA 448
QY      409 CACTAGT 415
Db      449 CTCTGGT 455

RESULT 12
AAV22331
ID      AAV22331 standard; cDNA to mRNA; 357 BP.
XX
AC      AAV22331;
XX
XX      06-JUL-1998 (first entry)
DT
XX
DE      Nucleic acid encoding synthetic branched mucin type glycolipid.
XX
XX      Branched mucin type glycolipid; V region; heavy chain; antibody;
KW      cancer treatment; diagnosis; ss.
XX
XX      Synthetic.
OS
XX      JP10084963-A.
PN
XX      07-APR-1998.
PD
XX      12-SEP-1996; 96JP-00241725.
PF
XX      12-SEP-1996; 96JP-00241725.
PR
XX      12-SEP-1996; 96JP-00241725.
XX
XX      (TOYU ) TOSOH CORP.
PA
XX      WPI; 1998-264850/24.
DR      P-PSDB; AAW46958.
XX
XX      Recognising branched mucin type synthetic glycolipid - using gene
PT      fragment of an antibody, useful in cancer treatment and diagnosis.
PS
XX      Claim 1; Page 4-5; 6pp; Japanese.
XX
XX      The present sequence encodes a branched mucin type synthetic glycolipid.
CC      A gene fragment encoding the V region of the heavy chain of an antibody
CC      recognising the protein encoded by the present sequence is claimed. The
CC      antibody gene fragment is useful for the development of cancer treatments
CC      and diagnosing agents
XX
XX      Sequence 357 BP; 99 A; 75 C; 93 G; 90 T; 0 U; 0 Other;
SQ
Query Match 65.5%; Score 272; DB 2; Length 357;
Best Local Similarity 94.9%; Pred. No. 1.5e-71;
Matches 281; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY      87 GAAGTCAAGCTTGAGGAGTCTGGAGGAGCTTGGTGCAACCTGGAGATCCCTGAACCTC 146

```

Db 1 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGGATCCATGAAATC 60
QY 147 TCCTGTGTAGCTCTGGATTACCTTTTCAGTGGCTTACTGGATGCTTGGGTCCGCGCAGTCT 206
Db 61 TCCTGTGTGCTCTGGATTACCTTTTCAGTGGCTTACTGGATGCTTGGGTCCGCGCAGTCT 120
QY 207 CCAGAGAAGGGGCTTGAGTGGTGGTGGTGAATAGATTGAATCTGAATTAATATGCAACA 266
Db 121 CCAGAGAAGGGGCTTGAGTGGTGGTGGTGAATAGATTGAATCTGAATTAATATGCAACA 180
QY 267 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCGT 326
Db 181 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCGT 240
QY 327 CTCCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 382
Db 241 GTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 296

RESULT 13

AAC90472
ID AAC90472 standard; DNA; 856 BP.
XX
AC AAC90472;
XX
DT 13-MAR-2001 (first entry)
XX
DE Antibody 33F12 catalytic fragment nucleotide sequence.
XX
KW Antibody 33F12; ketone compound; antitumour; cytotoxic;
KW targeted drug delivery; ds.
XX
OS Unidentified.
XX
PN WO200071556-A1.
XX
PD 30-NOV-2000.
XX
PF 24-MAY-2000; 2000WO-US014366.
XX
PR 25-MAY-1999; 99US-00318661.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Barbas CF, Shabat D, Rader C, List B, Lerner RA;
XX
DR WPI; 2001-061339/07.
XX P-FSDB; AAB50426.
PT New ketone compounds containing active agents useful as carriers for e.g.
PT antitumor agents, antibiotics or fluorescent molecules.
XX
PS Disclosure; Fig 10; 45pp; English.
XX

CC The present sequence may be used in the activation of new ketone produg
CC compounds containing active agents. The ketone derivatives are useful as
CC carriers for antitumour agents such as cytotoxic agents, where the
CC antitumour agent is a microtubule stabilising agent such as paclitaxel,
CC epothilone or its therapeutically active analogue or an anthracycline
CC antibiotic such as doxorubicin or its therapeutically active analogue.
CC The ketone derivatives are useful for targeted drug delivery. The
CC inactive molecules in the ketone compounds are converted to active
CC molecules by retro-Michael reaction. The antibody has bifunctional
CC activity and specifically immunoreacts with cell surface antigen of a
CC target cell. The active ingredients can be mixed effectively with
CC excipients as per desired amount along with the buffering agent to
CC enhance the effectiveness and activity of the compound
XX
SQ Sequence 856 BP; 195 A; 208 C; 228 G; 225 T; 0 U; 0 Other;

Query Match 65.4%; Score 271.6; DB 5; Length 856;
Best Local Similarity 92.3%; Pred. No. 2.7e-71;
Matches 286; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGGATCCATGAAATC 146
Db 460 GAGGTGATGCTGTGGTGGTCTGGAGGAGGCTTGGTGCACCTGGAGGATCCATGAAATC 519
QY 147 TCCTGTGTAGCTCTGGATTACCTTTTCAGTGGCTTACTGGATGCTTGGGTCCGCGCAGTCT 206
Db 520 TCCTGTGTGCTGTGGATTAACTTCAGTAGATTCTGGATGCTTGGGTCCGCGCAGTCT 579
QY 207 CCAGAGAAGGGGCTTGAGTGGTGGTGGTGAATAGATTGAATCTGAATTAATATGCAACA 266
Db 580 CCAGAGAAGGGGCTTGAGTGGTGGTGGTGAATAGATTGAATCTGAATTAATATGCAACA 639
QY 267 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCGT 326
Db 640 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCGT 699
QY 327 CTCCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
Db 700 CTCCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 759
QY 387 TTCATAGACT 396
Db 760 TATTTTACT 769

RESULT 14

ADR59058
ID ADR59058 standard; DNA; 408 BP.
XX
AC ADR59058;
XX
DT 18-NOV-2004 (first entry)
XX
DE Anti-K88 antibody VH codon optimised DNA, SEQ ID 9.
XX
KW Gastrointestinal; antibody; heavy chain; light chain; variable region;
KW enterotoxigenic Escherichia coli; ETEC; K88 antigen; K99 antigen;
KW animal food; enteric disease; ds.
XX
OS Synthetic.
XX
PN WO2004074491-A2.
XX
PD 02-SEP-2004.
XX
PF 16-FEB-2004; 2004WO-EP001427.
XX
PR 18-FEB-2003; 2003US-0448429P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Brown D, Campos M, Dalmia B, Demarest S, Hansen G, Heifetz PB;
XX WPI; 2004-635583/61.
XX
DR Novel immunoglobulin heavy chain comprising bovine CH3 or CH2 domain,
XX murine CH2CH3 domain or human CH2CH3 domain, useful in treatment or
XX prevention of enteric disease in animal.
XX
PS Claim 9; SEQ ID NO 9; 165pp; English.
XX
CC The present invention relates to coding sequences for mammalian antibody
CC heavy and light chains directed against enterotoxigenic Escherichia coli
CC (ETEC), in particular, ETEC of a strain possessing the K88 or K99
CC antigen. The heavy and light chain sequences are useful for producing
CC transgenic plants, which express the K88 or K99 antibody. The transgenic
CC plants are useful for producing animal feed, food product, animal feed
CC additive, feed pre-mix or nutritional supplement and are also useful for
CC treating or preventing enteric disease in an animal. The present sequence
CC is the coding sequence for an anti-K88 antibody heavy chain variable
CC region which has been codon optimised for expression in plants.
XX

SQ Sequence 408 BP; 105 A; 92 C; 105 G; 106 T; 0 U; 0 Other;
Query Match 65.1%; Score 270.2; DB 13; Length 408;
Best Local Similarity 94.0%; Pred. No. 5.5e-71;
Matches 281; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 84 AGTGAAGTGAAGCTTGAGAGCTGAGAGAGGCTTGGTGCACCTGGAGGATCCATGAA 143
DB 4 AGTGAAGTGAAGCTTGAGAGCTGAGAGAGGCTTGGTGCACCTGGAGGATCCATGAA 63
QY 144 CTCTCTGTAGCTCTCGATTTACTTTTCAGTGGCTACTGATGCTTGGGTCCGCCAG 203
DB 64 CTCTCTGTGTGCTTCTGATTCACCTTCAGTAACTACTGATGATGAGTGGTCCGCCAG 123
QY 204 TCTCCAGAGAAGGGGCTTGAGTGGTGTCTGAAATTTAGATTTGAAATTTGATGCA 263
DB 124 TCTCCAGAGAAGGGGCTTGAGTGGTGTCTGAAATTTAGATTTGACATCTAATTTTGA 183
QY 264 ACATATTCGGAGCTGTGAAAGGGAAGTTTACCACCTCAAGAGATGATTTCCAAAGT 323
DB 184 ACATATTCGGAGCTGTGAAAGGGAAGTTTACCACCTCAAGAGATGATTTCCAAAGT 243
QY 324 CGTCTCTACTCGCAATGAACAGCTTAAGAGCTGGAAGACAGTGGAGTTTATTACTGTAC 382
DB 244 AGTGTCTACTCGCAATGAACAGCTTAAGAGCTGGAAGACAGTGGAGTTTATTACTGTAC 302

RESULT 15

AAQ85386
ID AAQ85386 standard; DNA; 1979 BP.
XX AAQ85386;
AC
XX
DT 25-MAR-2003 (revised)
DT 31-AUG-1995 (first entry)
XX
DE Anti-cataract immunotoxin in pHB19.
XX
KW Immunotoxin; heavy chain; light chain; variable region; antibody;
KW ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
KW pHB19; 4197X; monoclonal antibody; MAB; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 115..1779
FT FT /*tag= a
FT sig_peptide 115..195
FT FT /*tag= b
FT FT /note= "phoA signal sequence"
FT mat_peptide 196..1776
FT FT /*tag= c
XX
XX WO9503828-A1.
XX
XX
PD 09-FEB-1995.
XX
XX 15-JUL-1994; 94WO-US007919.
XX
XX 02-AUG-1993; 93US-00101329.
XX
XX (HOUS-) HOUSTON BIOTECHNOLOGY INC.
XX
XX Wood MS, Gould RM, Kelleher PJ, Wallace TL;
XX
XX WPI; 1995-082036/11.
XX P-PSDB; AAR70827.
XX
XX New single chain immuno:toxin - binds specifically to epithelial cells,
XX for inhibiting development of sec. cataracts after extra:capsular
XX cataract extraction.
XX
XX Disclosure; Fig 4; 68pp; English.

XX The immunotoxin given in AAR70827 comprises the heavy and light chain
CC variable regions of anti-lens epithelium IgG3 MAb 4197X linked to ricin-A
CC and a hexa-histidine tag. The DNA construct encoding the immunotoxin was
CC expressed from pHB19 in E. coli. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 1979 BP; 558 A; 426 C; 459 G; 536 T; 0 U; 0 Other;
Query Match 65.0%; Score 269.8; DB 2; Length 1979;
Best Local Similarity 94.3%; Pred. No. 1.3e-70;
Matches 280; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 86 TGAAGTGAAGCTTGAGAGCTGAGAGGCTTGGTGCACCTGGAGGATCCATGAAACT 145
DB 198 TGAAGTGAAGCTTGAGAGCTGAGAGGCTTGGTGCACCTGGAGGATCCATGAAACT 257
QY 146 CTCTCTGTAGCTCTCGATTTACTTTTCAGTGGCTACTGATGTCTTGGGTCCGCCAGTC 205
DB 258 CTCTCTGTGTGCTTCTGATTTCACTTTTCAGTAACTTTCTGGATGAACCTGGTCCGCCAGTC 317
QY 206 TCCAGAGAAGGGGCTTGAGTGGTGTCTGAAATTTAGATTTGAAATTTGATGCAAC 265
DB 318 TCCAGAGAAGGGGCTTGAGTGGTGTCTGAAATTTAGATTTGAAATTTGATGCAAC 377
QY 266 ACATTTATCGGAGCTGTGAAAGGGAAGTTTACCACCTCTCAAGAGATGATTTCCAAAGTCG 325
DB 378 ACATTTATCGGAGCTGTGAAAGGGAAGTTTACCACCTCTCAAGAGATGATTTCCAAAGTAG 437
QY 326 TCTCTACCTCGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 382
DB 438 TGTCTACCTCGCAATGAACAGCTTAAGAGCTGAAGACAGTGGCATTATTACTGTAC 494

Search completed: April 18, 2005, 11:34:41
Job time : 235.448 secs

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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 14:42:49 ; Search time 1129.75 Seconds
(without alignments)

Title: US-09-674-716B-1

Perfect score:

Sequence: 1 aagctttacagttactcagc.....tggggccaaggacactagt 415

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

SUMMARIES

Result No.	Query			ID	Description
	Score	Match	Length		
1	310.4	74.8	453	US-09-564-329A-14	Sequence 14, Appl
2	310.4	74.8	453	US-09-855-153-14	Sequence 14, Appl
3	310.4	74.8	453	US-09-854-811-14	Sequence 14, Appl
4	310.4	74.8	453	US-09-934-773-14	Sequence 14, Appl
5	310.4	74.8	453	US-09-963-620-14	Sequence 14, Appl
6	310.4	74.8	453	US-09-855-632-14	Sequence 14, Appl
7	310.4	74.8	453	US-10-225-784-14	Sequence 14, Appl
8	310.4	74.8	453	US-10-324-720-14	Sequence 14, Appl
9	310.4	74.8	453	US-10-225-779-14	Sequence 14, Appl
10	310.4	74.8	453	US-10-374-381-14	Sequence 14, Appl
11	310.4	74.8	453	US-10-446-542-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-564-329A-14
; Sequence 14, Application US/09564329A
; Patent No. US20010055751A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Safran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/564,329A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25

; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-09-564-329A-14

Query Match 74.8%; Score 310.4; DB 9; Length 453;
Best Local Similarity 92.6%; Pred. No. 2.3e-85;
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 35 CATGGATTTGGCGTCATTTTTTTTATTTGTTCTTTTAAAGGGGTCCAGAGTGAAGTGA 94
Db 6 CTTGGGTTGAGCTGGGTTTTTATTTATTTGTTCTTTTAAAGGGGTCCGAGTGAAGTGA 65
QY 95 GCTTGAGGAGTCTGGAGGAGGCTTGGTGAACCTGGAGGATCCATGAACCTCTCTGTGT 154
Db 66 GCTTGAGGAGTCTGGAGGAGGCTGGGTGCAACCTGGAGGATCCATGAACCTCTCTGTGT 125
QY 155 AGCCTCTGGATTTACTTTTCTAGTGGCTTCTGGATGCTTGGTCCGCGAGTCTCCAGAA 214
Db 126 AGCCTCTGGATTTACTTTTCTAGTAAATTTACTGGATGACTTGGTCCGCGAGTCTCCAGAA 185
QY 215 GGGGCTTGAGTGGGTTGCTGAAATTTAGATTGAAATCTGATAATTATGCAACACATTATGC 274
Db 186 GGGGCTTGAGTGGGTTGCTGAAATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 245
QY 275 GAGTCTGTGAAAGGGAAGTTCCACATCTCAAGAGATGATTTCCAAAGTCTCTTACCT 334
Db 246 GAGTCTGTGAAAGGGAAGTTCCACATCTCAAGAGATGATTTCCAAAGTCTCTTACCT 305
QY 335 GCAATGACACAGCTTAAGAGCTGAAGACAGTGAAGTTTATTACTGTACAGAT 386
Db 306 GCAATGACACAGCTTAAGAGCTGAAGACAGTGAAGTTTATTACTGTACAGAT 357

RESULT 2

US-09-855-153-14
; Sequence 14, Application US/09855153
; Patent No. US20020102666A1
; GENERAL INFORMATION:
; APPLICANT: Witte, Robert E.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/855,153
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25

; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-09-855-153-14

Query Match 74.8%; Score 310.4; DB 9; Length 453;
Best Local Similarity 92.6%; Pred. No. 2.3e-85;
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 35 CATGGATTTGGCGTCATTTTTTTTATTTGTTCTTTTAAAGGGGTCCAGAGTGAAGTGA 94
Db 6 CTTGGGTTGAGCTGGGTTTTTATTTATTTGTTCTTTTAAAGGGGTCCGAGTGAAGTGA 65
QY 95 GCTTGAGGAGTCTGGAGGAGGCTTGGTGAACCTGGAGGATCCATGAACCTCTCTGTGT 154
Db 66 GCTTGAGGAGTCTGGAGGAGGCTGGGTGCAACCTGGAGGATCCATGAACCTCTCTGTGT 125
QY 155 AGCCTCTGGATTTACTTTTCTAGTGGCTTCTGGATGCTTGGTCCGCGAGTCTCCAGAA 214
Db 126 AGCCTCTGGATTTACTTTTCTAGTAAATTTACTGGATGACTTGGTCCGCGAGTCTCCAGAA 185
QY 215 GGGGCTTGAGTGGGTTGCTGAAATTTAGATTGAAATCTGATAATTATGCAACACATTATGC 274
Db 186 GGGGCTTGAGTGGGTTGCTGAAATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 245
QY 275 GAGTCTGTGAAAGGGAAGTTCCACATCTCAAGAGATGATTTCCAAAGTCTCTTACCT 334
Db 246 GAGTCTGTGAAAGGGAAGTTCCACATCTCAAGAGATGATTTCCAAAGTCTCTTACCT 305
QY 335 GCAATGACACAGCTTAAGAGCTGAAGACAGTGAAGTTTATTACTGTACAGAT 386
Db 306 GCAATGACACAGCTTAAGAGCTGAAGACAGTGAAGTTTATTACTGTACAGAT 357

RESULT 3

US-09-854-811-14
; Sequence 14, Application US/09854811
; Patent No. US20020119157A1
; GENERAL INFORMATION:
; APPLICANT: Witte, Robert E.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/854,811
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-09-854-811-14

Query Match 74.8%; Score 310.4; DB 9; Length 453;
Best Local Similarity 92.6%; Pred. No. 2.3e-85;
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 35 CATGGATTTGGCGTCATTTTTTTTATTTGTTCTTTTAAAGGGGTCCAGAGTGAAGTGA 94
Db 6 CTTGGGTTGAGCTGGGTTTTTATTTATTTGTTCTTTTAAAGGGGTCCGAGTGAAGTGA 65
QY 95 GCTTGAGGAGTCTGGAGGAGGCTTGGTGAACCTGGAGGATCCATGAACCTCTCTGTGT 154
Db 66 GCTTGAGGAGTCTGGAGGAGGCTGGGTGCAACCTGGAGGATCCATGAACCTCTCTGTGT 125

Qy	155	AGCCTCTGGAATTATCTTTTCAGTGGCTACTGGAGTCTTTGGTCCGCCAGTCTCCAGAGAA	214
Db	126	AGCCTCTGGAATTATCTTTTCAGTAAATTCTGATGACTTTGGTCCGCCAGTCTCCAGAGAA	185
Qy	215	GGGGCTTTGAGTCGGGTCTGAAATTTAGAGATTCGAATTCGAATTTATGCAACACATTATGC	274
Db	186	GGGGCTTTGAGTCGGGTCTGAAATTTGGAATTCGATTCGAAATTTATGCAACACATTATGC	245
Qy	275	GGAGTCTGTGAAAGGGAAGTTCCACCATCTCAAGAGATGATTCCAAAAAGTCGTCTCTACCT	334
Db	246	GGAGTCTGTGAAAGGGAATTTCCACCATCTCAAGAGATGATTCCAAGAAAGTCGTCTCTACCT	305
Qy	335	GCAATGAAACAGCTTAAGAGCTGGAAGACAGTCGGAGTTTATTCGTGTACAGAT	386
Db	306	GCAATGAAACACTTAAGACCTTGAAGACAGTCGGAAATTTATTCGTGTACAGAT	357

RESULT 6
US-09-855-632-14
; Sequence 14, Application US/09855632
; Publication No. US20030113818A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

	Query Match	74.8%	Score 310.4;	DB 10;	Length 453;
	Best Local Similarity	92.6%;	Pred. NO. 2.3e-85;		
	Matches 326;	Conservative 0;	Mismatches 26;	Indels 0;	Gaps 0;
Qy	35	CATGGATTTTCGGCTGATTTTTTTTATTGTCTCTTTTAAAGGGGTCAGAGTGAAGTGAA	94		
Db	6	CTTCGGGTGAGTCGGGTTTTTATTATTGTCTCTTTTAAAGGGGTCGAGTGAAGTCAG	65		
Qy	95	GCTTGAAGAGTCTGGAGAGAGCGCTGGTGCACCTCGGAGATCCATGAACCTCTCCTGTGT	154		
Db	66	GCTTGAGAGGTCTGGAGAGGCTGGGTGCACCTCGGAGATCCATGAACCTCTCCTGTGT	125		

Qy	155	AGCCTCGGATTTACTTTTCAGTGGCTACTGATGTCCTGGTCCGCCAGTCTCCAGAGNA	214
Db	126	AGCCTCGGATTTACTTTTCAGTAAATTACTGATGACCTGGGTCCGCCAGTCTCCAGAGAA	185
Qy	215	GGGCTTGAGTGGGTCTGTAATTCGAAATTCGATTAATATGCAACACATTATGC	274
Db	186	GGGCTTGAGTGGGTCTGTAATTCGAAATTCGATTAATATGCAACACATTATGC	245
Qy	275	GGAGTCTGTGAAAGGGGAAGTTCCACCATCTCAAGAGATGATTCCTCAAGTTCGTCTCTACCT	334
Db	246	GGAGTCTGTGAAAGGGGAATTCACCATCTCAAGAGATGATTCCTCAAGTTCGTCTCTACCT	305
Qy	335	GCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT	386
Db	306	GCAATGAACAACTTAAAGACTGAAGACAGTGGAAATTTATTACTGTACAGAT	357

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RESULT 7
; US-10-225-784-14
; Sequence 14, Application US/10225784
; Publication No. US20030113820A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Reiter, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PCSA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

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Query Match	74.8%;	Score 310.4;	DB 15;	Length 453;
Best Local Similarity	92.6%;	Pred. No. 2.3e-85;		
Matches 326;	Conservative	0;	Mismatches 26;	Indels 0;
			Gaps	0;

Qy	35	CATGGATTTTGGGCTGATATTTTTTTTAAATGTTCTTTTTAAAGGGGTCCAGAGTGAAGTAA	94
Db	6	CTTCGGGTTGAGCTGGGTTTTTTATTAATGTTCTTTTTAAAGGGGTCCGAGTGAAGTGAG	65
Qy	95	GCTTTGAGAGTCTGGAGAGCGCTTGGTGCACCTGGAGGATCCATGAACAATCTCCTGTGT	154
Db	66	GCTTTGAGAGTCTGGAGAGCGCTGGGTGCACCTGGAGGATCCATGAACAATCTCCTGTGT	125
Qy	155	AGCCTCTGGATTTACTTCTCAGTGCGCTACTGGATGTCCTTGGTCCGCCAGTCTCCAGAA	214
Db	126	AGCCTCTGGATTTACTTCTCAGTAAATTACTCGATGACTTGGGTCCGCCAGTCTCCAGAA	185

Db	246	GGAGTCTGTGAAGGAAATTACCATCTCAAGAGATGATTCCAGAAAGTGGTCTTACCT	305
Qy	335	GCAATGAACACGCTTAAGAGCTGAAGACAGTGGAGTTATTACTGTACAGAT	386
Db	306	GCAATGAACAACTTAAAGCTCTGAAGACAGTGGAAATTTATTACTGTACAGAT	357

RESULT 10
US-10-374-381-14
; Sequence 14, Application US/10374381
; Publication No. US20030228318A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/374,381
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US/09/564,329A
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID-Mice
US-10-374-381-14

	Query Match	74.8%;	Score 310.4;	DB 17;	Length 453;
	Best Local Similarity	92.6%;	Pred. No. 2.3e-85;		
	Matches 326;	Conservative 0;	Mismatches 26;	Indels 0;	Gaps 0
QY	35	CATGGATTTCGGCTGATTTTTTTTATTGTCTTTTAAAAAGGGTGCCAGAGTGAAGTAA	94		
Db	6	CTTCGGGTTCAGCTCGGGTTTTTATTATTGTCTTTTAAAAAGGGTCCGAGTGAAGTCAG	65		
QY	95	GCTTCAGAGAGTCTGAGAGAGGCTTGGTCGCAACTCGGAGATCCATGAACTCCTCTGT	154		
Db	66	GCTTCAGAGAGTCTGAGAGAGGCTGGGTCAACCTCGGAGATCCATGAACTCCTCTGT	125		
QY	155	AGCCTCTGGATTACTTTTCAGTGGCTACTCGGATGTCCTTGGGTCCGCCAGTCTCCAGAAA	214		
Db	126	AGCCTCTGGATTACTTTTCAGTAAATACTTCGGATGACTTGGGTCCGCCAGTCTCCAGAAA	185		
QY	215	GGGGCTTCAGTGGGTTCGTAATTAGATTGAAATCTGATAATTATGCAACACATTATGC	274		
Db	186	GGGGCTTCAGTGGGTTCGTAATTCGATTGAGATCTGNAATATTGCACACATTATGC	245		
QY	275	GGAGTCTGTGAAGGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGATCGTCTCTACT	334		
Db	246	GGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCCAAAGATCGTCTCTACT	305		

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335 GCAGATGACACGCTTAAGACGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
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306 GCAGATGACACGCTTAAGACGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 357
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RESULT 11
US-10-446-542-14
; Sequence 14, Application US/10446542
; Publication No. US20040018571A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/446,542
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/855,153
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-10-446-542-14

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Query Match	74.8%;	Score 310.4;	DB 17;	Length 453;
Best Local Similarity	92.6%;	Pred. No. 2.3e-8;		
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QY	35	CATCGATTTGGCGCTGATTTTTTTTATTTATGTTCTTTTAAAGGGGTCACAGAGTGAAGTGAA	94	
DB	6	CTTGGGGTGAAGCTGGGGTTTTTATTTATGTTCTTTTAAAGGGGTCGGAGTGAAGTGAG	65	
QY	95	GCTTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCTCCTGTGT	154	
DB	66	GCTTTGAGGAGTCTGGAGGAGGCTGGGTGCAACCTGGAGGATCCATGAAACTCTCCTGTGT	125	
QY	155	AGCCTCTGGATTTACTTTCTGAGTGCTACTGAGTGTCTTTGGTCCGCAGCTCTCCAGAGAA	214	
DB	126	AGCCTCTGGATTTACTTTTCAGTAATTTACTGGATGACTTGGGTCCGCAGCTCTCCAGAGAA	185	
QY	215	GGGGCTTGAGTGGGGTTCGTGAAATTTAGATTTGAAATCTGATAATTTATGCAACACATTTATGC	274	
DB	186	GGGGCTTGAGTGGGGTTCGTGAAATTTGATTTGAAATCTGATTTGAAATTTATGCAACACATTTATGC	245	
QY	275	GGAGTCTCTGAAAGGGAAGTTTCACCATCTCAAGAGATGATTTCCAAAAGTCGTCTCTACCT	334	
DB	246	GGAGTCTGTGAAGGGGAATTTCCCATCTCAAGAGATGATTTCCAGAAGTCGTCTCTACCT	305	
QY	335	GCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT	386	
DB	306	GCAATGAACAACTTAAGACCTGAAGACAGTGGGAATTTATTACTGTACAGAT	357	

Qy	275	GGAGTCTGTGAAGGGGAAGTTCCACATCTCAAGAGATGATTCCAAAGTCGTCTCTACCT	334
Db	246	GGAGTCTGTGAAGGGGAAATTCACATCTCAAGAGATGATTCCAAAGTCGTCTCTACCT	305
Qy	335	GCAATGAACACAGCTTAAGAGCTGAAGACAGTCGGAGTTTATTACTGTACAGAT	386
Db	306	GCAATGAACAACTTAAAGCTGAAGACAGTCGGAAATTTATTACTGTACAGAT	357

RESULT 13

US-10-769-074-26

Sequence 26, Application US/10769074
Publication No. US2005005909A1

GENERAL INFORMATION:

APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Safftan, Douglas C.
APPLICANT: Jakobovits, Aya
APPLICANT: The Regents of the University of California
APPLICANT: Agensys, Inc.

TITLE OF INVENTION: PSCA: Prostate Stem Cell Antigen and Uses Thereof

FILE REFERENCE: 02307K-141589US

CURRENT APPLICATION NUMBER: US/10769,074

CURRENT FILING DATE: 2004-01-29

PRIOR APPLICATION NUMBER: US/10769,308

PRIOR FILING DATE: 2004-01-29

PRIOR APPLICATION NUMBER: US 08/814,279

PRIOR FILING DATE: 1997-03-10

PRIOR APPLICATION NUMBER: US 60/228,816

PRIOR FILING DATE: 1997-03-10

PRIOR APPLICATION NUMBER: US 60/071,141

PRIOR FILING DATE: 1998-01-12

PRIOR APPLICATION NUMBER: US 60/074,675

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 09/038,261

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: US 09/203,939

PRIOR FILING DATE: 1998-12-02

PRIOR APPLICATION NUMBER: US 60/113,230

PRIOR FILING DATE: 1998-12-21

PRIOR APPLICATION NUMBER: US 09/251,835

PRIOR FILING DATE: 1999-02-17

PRIOR APPLICATION NUMBER: US 60/120,536

PRIOR FILING DATE: 1999-02-17

Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 26

Query Match	74.8%	Score	310.4	DB	19	Length	453
Best Local Similarity	92.6%	Pred.	No. 2.3e-85				
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			0	Mismatches	26		

35	CATGGATTTTGGGCTGATTTTTTTTTTATTGTCTCTTTAAAGGGGTCCAGAGTGAAGTGAA	94
Qy		
6	CTTCGGGTTGAGCTGGGTTTTTATATTGTCTTTTAAAGGGGTCCGAGTGAAGTGAG	65
Db		
95	GCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGGATCCATGAACCTCTCTGTGT	154
Qy		
66	GCTTGAGGAGTCTGGAGGAGGCTGGGTGCACCTGGAGGATCCATGAACCTCTCTGTGT	125
Db		
155	AGCCTCTGGATTACTTTTCAGTGGCTACTGGATGTCTTTGGGTCCGCCAGTCTCCAGAGAA	214
Qy		

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RESULT 12
US-10-769-308-26
; Sequence 26, Application US/10769308
; Publication No. US20050003465A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Jakobovits, Ava
; APPLICANT: The Regents of the University of California
; APPLICANT: Agensys, Inc.
; TITLE OF INVENTION: PSCA: Prostate Stem Cell Antigen and Uses Thereof
; FILE REFERENCE: 02307K-141583US
; CURRENT APPLICATION NUMBER: US/10/769,308
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 60/228,816
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: US 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: US 09/251,835.
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 60/124,658
; PRIOR FILING DATE: 1999-03-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:heavy chain
; OTHER INFORMATION: variable domain region of PSCA monoclonal antibody
; OTHER INFORMATION: 2H9
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(453)
US-10-769-308-26

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Query Match	74.8%;	Score 310.4;	DB 18;	Length 453;
Best Local Similarity	92.6%;	Pred. No. 2.3e-85;		
Matches 326;	Conservative	0;	Mismatches 26;	Indels 0;
Gaps 0;				

35	QY	CATGGAATTTGGCGTGAATTTTTTTTTTATATGTTCTTTTAAAGGGGTCCAGAGTGAATGAA	94
6	Db	CTTCGGGTGAGCTGGGTTTTTATATGTTCTTTTAAAGGGGTCCGGAGTGAAGTGAAG	65
95	QY	GCTTCAGAGATCTGGAGAGAGCTTGGTGCAACTGGAGGATCATGAAACTCTCTGTGT	154
66	Db	GCTTCAGAGATCTGGAGAGAGCTGGTGCAACTGGAGGATCATGAAACTCTCTGTGT	125
155	QY	AGCCTCTGGAATTTACTTTTCAGTGGCTACTGGATGTCCTTGGGTCCGCCAGTCTCCAGAGAA	214
126	Db	AGCCTCTGGAATTTACTTTTCAGTAAATTAAGTGAATGACTTGGGTCCGCCAGTCTCCAGAGAA	185
215	QY	GGGGCTTCAGTGGGTGCTGAAATAGATTGAAATCTGATAATTTATGCAACACATTATGC	274
186	Db	GGGGCTTCAGTGGGTGCTGAAATTCGATTCGATCTGAAATTTATGCAACACATTATGC	245

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Db 126 AGCTCTGATTTACTTTTCAGTAATTTACTGGATGACTTGGTCCGCGAGTCTCCAGAGAA 185
QY 215 GGGGCTTGAGTGGTTCGTAATTTAGATTGAAATCTGATAATTTATGCAACATTTATGC 274
Db 186 GGGGCTTGAGTGGTTCGTAATTTAGATTGAAATCTGATAATTTATGCAACATTTATGC 245
QY 275 GGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCTCTTACCT 334
Db 246 GGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCTCTTACCT 305
QY 335 GCAATGAAACAGCTTAAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
Db 306 GCAATGAAACAGCTTAAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 357

RESULT 14
US-09-883-758-3
; Sequence 3, Application US/09883758
; Patent No. US20020058804A1
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: Lerner, Benjamin
; APPLICANT: List, Benjamin
; APPLICANT: Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF0011S
; CURRENT APPLICATION NUMBER: US/09/883,758
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/318,661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment.
; LOCATION: (1)..(855)
US-09-883-758-3

Query Match 65.4%; Score 271.6; DB 9; Length 856;
Best Local Similarity 92.3%; Pred. No. 3e-73;
Matches 286; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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Db 460 GAGGTGATGCTGGTGAGTCTGGAGGAGGCTTGGTGCACCTGGAGGATCCATGAACCTC 519
QY 147 TCCTGTGTAGCTCTCGATTTACTTTTCAGTGGCTACTGGATGCTTTGGGTCCGCCAGTCT 206
Db 520 TCCTGTGTGTCTCGATTTAACTTCAGTAGATTCAGTAGTCTTTGGGTCCGCCAGTCT 579
QY 207 CCAGAGAAGGGCTTGAGTGGGTTGCTGAAATTTAGATTGAAATCTGATAATTTATGCAACA 266
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QY 267 CATTATGCGGAGTCTGTGAAGGGAAGTTCCACATCTCAAGAGATGATTCCAAAGTCTGT 326
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; Sequence 6, Application US/09883758
; Patent No. US20020058804A1
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: Lerner, Benjamin
; APPLICANT: List, Benjamin
; APPLICANT: Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF0011S
; CURRENT APPLICATION NUMBER: US/09/883,758
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/318,661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment.
; LOCATION: (1)..(855)
US-09-883-758-6

Query Match 65.4%; Score 271.6; DB 9; Length 856;
Best Local Similarity 92.3%; Pred. No. 3e-73;
Matches 286; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGGATCCATGAACCTC 146
Db 397 GAGGTGATGCTGGTGAGTCTGGAGGAGGCTTGGTGCACCTGGAGGATCCATGAACCTC 338
QY 147 TCCTGTGTAGCTCTCGATTTACTTTTCAGTGGCTACTGGATGCTTTGGGTCCGCCAGTCT 206
Db 337 TCCTGTGTGTCTCGATTTAACTTCAGTAGATTCAGTAGTCTTTGGGTCCGCCAGTCT 278
QY 207 CCAGAGAAGGGCTTGAGTGGGTTGCTGAAATTTAGATTGAAATCTGATAATTTATGCAACA 266
Db 277 CCAGAGAAGGGCTTGAGTGGGTTGCTGAAATTTAGATTGAAATCTGATAATTTATGCAACA 218
QY 267 CATTATGCGGAGTCTGTGAAGGGAAGTTCCACATCTCAAGAGATGATTCCAAAGTCTGT 326
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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125: /cgn2_6/ptodata/1/pna/US6055_COMB.seq.*
126: /cgn2_6/ptodata/1/pna/US6056_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	415	100.0	415	US-09-674-716B-46	Sequence 46, Appl
3	310.4	74.8	453	US-09-359-326A-14	Sequence 14, Appl
4	310.4	74.8	453	US-09-854-811-14	Sequence 14, Appl
5	310.4	74.8	453	US-09-855-153-14	Sequence 14, Appl
6	310.4	74.8	453	US-10-224-720-14	Sequence 14, Appl
7	310.4	74.8	453	US-10-225-779-14	Sequence 14, Appl
8	310.4	74.8	453	US-10-225-784-14	Sequence 14, Appl
9	310.4	74.8	453	US-10-374-381-14	Sequence 14, Appl
10	310.4	74.8	453	US-10-446-542-14	Sequence 14, Appl
11	310.4	74.8	453	US-10-769-074-26	Sequence 26, Appl
12	310.4	74.8	453	US-10-769-308-26	Sequence 26, Appl
13	310.4	74.8	453	US-10-997-735-14	Sequence 14, Appl
14	310.4	74.8	453	US-11-021-950-14	Sequence 14, Appl
15	294.2	70.9	412	US-09-724-671-4993	Sequence 4993, Ap
16	294.2	70.9	924	US-10-144-771-46557	Sequence 46557, A
17	294.2	70.9	924	US-60-360-207-46557	Sequence 46557, A
18	293.4	70.7	435	US-09-724-671-4676	Sequence 4676, Ap
19	291.2	70.2	400	US-09-724-671-5111	Sequence 5111, Ap
20	291	70.1	481	US-08-101-329-1	Sequence 1, Appli
21	289.8	69.8	839	US-10-144-771-14209	Sequence 14209, A
22	289.8	69.8	839	US-60-360-207-14209	Sequence 4759, Ap
23	282.2	68.0	431	US-09-724-671-4759	Sequence 4435, Ap
24	279.6	67.4	463	US-09-724-671-4435	Sequence 5070, Ap
25	272	65.5	389	US-09-724-671-5070	Sequence 65, Appl
26	270.4	65.2	366	US-10-879-994-65	Sequence 5, Appli
27	269.8	65.0	1979	US-08-101-329-5	Sequence 12, Appl
28	269.4	64.9	403	US-07-977-706A-12	Sequence 12, Appl
29	269.4	64.9	403	US-07-977-706B-12	Sequence 12, Appl
30	269.4	64.9	403	US-07-977-707B-12	Sequence 12, Appl
31	269.4	64.9	403	US-08-128-015-12	Sequence 12, Appl
32	269.4	64.9	403	US-09-947-839-12	Sequence 12, Appl
33	269.4	64.9	403	US-09-947-839B-12	Sequence 1, Appli
34	269.2	64.9	445	US-10-507-941-1	Sequence 1, Appli
35	267.8	64.5	360	US-08-541-373-27	Sequence 27, Appl
36	267.8	64.5	360	US-08-541-373A-27	Sequence 27, Appl
37	267.2	64.4	366	US-08-477-512A-1	Sequence 1, Appli
38	267.2	64.4	366	US-08-486-817A-1	Sequence 1, Appli
39	266.2	64.1	1515	PCT-US02-25766-11314	Sequence 11314, A
40	265.4	64.0	765	US-10-239-656-68	Sequence 68, Appl
41	265.2	63.9	809	US-07-900-407D-1	Sequence 1, Appli
42	263	63.4	403	US-09-947-839-65	Sequence 65, Appl
43	263	63.4	403	US-09-947-839B-65	Sequence 65, Appl
44	262.4	63.2	768	US-10-239-656-60	Sequence 60, Appl
45	262.4	63.2	1509	US-10-239-656-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1

US-09-674-716B-1
; Sequence 1, Application US/09674716B
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, Jean-Yves M.P.
; APPLICANT: CROWE, James S.
; APPLICANT: ELLIS, Jonathan H.
; APPLICANT: RAPSON, Nicholas T.
; APPLICANT: SHEARIN, Jean
; TITLE OF INVENTION: Antibodies to CD23, derivatives thereof, and their therapeutic u
; FILE REFERENCE: 1430-256 / PG3433USW0
; CURRENT APPLICATION NUMBER: US/09/674,716B
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: CA 2,328,606
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: PCT/GB99/01434
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: GB 9809839.5
; PRIOR FILING DATE: 1998-05-09
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: MS Word
; SEQ ID NO 1
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(413)
US-09-674-716B-1

Query Match 100.0%; Score 415; DB 30; Length 415;
Best Local Similarity 100.0%; Pred. No. 2.3e-108;
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCTTACAGTTACTCAGCAGCAGGACCTCACCATGATTTGGGCTGATTTTTTA 60
Db 1 AAGCTTACAGTTACTCAGCAGCAGGACCTCACCATGATTTGGGCTGATTTTTTA 60
QY 61 TTGTTCTTTTAAAGGGTCCAGAGTGAAGTCAAGCTTGAGGAGTCTGGAGGAGGCTTGG 120
Db 61 TTGTTCTTTTAAAGGGTCCAGAGTGAAGTCAAGCTTGAGGAGTCTGGAGGAGGCTTGG 120
QY 121 TGCAACCTGAGGATCCATGAAACTCTCTGTAGACCTCTCGATTTACTTTCACTGGCT 180
Db 121 TGCAACCTGAGGATCCATGAAACTCTCTGTAGACCTCTCGATTTACTTTCACTGGCT 180
QY 181 ACTGATGTCTTGGTCCGCCAGTCTCCAGAGAGGGGCTTCAGTGGGTTGCTGAAATTA 240
Db 181 ACTGATGTCTTGGTCCGCCAGTCTCCAGAGAGGGGCTTCAGTGGGTTGCTGAAATTA 240
QY 241 GATTGAAATCTGATTAATTATGCAACACATTTATGCGGAGTCTGTAAAGGGAAGTTCA 300
Db 241 GATTGAAATCTGATTAATTATGCAACACATTTATGCGGAGTCTGTAAAGGGAAGTTCA 300
QY 301 TCTCAAGAGATGATTCCAAAGTCTCTCTACTCTGCAAAATGAACAGCTTAAGAGCTGAAG 360
Db 301 TCTCAAGAGATGATTCCAAAGTCTCTCTACTCTGCAAAATGAACAGCTTAAGAGCTGAAG 360
QY 361 ACAGTGGAGTTTATTACTCTAGATTTTATAGCTGGGGCCCAAGGACACTAGT 415
Db 361 ACAGTGGAGTTTATTACTCTAGATTTTATAGCTGGGGCCCAAGGACACTAGT 415

RESULT 2

US-09-674-716B-46/c
; Sequence 46, Application US/09674716B
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, Jean-Yves M.P.
; APPLICANT: CROWE, James S.
; APPLICANT: ELLIS, Jonathan H.
; APPLICANT: RAPSON, Nicholas T.
; APPLICANT: SHEARIN, Jean
; TITLE OF INVENTION: Antibodies to CD23, derivatives thereof, and their therapeutic u

FILE REFERENCE: 1430-256 / PG3433USW0
CURRENT APPLICATION NUMBER: US/09/674,716B
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: CA 2,328,606
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: PCT/GB99/01434
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: GB 9809839.5
PRIOR FILING DATE: 1998-05-09
NUMBER OF SEQ ID NOS: 54
SOFTWARE: MS Word
SEQ ID NO 46
LENGTH: 415
TYPE: DNA
ORGANISM: Mus musculus
US-09-674-716B-46

Query Match 100.0%; Score 415; DB 30; Length 415;
Best Local Similarity 100.0%; Pred. No. 2.3e-108;
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 TTGTTCTTTTAAAGGGGTCAGAGTGAAGTGAAGTCTGAGGAGTCTGAGGAGGCTTGG 120
DB 355 TTGTTCTTTTAAAGGGGTCAGAGTGAAGTGAAGTCTGAGGAGTCTGAGGAGGCTTGG 296
QY 121 TGCNACCTGGAGGATCCATGAACCTCTCTGTGTAGGCTCTGATTTTACGTTGCTGCCT 180
DB 295 TGCNACCTGGAGGATCCATGAACCTCTCTGTGTAGGCTCTGATTTTACGTTGCTGCCT 236
QY 181 ACTGGATGCTTGGGTCGCCAGTCTCCAGAGAGGGGCTTGAGTGGGTTGCTGAATTA 240
DB 235 ACTGGATGCTTGGGTCGCCAGTCTCCAGAGAGGGGCTTGAGTGGGTTGCTGAATTA 176
QY 241 GATTGAATCTGATAATTTATGCAACACATTTATGCGAGTCTGTGAAAGGGAAGTTACCCA 300
DB 175 GATTGAATCTGATAATTTATGCAACACATTTATGCGAGTCTGTGAAAGGGAAGTTACCCA 116
QY 301 TCTCAAGAGATGATTCAAAAGTCTCTACCTGCAATTAAGACAGCTTAAGAGCTGAAG 360
DB 115 TCTCAAGAGATGATTCAAAAGTCTCTACCTGCAATTAAGACAGCTTAAGAGCTGAAG 56
QY 361 ACAGTGAGTTTATTACTGTACAGATTTTATAGACTCGGGCCAGGACACTAGT 415
DB 55 ACAGTGAGTTTATTACTGTACAGATTTTATAGACTCGGGCCAGGACACTAGT 1

RESULT 3
US-09-359-326A-14
Sequence 14, Application US/09359326A
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSMA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/09/359,326A
CURRENT FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16

PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 453
TYPE: DNA
ORGANISM: SCID Mice
US-09-359-326A-14
Query Match 74.8%; Score 310.4; DB 21; Length 453;
Best Local Similarity 92.6%; Pred. No. 3.2e-78;
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 35 CATGGATTTGGGCTGATTTTTTTTATTTTAAAGGGGTCAGAGTGAAGTGAA 94
DB 6 CTTGGGTTGAGCTGGGTTTTTATTTTATTTTAAAGGGGTCGAGTGAAGTGAG 65
QY 95 GCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGGATCCATGAACCTCTCTGTGT 154
DB 66 GCTTGAGGAGTCTGGAGGAGGCTGGGTGCAACCTGGAGGATCCATGAACCTCTCTGTGT 125
QY 155 AGCTCTCGATTTTACCTTTCAGTGGCTACTGGATGTCTTGGGTCGCCAGTCTCCAGAGAA 214
DB 126 AGCTCTCGATTTTACCTTTCAGTAAATTTAGTGGATGACTTGGGTCGCCAGTCTCCAGAGAA 185
QY 215 GGGGCTTGAGTGGGTTGCTGAAATTTAGATTTGAATCTGATAATTATGCAACACATATGC 274
DB 186 GGGGCTTGAGTGGGTTGCTGAAATTTAGATTTGATTTGATTTGATTTGATTTGATTTGAT 245
QY 275 GGAGTCTGTGAAAGGGAAGTTACCATCTCAAGAGATGATTTCCAAAAGTCTCTCTACCT 334
DB 246 GGAGTCTGTGAAAGGGAAGTTACCATCTCAAGAGATGATTTCCAAAAGTCTCTCTACCT 305
QY 335 GCNAATGAACAGCTTAAAGCTTGAAGCTGACAGACAGTGGAGTTTATTACTGTACAGAT 386
DB 306 GCNAATGAACAGCTTAAAGCTTGAAGCTGACAGACAGTGGAGTTTATTACTGTACAGAT 357
RESULT 4
US-09-854-811-14
Sequence 14, Application US/09854811
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSMA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/09/854,811
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 453
TYPE: DNA
ORGANISM: SCID Mice
US-09-854-811-14
Query Match 74.8%; Score 310.4; DB 36; Length 453;
Best Local Similarity 92.6%; Pred. No. 3.2e-78;
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 35 CATGGATTTGGGCTGATTTTTTTTATTTTAAAGGGGTCAGAGTGAAGTGAA 94

6	CTTCGGGTGAGCTGGGGTTTTATTATGTCTTTTTAAAGGGTCCGGAGTGAAGTGAG	65
95	GCTTCAGAGAGTCTGGAGGAGGCTTGGTGCACCTGGAGGATCATGAAACTCTCTCGTGCT	154
66	GCTTCAGAGAGTCTGGAGGAGGCTGGGTGCACCTGGAGGATCATGAAACTCTCTCGTGCT	125
155	AGCCTCTCGAATTTACTTTTCAGTGGCTACTGATGCTCTTGGGTCGGCAGGTCTCCAGAGAA	214
126	AGCCTCTCGAATTTACTTTTCAGTGAATTACTGATGACTTGGGTCCGCCAGTCTCCAGAGAA	185
215	GGGGCTTCAGTGGGTTGCTGAAATTAGATTGAATTCGATAATTATGCAACACATTATGC	274
186	GGGGCTTCAGTGGGTTGCTGAAATTCGATTTGAGATCTGAAAAATTATGCAACACATTATGC	245
275	GGAGTCTGTGAAGGGAAGTTCCACATCTCAAGAGATGATTCCAAAGTCGTCTCTACCT	334
246	GGAGTCTGTGAAGGGAATTCACATCTCAAGAGATGATTCAGAAAGTCGTCTCTACCT	305
335	GCAAAATGAACAGCTTTAAGAGCTGAAGCAGTGGAGTTTATTACTGTACAGAT	386
306	GCAATGAACACTTTAAGACTGAAGCAGTGGAAATTTATTACTGTACAGAT	357

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US-09-855-153-14
; Sequence 14, Application US/09855153
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Safiran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54U314
; CURRENT APPLICATION NUMBER: US/09/855,153
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-09-855-153-14

Dd	6	CTTCGGGTTGAGCTGGGTTTTTAATTATGTTCTTTTAAAAGGGGTCCGGAGTGAAGTGAG	65
Qy	95	GCTTTGAGGAGCTCTGGAGGAGCGTTGGTGCACACCTGGAGGATCCATGAAAACCTCTCTGTGT	154
Dd	66	GCTTTGAGGAGCTCTGGAGGAGCGTTGGTGCACACCTGGAGGATCCATGAAAACCTCTCTGTGT	125
Qy	155	AGCCTCTGGATTTACTTTTCACTGCTACTCGATGTCTTTGGGTCCGCCAGTCTCCAGAGAA	214
Dd	126	AGCCTCTGGATTTACTTTTCACTGCTACTCGATGTCTTTGGGTCCGCCAGTCTCCAGAGAA	185
Qy	215	GGGCGCTTGAGTGGGTTGCTGCAAAATTAGATTGMAATCTGATAATTATGCAACACATTAATGC	274
Dd	186	GGGCGCTTGAGTGGGTTGCTGCAAAATTAGATTGMAATCTGATAATTATGCAACACATTAATGC	245
Qy	275	GGAGTCTGTGAAAGGGGAAGTTCACCACTCTCAAGAGATGATTCCAAAAGTCTGTCTTCACT	334
Dd	246	GGAGTCTGTGAAAGGGGAAGTTCACCACTCTCAAGAGATGATTCCAAAAGTCTGTCTTCACT	305
Qy	335	GCAAAATGAAACAGCTTAAGAGCTGAGACAGTGGAGTTTATTACTGTACAGAT	386
Dd	306	GCAAAATGAAACAGCTTAAGAGCTGAGACAGTGGAGTTTATTACTGTACAGAT	357

RESULT 6
 US-10-224-720-14
 ; Sequence 14, Application US/10224720
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; APPLICANT: Saffran, Douglas C.
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 30435.54US14
 ; CURRENT APPLICATION NUMBER: US/10/224,720
 ; CURRENT FILING DATE: 2002-08-20
 ; PRIOR APPLICATION NUMBER: US/09/359,326
 ; PRIOR FILING DATE: 1999-07-20
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 60/113,230
 ; PRIOR FILING DATE: 1998-12-21
 ; PRIOR APPLICATION NUMBER: 60/120,536
 ; PRIOR FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 60/124,658
 ; PRIOR FILING DATE: 1999-03-16
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 09/203,939
 ; PRIOR FILING DATE: 1998-12-02
 ; PRIOR APPLICATION NUMBER: 09/251,835
 ; PRIOR FILING DATE: 1999-02-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 453
 ; TYPE: DNA
 ; ORGANISM: SCID Mice
 US-10-224-720-14

RESULT 6
 US-10-224-720-14
 ; Sequence 14, Application US/10224720
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; APPLICANT: Saffran, Douglas C.
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 30435.54US14
 ; CURRENT APPLICATION NUMBER: US/10/224,720
 ; CURRENT FILING DATE: 2002-08-20
 ; PRIOR APPLICATION NUMBER: US/09/359,326
 ; PRIOR FILING DATE: 1999-07-20
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 60/113,230
 ; PRIOR FILING DATE: 1998-12-21
 ; PRIOR APPLICATION NUMBER: 60/120,536
 ; PRIOR FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 60/124,658
 ; PRIOR FILING DATE: 1999-03-16
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 09/203,939
 ; PRIOR FILING DATE: 1998-12-02
 ; PRIOR APPLICATION NUMBER: 09/251,835
 ; PRIOR FILING DATE: 1999-02-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 453
 ; TYPE: DNA
 ; ORGANISM: SCID Mice
 US-10-224-720-14

Query Match	74.8%;	Score 310.4;	DB 36;	Length 453;
Best Local Similarity	92.6%;	Pred. No. 3.2e-78;		
Matches 326;	Conservative	0;	Mismatches 25;	Indels 0;
Gaps	0;			
Qy	35	CATGGATTTTGGCGTGATTTTTTTTATTGTCTCTTTTAAAGGGGTCACAGAGTGAAGTGAA	94	

35 CATGGATTTGGCGTGATTTTTTTTATTGTTCTTTTAAAGGGGTCGAGTGAAGTGAA 94
6 CTTGGGTTGAGCTGGGGTTTTTATTATTGTTCTTTTAAAGGGGTCGAGTGAAGTGAG 65
95 GCTTTGAGGAGTCTGGAGAGCGTTGGTCAACCTGGAGGATCCATGAACCTCCTGTGCT 154

Db 66 GCTTGAGGAGTCTGGGAGGAGCTGGGTGCAACCTGGAGGATCCATGAACTCTCTGTGT 125
QY 155 AGCCTCTGGATTACTTTTCAGTGGCTACTCGATGCTTGGGTCCGCCAGTCTCCAGAGAA 214
Db 126 AGCCTCTGGATTACTTTTCAGTAAATTTACTGGATGACTTGGGTCCGCCAGTCTCCAGAGAA 185
QY 215 GGGGCTTGAGTGGGTGCTGAAATTCAGATTCGAAATTCGATTAATTCGACACATTTATGC 274
Db 186 GGGGCTTGAGTGGGTGCTGAAATTCGATTCGAAATTCGATTAATTCGACACATTTATGC 245
QY 275 GGAGTCTGTGAAAGGAGGAGTTCACCATCTCAAGAGATGATTCGAAAGTCTCTCTACCT 334
Db 246 GGAGTCTGTGAAAGGAGGAGTTCACCATCTCAAGAGATGATTCGAAAGTCTCTCTACCT 305
QY 335 GCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
Db 306 GCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 357

RESULT 7

US-10-225-779-14
; Sequence 14, Application US/10225779
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/225,779
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/203,939
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-10-225-779-14

Query Match 74.8%; Score 310.4; DB 50; Length 453;
Best Local Similarity 92.6%; Pred. No. 3.2e-78;
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 35 CATGGATTTTGGGCTGATTTTTTTTATTGTTCTTTTAAAGGGGTCCAGAGTCAAGTGAA 94
Db 6 CTTCCGGTTCAGCTGGGTTTTTATTGTTCTTTTAAAGGGGTCCGAGTCAAGTGAG 65
QY 95 GCTTGAGGAGTCTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAAACTCTCTGTGT 154
Db 66 GCTTGAGGAGTCTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAAACTCTCTGTGT 125
QY 155 AGCCTCTGGATTACTTTTCAGTGGCTACTCGATGCTTGGGTCCGCCAGTCTCCAGAGAA 214

Db 126 AGCCTCTGGATTACTTTTCAGTAAATTTACTCGATGACTTGGGTCCGCCAGTCTCCAGAGAA 185
QY 215 GGGGCTTGAGTGGGTGCTGAAATTCAGATTCGAAATTCGATTAATTCGACACATTTATGC 274
Db 186 GGGGCTTGAGTGGGTGCTGAAATTCGATTCGAAATTCGATTAATTCGACACATTTATGC 245
QY 275 GGAGTCTGTGAAAGGAGGAGTTCACCATCTCAAGAGATGATTCGAAAGTCTCTCTACCT 334
Db 246 GGAGTCTGTGAAAGGAGGAGTTCACCATCTCAAGAGATGATTCGAAAGTCTCTCTACCT 305
QY 335 GCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
Db 306 GCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 357

RESULT 8

US-10-225-784-14
; Sequence 14, Application US/10225784
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/225,784
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-10-225-784-14

Query Match 74.8%; Score 310.4; DB 50; Length 453;
Best Local Similarity 92.6%; Pred. No. 3.2e-78;
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 35 CATGGATTTTGGGCTGATTTTTTTTATTGTTCTTTTAAAGGGGTCCAGAGTCAAGTGAA 94
Db 6 CTTCCGGTTCAGCTGGGTTTTTATTGTTCTTTTAAAGGGGTCCGAGTCAAGTGAG 65
QY 95 GCTTGAGGAGTCTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAAACTCTCTGTGT 154
Db 66 GCTTGAGGAGTCTGGAGAGGCTTGGTGCACCTGGAGGATCCATGAAACTCTCTGTGT 125
QY 155 AGCCTCTGGATTACTTTTCAGTGGCTACTCGATGCTTGGGTCCGCCAGTCTCCAGAGAA 214
Db 126 AGCCTCTGGATTACTTTTCAGTAAATTTACTGGATGACTTGGGTCCGCCAGTCTCCAGAGAA 185
QY 215 GGGGCTTGAGTGGGTGCTGAAATTCAGATTCGAAATTCGATTAATTCGACACATTTATGC 274

Db 186 GGGCTTGGTGGTGGTCTGAAATTCGATTGAGATCTGAAATATTGAAATTCGAAACACATTATG 245
QY 275 GGAGTCTGTAAGGGAAGTTACCATCTCAAGAGATGATTCGAAAGTCGTCTTACCT 334
Db 246 GGAGTCTGTAAGGGAATTCACCATCTCAAGAGATGATTCGAAAGTCGTCTTACCT 305
QY 335 GCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
Db 306 GCAAAATGAACACTTAAGACCTGAAGACAGTGGAAATTTATTACTGTACAGAT 357

RESULT 9
US-10-374-381-14
; Sequence 14, Application US/10374381
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.5AUS14
; CURRENT APPLICATION NUMBER: US/10/374,381
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US/09/564,329A
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-10-374-381-14

Query Match 74.8%; Score 310.4; DB 53; Length 453;
Best Local Similarity 92.6%; Pred. No. 3.2e-78;
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 35 CATGGATTTGGGCTGATTTTTTTTATTGTTCTTTTAAAGGGGTCCAGAGTGAAGTGA 94
Db 6 CTTCGGGTGAGCTGGGTTTTTATTGTTCTTTTAAAGGGGTCCGAGTGAAGTGA 65
QY 95 GCTTGAGGAGTCTGGAGGAGCTGGTGCACCTGGAGATCCATGAACTCTCTGTGT 154
Db 66 GCTTGAGGAGTCTGGAGGAGCTGGTGCACCTGGAGATCCATGAACTCTCTGTGT 125
QY 155 AGCTCTGATTTACTTTTCACTGGTCTTGGTCCGCGAGTCTCCAGAA 214
Db 126 AGCTCTGATTTACTTTTCACTGGTCTTGGTCCGCGAGTCTCCAGAA 185
QY 215 GGGCTTGGTGGTCTGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCG 274
Db 186 GGGCTTGGTGGTCTGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCG 245
QY 275 GGGCTTGGTGGTCTGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCG 274
Db 186 GGGCTTGGTGGTCTGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCG 245
QY 275 GGAGTCTGTAAGGGAAGTTACCATCTCAAGAGATGATTCGAAAGTCGTCTTACCT 334

Db 246 GGAGTCTGTAAGGGAATTCACCATCTCAAGAGATGATTCGAAAGTCGTCTTACCT 305
QY 335 GCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
Db 306 GCAAAATGAACACTTAAGACCTGAAGACAGTGGAAATTTATTACTGTACAGAT 357

RESULT 10
US-10-446-542-14
; Sequence 14, Application US/10446542
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.5AUS14
; CURRENT APPLICATION NUMBER: US/10/446,542
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/855,153
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-10-446-542-14

Query Match 74.8%; Score 310.4; DB 54; Length 453;
Best Local Similarity 92.6%; Pred. No. 3.2e-78;
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 35 CATGGATTTGGGCTGATTTTTTTTATTGTTCTTTTAAAGGGGTCCAGAGTGAAGTGA 94
Db 6 CTTCGGGTGAGCTGGGTTTTTATTGTTCTTTTAAAGGGGTCCGAGTGAAGTGA 65
QY 95 GCTTGAGGAGTCTGGAGGAGCTGGTGCACCTGGAGATCCATGAACTCTCTGTGT 154
Db 66 GCTTGAGGAGTCTGGAGGAGCTGGTGCACCTGGAGATCCATGAACTCTCTGTGT 125
QY 155 AGCTCTGATTTACTTTTCACTGGTCTTGGTCCGCGAGTCTCCAGAA 214
Db 126 AGCTCTGATTTACTTTTCACTGGTCTTGGTCCGCGAGTCTCCAGAA 185
QY 215 GGGCTTGGTGGTCTGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCG 274
Db 186 GGGCTTGGTGGTCTGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCG 245
QY 275 GGAGTCTGTAAGGGAAGTTACCATCTCAAGAGATGATTCGAAAGTCGTCTTACCT 334
Db 246 GGAGTCTGTAAGGGAATTCACCATCTCAAGAGATGATTCGAAAGTCGTCTTACCT 305
QY 335 GCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386

Db 306 GCAATGAACAACCTTAAGACCTGAAGACAGCTGGAATTTATTACTGTACAGAT 357
US-10-769-074-26
; Sequence 26, Application US/10769074
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Jakobovits, Aya
; APPLICANT: The Regents of the University of California
; APPLICANT: Agensys, Inc.
; TITLE OF INVENTION: PSCA: Prostate Stem Cell Antigen and Uses Thereof
; FILE REFERENCE: 02307K-141589US
; CURRENT APPLICATION NUMBER: US/10/769,074
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US/10/769,308
; PRIOR FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 05/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: US 05/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 60/120,536
; PRIOR FILING DATE: 1999-02-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:heavy chain
; OTHER INFORMATION: variable domain region of PSCA monoclonal antibody
; OTHER INFORMATION: 2H9
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(453)
US-10-769-074-26
Query Match 74.8%; Score 310.4; DB 62; Length 453;
Best Local Similarity 92.6%; Pred. No. 3.2e-78;
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Qy 35 CATGGATTTGGCTGATTTTTTTTATTTGTTCTTTTAAAGGGGTCAGAGTGAAGTAA 94
Db 6 CTTGGGTTGAGCTGGGTTTTTTATTTATTTGTTCTTTTAAAGGGGTCAGAGTGAAGTAA 65
Qy 95 GCTTGAGGAGCTGGAGGAGGCTTGGTGCAACTGGAGGATCCATGAACTCTCCTGTGT 154
Db 66 GCTTGAGGAGCTGGAGGAGGCTTGGTGCAACTGGAGGATCCATGAACTCTCCTGTGT 125
Qy 155 AGCCTCTGGATTTACTTTTCACTGGCTACTGGATGTCTTGGGTCGCCAGTCTCCAGAGAA 214
Db 126 AGCCTCTGGATTTACTTTTCACTGGCTACTGGATGTCTTGGGTCGCCAGTCTCCAGAGAA 185
Qy 215 GGGGCTTGAGTGGGTTGCTGAAATTTAGATTGAATCTGATAATTTATGCAACATTTATGC 274
Db 186 GGGGCTTGAGTGGGTTGCTGAAATTTGATTGAGATCTGAAATTTATGCAACATTTATGC 245

Qy 275 GGAGTCTGTGAAGGGAAGTTTCAACATCTCAAGAGATGATTTCCAAAGTGTCTCTACCT 334
Db 246 GGAGTCTGTGAAGGGAAGTTTCAACATCTCAAGAGATGATTTCCAAAGTGTCTCTACCT 305
Qy 335 GCAATGAACAACCTTAAGACCTGAAGACAGCTGGAATTTATTACTGTACAGAT 386
Db 306 GCAATGAACAACCTTAAGACCTGAAGACAGCTGGAATTTATTACTGTACAGAT 357
RESULT 12
US-10-769-308-26
; Sequence 26, Application US/10769308
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Jakobovits, Aya
; APPLICANT: The Regents of the University of California
; APPLICANT: Agensys, Inc.
; TITLE OF INVENTION: PSCA: Prostate Stem Cell Antigen and Uses Thereof
; FILE REFERENCE: 02307K-141589US
; CURRENT APPLICATION NUMBER: US/10/769,308
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 60/228,816
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: US 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: US 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 60/124,658
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:heavy chain
; OTHER INFORMATION: variable domain region of PSCA monoclonal antibody
; OTHER INFORMATION: 2H9
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(453)
US-10-769-308-26
Query Match 74.8%; Score 310.4; DB 62; Length 453;
Best Local Similarity 92.6%; Pred. No. 3.2e-78;
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Qy 35 CATGGATTTGGCTGATTTTTTTTATTTGTTCTTTTAAAGGGGTCAGAGTGAAGTAA 94
Db 6 CTTGGGTTGAGCTGGGTTTTTTATTTATTTGTTCTTTTAAAGGGGTCAGAGTGAAGTAA 65
Qy 95 GCTTGAGGAGCTGGAGGAGGCTTGGTGCAACTGGAGGATCCATGAACTCTCCTGTGT 154
Db 66 GCTTGAGGAGCTGGAGGAGGCTTGGTGCAACTGGAGGATCCATGAACTCTCCTGTGT 125
Qy 155 AGCCTCTGGATTTACTTTTCACTGGCTACTGGATGTCTTGGGTCGCCAGTCTCCAGAGAA 214

Db 126 AGCTCTGGATTACTTTTCAGTAATTTACTGGATGACTTGGGTCGCCAGCTCTCCAGAA 185
Qy 215 GGGGCTTGAGTGGGTGCTGAAATAGATTGAAATCTGATATTAATGCAACATTATGC 274
Db 186 GGGGCTTGAGTGGGTGCTGAAATAGATTGAAATCTGATATTAATGCAACATTATGC 245
Qy 275 GGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCACCAAGTCTCTACCT 334
Db 246 GGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCACCAAGTCTCTACCT 305
Qy 335 GCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
Db 306 GCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 357

RESULT 13

US-10-997-735-14
; Sequence 14, Application US/10997735
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSMA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/997,735
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US/10/225,779
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-10-997-735-14

Query Match 74.8%; Score 310.4; DB 67; Length 453;
Best Local Similarity 92.6%; Pred. No. 3.2e-78; Indels 0; Gaps 0;
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Qy 35 CATGGATTTTGGGCTGATTTTTTTTATTTGTTCTTTTAAAGGGGTCAGAGTGAAGTGA 94
Db 6 CTTCCGGTTGAGCTGGGTTTTTATTTATTTGTTCTTTTAAAGGGGTCAGAGTGAAGTGA 65
Qy 95 GCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGATCCATGAATCTCTCTGTGT 154
Db 66 GCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGATCCATGAATCTCTCTGTGT 125
Qy 155 AGCTCTGATTTTACTTTTCAGTGGCTTCTGATGTTCTTGGTCCGCGAGTCTCCAGAGAA 214
Db 126 AGCTCTGATTTTACTTTTCAGTGAATTTAGATTGAAATCTGATAATTATGCAACATTATGC 185
Qy 215 GGGGCTTGAGTGGGTGCTGAAATAGATTGAAATCTGATAATTATGCAACATTATGC 274

Db 186 GGGGCTTGAGTGGGTGCTGAAATAGATTGAAATCTGATATTAATGCAACATTATGC 245
Qy 275 GGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCACCAAGTCTCTACCT 334
Db 246 GGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCACCAAGTCTCTACCT 305
Qy 335 GCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
Db 306 GCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 357

RESULT 14

US-11-021-950-14
; Sequence 14, Application US/11021950
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSMA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/11/021,950
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/225,784
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-11-021-950-14

Query Match 74.8%; Score 310.4; DB 68; Length 453;
Best Local Similarity 92.6%; Pred. No. 3.2e-78; Indels 0; Gaps 0;
Matches 326; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Qy 35 CATGGATTTTGGGCTGATTTTTTTTATTTGTTCTTTTAAAGGGGTCAGAGTGAAGTGA 94
Db 6 CTTCCGGTTGAGCTGGGTTTTTATTTATTTGTTCTTTTAAAGGGGTCAGAGTGAAGTGA 65
Qy 95 GCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGATCCATGAATCTCTCTGTGT 154
Db 66 GCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGATCCATGAATCTCTCTGTGT 125
Qy 155 AGCTCTGATTTTACTTTTCAGTGGCTTCTGATGTTCTTGGTCCGCGAGTCTCCAGAGAA 214
Db 126 AGCTCTGATTTTACTTTTCAGTGAATTTAGATTGAAATCTGATAATTATGCAACATTATGC 185
Qy 215 GGGGCTTGAGTGGGTGCTGAAATAGATTGAAATCTGATAATTATGCAACATTATGC 274
Db 186 GGGGCTTGAGTGGGTGCTGAAATAGATTGAAATCTGATAATTATGCAACATTATGC 245
Qy 275 GGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCACCAAGTCTCTACCT 334

Db 246 GGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCACAGAGTCTCTCTACCT 305
 Qy 335 GCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
 Db 306 GCAAATGAACAACTTAAGACCTGAAGACAGTGGAAATTTATTACTGTACAGAT 357

RESULT 15

US-09-724-671-4993
 ; Sequence 4993, Application US/09724671
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D
 ; APPLICANT: Murison, James G
 ; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
 ; FILE REFERENCE: 105002
 ; CURRENT APPLICATION NUMBER: US/09/724,671
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: U.S. No. 60/171,678
 ; NUMBER OF SEQ ID NOS: 21907
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4993
 ; LENGTH: 412
 ; TYPE: DNA
 ; ORGANISM: Mouse
 ; US-09-724-671-4993

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 Best Local Similarity 93.1%; Pred. No. 1.4e-73;
 Matches 308; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 Qy 52 TTTTITTTTATTTCTTTTAAAGGGGTCCAGAGTGAAGTGAAGCTTTGAGGAGTCTGGAG 111
 Db 73 TATTCATAGTTTCTCTTAAAGGTGTCCAGAGTGAAGTGAAGCTTTGAGGAGTCTGGAG 132
 Qy 112 GAGCTTGGTGCACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTTACTT 171
 Db 133 GAGGCTTGGTGCACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTTACTT 192
 Qy 172 TCAGTGGCTACTGGATCTTTGGTCCGCGAGTCTCCAGAGAGGGGCTTGAGTGGGTG 231
 Db 193 TCAGTAACTACTGGATGAACCTGGTCCGCGAGTCTCCAGAGAGGGGCTTGAGTGGGTG 252
 Qy 232 CTGAAATTAGATTGAAATCTGATAATTATGCAACACATTATGGGAGTCTGTGAAAGGGA 291
 Db 253 CTGAAATTAGATTGAAATCTGATAATTATGCAACACATTATGGGAGTCTGTGAAAGGGA 312
 Qy 292 AGTTACCATCTCAGAGATGATTCGAAAGTGTCTCTACCTGCAAAATGAACAGCTTAA 351
 Db 313 GGTTACCATCTCAGAGATGATTCGAAAGTGTCTCTACCTGCAAAATGAACAGCTTAA 372
 Qy 352 GAGCTGAAGACAGTGGAGTTTATTACTGTAC 382
 Db 373 GAGCTGAAGACAGTGGCATTATTACTGTAC 403

Search completed: April 18, 2005, 21:04:44
 Job time : 2123.49 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 1941.07 Seconds
(without alignments)
10908.879 Million cell updates/sec

Title: US-09-674-716B-2

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_ba:.*
2: gb_hgt:.*
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4: gb_on:.*
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6: gb_pat:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_sts:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vi:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	437	100.0	437	6 BD232418	BD232418 Antibodie
2	437	100.0	437	6 BD232450	BD232450 Antibodie
3	437	100.0	437	6 AX010601	AX010601 Sequence
4	437	100.0	437	6 AX010644	AX010644 Sequence
5	373.2	85.4	431	10 MUSIGKNG	M19910 Mouse Ig re
6	371.6	85.0	458	10 MUSIGKCNF	M19909 Mouse Ig re
7	333.4	76.3	1400	10 MUSIGKAH	J00553 Mouse ig ka
8	326.8	74.8	339	10 MMU29425	U29425 Mus musculus
9	317.2	72.6	339	6 AR072863	AR072863 Sequence
10	317.2	72.6	339	6 AR166313	AR166313 Sequence
11	317.2	72.6	368	6 AR072861	AR072861 Sequence
12	317.2	72.6	368	6 AR166317	AR166317 Sequence
13	316	72.3	420	6 AR166319	AR166319 Sequence
14	313.2	71.7	744	6 AX935403	AX935403 Sequence
15	313.2	71.7	951	6 AX935454	AX935454 Sequence
16	309.2	70.8	368	6 AR072865	AR072865 Sequence
17	309.2	70.8	368	6 AR166315	AR166315 Sequence
18	308	70.5	825	10 MMUG28	V00779 Mouse immun
19	308	70.5	899	10 MMU231264	AJ231264 Mus muscu

20	308	70.5	1047	10 MUSIGKVH2	J00562 Mouse ig ka
21	308	70.5	1060	10 MUSIGKVT1	K02415 Mouse Ig ge
22	308	70.5	3101	10 AY591709	AY591709 Mus muscu
23	308	70.5	33428	2 AC101099	AC101099 Mus muscu
24	308	70.5	194119	2 AC140374	AC140374 Mus muscu
25	308	70.5	203073	10 AC123322	AC123322 Mus muscu
26	308	70.5	318959	2 AY657023	AY657023 Mus muscu
27	296.8	67.9	1149	10 MUSIGKVA	M80407 Mouse Ig ge
28	293.6	67.2	396	10 MMU277812	AJ277812 Mus muscu
29	293.2	67.1	464	6 A29573	A29573 M.musculus
30	293.2	67.1	464	6 I25724	I25724 Sequence 15
31	293.2	67.1	958	10 MMU55479	AJ555479 Mus muscu
32	293.2	67.0	451	10 MMSV5PKL	Z49934 M.musculus
33	288.8	66.1	396	10 AF045509	AF045509 Mus muscu
34	287.4	65.8	773	6 AX825304	AX825304 Sequence
35	286.8	65.6	961	6 E08433	E08433 cDNA encodi
36	286.4	65.5	978	10 MUSIGKVB	M15553 Mouse germi
37	284.4	65.1	399	10 MMU92070	U92070 Mus musculu
38	284.4	65.1	426	6 AX825286	AX825286 Sequence
39	284.4	65.1	982	10 MUSIGKVA	M15552 Mouse germi
40	284	65.0	396	10 AF045515	AF045515 Mus muscu
41	280	64.1	593	10 MMIGMM65A	X57856 M.musculus
42	280	64.1	935	10 BC031349	BC031349 Mus muscu
43	276.4	63.2	399	6 A23299	A23299 M.musculus
44	276.4	63.2	399	6 AR013733	AR013733 Sequence
45	276.4	63.2	399	6 AR275126	AR275126 Sequence

ALIGNMENTS

RESULT 1	BD232418	437 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD232418	Antibodies against CD23, derivatives thereof and therapeutic			
DEFINITION	BD232418	utilization of the same.			
ACCESSION	BD232418	VERSION	BD232418.1	GI:33042188	
KEYWORDS	JP 2002514421-A/2.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 437)				
AUTHORS	Bonnefoy, J.Y.M.P., Crowe, S.J., Ellis, J.H., Rapson, N.T. and Shearin, J.				
TITLE	Antibodies against CD23, derivatives thereof and therapeutic				
JOURNAL	utilization of the same				
COMMENT	Patent: JP 2002514421-A 2 21-MAY-2002; GLAXO GROUP LTD				
	OS Mus musculus (mouse)				
	PN JP 2002514421-A/2				
	PD 21-MAY-2002				
	PF 07-MAY-1999 JP 2000548470				
	PR 09-MAY-1998 GB 9809839.5				
	PI JEAN YVES MARCEL PAUL BONNEFOY, SCOTT JAMES CROWE, JONATHAN PI HENRY ELLIS,				
	PI NICHOLAS TIMOTHY RAPSON, JEAN SHEARIN				
	PC C12N15/02,A61K39/395,C07K16/28,C12N15/00				
	CC Antibodies against CD23, derivatives thereof and therapeutic				
	CC utilization				
	CC of the same				
	FT Key				
	CDS Location/Qualifiers				
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	/organism="Mus musculus"				
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ORIGIN					
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Best Local Similarity	100.0%;	Pred.	No. 6.1e-134;	Length	437;

Matches	437;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
1	QY	AAGCTTTACAGTTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTCAGTTTCTGG	60						
1	Db	AAGCTTTACAGTTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTCAGTTTCTGG	60						
61	QY	GGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGGGATATTCTGTATACCCAGGATGAAC	120						
61	Db	GGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGGGATATTCTGTATACCCAGGATGAAC	120						
121	QY	TCTCCAAATCCTGTACACTTCTCGAGAAATCAGTTTCCATCTCTCGAGGTCCTAGTAAGATC	180						
121	Db	TCTCCAAATCCTGTACACTTCTCGAGAAATCAGTTTCCATCTCTCGAGGTCCTAGTAAGATC	180						
181	QY	TCCTGTATAGGATGGGAAGACATACCTTGAATTTGGTTTCTGCAGAGACAGGACAAATCTC	240						
181	Db	TCCTGTATAGGATGGGAAGACATACCTTGAATTTGGTTTCTGCAGAGACAGGACAAATCTC	240						
241	QY	CTCAGCTCCTGATCTATTTGATGTCCACCCGTGCATCAGGAGTCTCAGACCGGTTTAGTG	300						
241	Db	CTCAGCTCCTGATCTATTTGATGTCCACCCGTGCATCAGGAGTCTCAGACCGGTTTAGTG	300						
301	QY	CGATGGGTGAGGCACAGATTTTCCCTCGAAATCAGTAGAGTGAAGGCTGAGGATGTGG	360						
301	Db	CGATGGGTGAGGCACAGATTTTCCCTCGAAATCAGTAGAGTGAAGGCTGAGGATGTGG	360						
361	QY	GTGTGTATTACTGTCAACAACCTTGTAGAGTATCCATTTCAGTTTCGGCTCGGGGACAAAGT	420						
361	Db	GTGTGTATTACTGTCAACAACCTTGTAGAGTATCCATTTCAGTTTCGGCTCGGGGACAAAGT	420						
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421	Db	TGGAATAAACAACGTACG	437						

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LOCUS	BD232450/c	Antibodies against CD23, derivatives thereof and therapeutic										
DEFINITION	utilization of the same.											
ACCESSION	BD232450											
VERSION	BD232450.1	GI:33042220										
KEYWORDS	JP 2002514421-A/34.											
SOURCE	Mus musculus (house mouse)											
ORGANISM	Mus musculus											
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;											
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.											
	1 (bases 1 to 437)											
	Bonnefoy,J.Y.M.P., Crowe,S.J., Ellis,J.H., Rapson,N.T. and Shearin,J.											
TITLE	Antibodies against CD23, derivatives thereof and therapeutic											
JOURNAL	utilization of the same											
	Patent: JP 2002514421-A 34	21-MAY-2002;										
	GLAXO GROUP LTD											
COMMENT	OS	Mus musculus (mouse)										
	PN	JP 2002514421-A/34										
	PD	21-MAY-2002										
	PP	07-MAY-1999	JP 2000548470									
	PR	09-MAY-1998	GB 9809839.5									
	PI	JEAN YVES MARCEL PAUL BONNEFOY, SCOTT JAMES CROWE, JONATHAN PI HENRY ELLIS,										
	PI	NICHOLAS TIMOTHY RAPSON, JEAN SHEARIN										
	CC	C12N15/02,A61K39/395,C07K16/28,C12N15/00										
	CC	Antibodies against CD23, derivatives thereof and therapeutic										
	CC	utilization										
	CC	of the same										
	FH	Key	Location/Qualifiers									
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Best Local Similarity 100.0%; Pred. No. 6.1e-134;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTTCAAGTTCTGG 60
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Qy 61 GGGTGCCTTATGTTCTCGGATCTCTCGAGTCAGTGGGGATATTTGATAAACCCAGGATGAAC 120
Db 61 GGGTGCCTTATGTTCTCGGATCTCTCGAGTCAGTGGGGATATTTGATAAACCCAGGATGAAC 120

Qy 121 TCTCCAAATCCCTGTCACCTTCTGGAGAACATCAGTTTCCATCTCTCGCAGGTCAGTAAAGATC 180
Db 121 TCTCCAAATCCCTGTCACCTTCTGGAGAACATCAGTTTCCATCTCTCGCAGGTCAGTAAAGATC 180

Qy 181 TCCGTGTATAGGATGGGAGACATCTTGAATGGTTTCTGCAGAGACCAAGGCTTAAAGTGG 240
Db 181 TCCGTGTATAGGATGGGAGACATCTTGAATGGTTTCTGCAGAGACCAAGGCTTAAAGTGG 240

Qy 241 CTACAGCTCCTGATGATTTGATGTCACCCCGTGCATCAGGAGTCTCAGACCGGTTTAAAGT 300
Db 241 CTACAGCTCCTGATGATTTGATGTCACCCCGTGCATCAGGAGTCTCAGACCGGTTTAAAGT 300

Qy 301 GCAGTGGGTGAGGACAGATTTACCTCGGAAATCAGTAGAGTGAAGGCTGAGGATGTTGG 360
Db 301 GCAGTGGGTGAGGACAGATTTACCTCGGAAATCAGTAGAGTGAAGGCTGAGGATGTTGG 360

Qy 361 GTGTGTATTACTGTCACAACTTTGATAGATGTTTCCAGTTCATTCAGTTCCGGTCCGGGACAAAGT 420
Db 361 GTGTGTATTACTGTCACAACTTTGATAGATGTTTCCAGTTCATTCAGTTCCGGTCCGGGACAAAGT 420

Qy 421 TGGAAATATAAACGTACG 437
Db 421 TGGAAATATAAACGTACG 437

RESULT 4
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LOCUS      AX010644      437 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 47 from Patent WO9958679.
ACCESSION  AX010644
VERSION     AX010644.1  GI:9997453
KEYWORDS
SOURCE      Mus musculus
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE   1
AUTHORS     Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.
TITLE       Antibodies to cd23, derivatives thereof, and their therapeutic uses
JOURNAL     Patent: WO 9958679-A 47 19-NOV-1999; and their therapeutic uses
            BONNEFOY JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON
            NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY
            (GB); SHEARIN JEAN (US)
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Best Local Similarity 100.0%; Pred. No. 6.1e-134;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTTCAAGTTCTGG 60
Db 437 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTTCAAGTTCTGG 378

Qy 61 GGGTGCCTTATGTTCTCGGATCTCTCGAGTCAGTGGGGATATTTGATAAACCCAGGATGAAC 120
Db 377 GGGTGCCTTATGTTCTCGGATCTCTCGAGTCAGTGGGGATATTTGATAAACCCAGGATGAAC 318
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Qy 121 TCTCCAAATCCCTGTCACCTTCTGGAGAACATCAGTTTCCATCTCTCGCAGGCTCTAGTAAAGATC 180
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Qy 181 TCTGTATATAGGATGGGAGACATATCTTGAATGGTTTCTGCAGAGACCAAGGACAAATCTC 240
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Qy 241 CTACAGCTCCTGATGATTTGATGTCACCCCGTGCATCAGGAGTCTCAGACCGGTTTAAAGT 300
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Qy 301 GCAGTGGGTGAGGACAGATTTACCTCGGAAATCAGTAGAGTGAAGGCTGAGGATGTTGG 360
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Qy 421 TGGAAATATAAACGTACG 437
Db 17 TGGAAATATAAACGTACG 1

RESULT 5
MUSIGKNG
LOCUS      MUSIGKNG      431 bp      mRNA      linear      ROD 26-MAR-1994
DEFINITION Mouse Ig rearranged kappa-chain mRNA, clone AN06K.
ACCESSION  M19910.1  GI:197027
VERSION     M19910.1  GI:197027
KEYWORDS    C-region; immunoglobulin light chain; immunoglobulin-kappa;
            processed gene.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE   1 (bases 1 to 56)
AUTHORS     Rule,G.S.
JOURNAL     Unpublished (1988)
REFERENCE   2 (bases 1 to 431)
AUTHORS     Leahy,D.J., Rule,G.S., Whittaker,M.M. and McConnell,H.M.
TITLE       Sequences of 12 monoclonal anti-dinitrophenyl spin-label antibodies
            for NMR studies
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 85 (11), 3661-3665 (1988)
MEDLINE     88234486
PUBMED      3375235
COMMENT     Original source text: Mouse (BALB/c) mature B cell, cDNA to mRNA,
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            Draft entry and computer-readable sequence [2] kindly submitted by
            G. Rule, 20-JUL-1988.
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Db      831 AACTTTAGAGTATCGCTCACGTTCCGTTGGGACCAAGCTGGAGCTGAAACGTAAG 899

RESULT 8
MMU29425      339 bp mRNA linear ROD 03-FEB-1998
DEFINITION Mus musculus anti-PC rearranged Ig kappa chain V-J region mRNA,
ACCESSION U29425
VERSION U29425.1 GI:2745913
KEYWORDS Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 339)
AUTHORS Guo,W.X., Burger,A., Fischer,R.T., Sieckman,D.G., Longo,D.L. and
Kenny,J.J.
TITLE Sequence changes at the V-D junction of the VH1 heavy chain of
anti-phosphocholine antibodies alter binding to and protection
against Streptococcus pneumoniae
JOURNAL Int. Immunol. 9 (5), 665-677 (1997)
MEDLINE 97328374
PUBMED 9184912
REFERENCE 2 (bases 1 to 339)
AUTHORS Guo,W.X., Burger,A., Fischer,R.T., Sieckman,D.G., Longo,D.L. and
Kenny,J.J.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-1995) FCRDC, NCI, P.O. Box B, Frederick, MD
21702-1201, USA
REFERENCE 3 (bases 1 to 339)
AUTHORS Guo,W.X., Burger,A., Fischer,R.T., Sieckman,D.G., Longo,D.L. and
Kenny,J.J.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-1998) FCRDC, NCI, P.O. Box B, Frederick, MD
21702-1201, USA
REMARK Nucleotide and protein sequence update by submitter
COMMENT On Jan 5, 1998 this sequence version replaced gi:903959.
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Query Match 74.8%; Score 326.8; DB 10; Length 339;
Best Local Similarity 97.9%; Pred. No. 3.2e-97;
Matches 33; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 156 ATCTCTGCAGGCTTAGTAAGATCTCTCTATAGGATGGAGACATACACTTGAATTGG 215
Db 61 ATCTCTGCAGGCTTAGTAAGATCTCTCTATAGGATGGAGACATACACTTGAATTGG 120

QY 216 TTTCTGCAGAGACACAGGACAAATCTCTCAGCTCTCTGATGTATTTGATGTCCACCGTGCA 275
Db 121 TTTCTGCAGAGACACAGGACAAATCTCTCAGCTCTCTGATGTATTTGATGTCCACCGTGCA 180

QY 276 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTCACCTCGGAATC 335
Db 181 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTCACCTCGGAATC 240

QY 336 AGTAGAGTGAAGCTGAGGATGCGGTGTGTTACTTACTGTCAACAACCTTGTAGAGTATCCA 395
Db 241 AGTAGAGTGAAGCTGAGGATGCGGTGTGTTACTTACTTACTGTCAACAACCTTGTAGAGTATCCA 300

ORIGIN
Query Match 72.6%; Score 317.2; DB 6; Length 339;
Best Local Similarity 96.2%; Pred. No. 5e-94;
Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 96 GATATTGTGATAACCCAGGATGAACCTCCAACTCTGCTCACTCTGAGGAATCAGTTTCC 155
Db 1 GATATTGTGATGACCCAGGATGAACCTCCAACTCTGCTCACTCTGAGGAATCAGTTTCC 60

QY 156 ATCTCTGCAGGCTTAGTAAGATCTCTCTATAGGATGGAGACATACACTTGAATTGG 215
Db 61 ATCTCTGCAGGCTTAGTAAGATCTCTCTATAGGATGGAGACATACACTTGAATTGG 120

QY 216 TTTCTGCAGAGACACAGGACAAATCTCTCAGCTCTCTGATGTATTTGATGTCCACCGTGCA 275
Db 121 TTTCTGCAGAGACACAGGACAAATCTCTCAGCTCTCTGATGTATTTGATGTCCACCGTGCA 180

QY 276 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTCACCTCGGAATC 335
Db 181 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTCACCTCGGAATC 240

QY 336 AGTAGAGTGAAGCTGAGGATGCGGTGTGTTACTTACTGTCAACAACCTTGTAGAGTATCCA 395
Db 241 AGTAGAGTGAAGCTGAGGATGCGGTGTGTTACTTACTTACTGTCAACAACCTTGTAGAGTATCCA 300

RESULT 10
AR166313      339 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 99 from patent US 6280987.
ACCESSION AR166313
VERSION AR166313.1 GI:16241580
KEYWORDS

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QY 216 TTTCTGCAGAGACACAGGACAAATCTCTCAGCTCTCTGATGTATTTGATGTCCACCGTGCA 275
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QY 276 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTCACCTCGGAATC 335
Db 181 TCAGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTCACCTCGGAATC 240
QY 336 AGTAGAGTGAAGCTGAGGATGCGGTGTGTTACTTACTGTCAACAACCTTGTAGAGTATCCA 395
Db 241 AGTAGAGTGAAGCTGAGGATGCGGTGTGTTACTTACTTACTGTCAACAACCTTGTAGAGTATCCT 300
QY 396 TTCACGTTCCGTCGGGACAAAGTTGGAAATAAAACG 433
Db 301 TTCACGTTCCGTCGGGACAAAGTTGGAAATAAAACG 338

RESULT 9
AR072863      339 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 88 from patent US 5948658.
ACCESSION AR072863
VERSION AR072863.1 GI:9999626
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 339)
AUTHORS Landry,D.W.
TITLE Anti-cocaine catalytic antibody
JOURNAL Patent: US 5948658-A 88 07-SEP-1999;
FEATURES Location/Qualifiers
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Qy	276	TCAGGAGTCTCAGACCCGGTTTATGTGGCAGTGGGTGAGGCACAGATTTTCAACCTCGGAATC	335
Db	181	TCAGGAGTCTCAGACCCGGTTTATGTGGCAGTGGGTGAGGAACAGATTTCAACCTCGGAATC	240
Qy	336	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTCAACAACTTGTAGAGTATCCA	395
Db	241	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTCAACAACTTGTAGAGTATCCA	300
Qy	396	TTACAGTTTCGGCTCGGGGACAAAGTTTGGAAATAAAGC	433
Db	301	TTACAGTTTCGGCTCGGGGACAAAGTTTGGAAATAAAGC	338
RESULT 12			
AR166317	AR166317	368 bp	DNA
LOCUS	Sequence 107 from patent US 6280987.	linear	PAT 17-OCT-2001
DEFINITION	AR166317		
ACCESSION	AR166317		
VERSION	AR166317.1	GI:16241584	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 368)		
AUTHORS	Landry,D.W.		
TITLE	Anti-cocaine catalytic antibody		
JOURNAL	Patent: US 6280987-A 107 28-AUG-2001;		
FEATURES	location/Qualifiers		
source	1. 368		
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ORIGIN	/mol_type="unassigned DNA"		
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Best Local Similarity 96.2%; Pred. No. 5.1e-94;			
Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;			
Qy	96	GATATTGTGATAACCCAGGATGAACCTCTCAATCCTGTCACTTCTCGAGAAATCAAGTTTCC	155
Db	1	GATATGTTGATGACGCAAGACGAACTCTCAATCCTGTCACTTCTCGAGAAATCAAGTTTCC	60
Qy	156	ATCTCTGCAAGTCTAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTCAATTTGG	215
Db	61	ATCTCTGCAAGTCTAGTAAGAGTCTCCTATATGAGGATGGGAAGACATACTTCAATTTGG	120
Qy	216	TTTTCTGACAGACACAGACAATCTCTCAGCTCTGTATGTATTTGATGTCTCACCCGGTCCA	275
Db	121	TTTTCTGACAGACACAGACAATCTCTCAGCTCTGTATGTATTTGATGTCTCACCCGGTCCA	180
Qy	276	TCAGGAGTCTCAGACCCGGTTTATGTGGCAGTGGGTGAGGCACAGATTTTCAACCTCGGAATC	335
Db	181	TCAGGAGTCTCAGACCCGGTTTATGTGGCAGTGGGTGAGGAACAGATTTTCAACCTCGGAATC	240
Qy	336	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTCAACAACTTGTAGAGTATCCA	395
Db	241	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTCAACAACTTGTAGAGTATCCA	300
Qy	396	TTACAGTTTCGGCTCGGGGACAAAGTTTGGAAATAAAGC	433
Db	301	TTACAGTTTCGGCTCGGGGACAAAGTTTGGAAATAAAGC	338
RESULT 13			
AR166319	AR166319	420 bp	DNA
LOCUS	Sequence 111 from patent US 6280987.	linear	PAT 17-OCT-2001
DEFINITION	AR166319		
ACCESSION	AR166319		
VERSION	AR166319.1	GI:16241586	

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KEYWORDS      Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 420)
AUTHORS        Landry, D.W.
TITLE          Anti-cocaine catalytic antibody
JOURNAL        Patent: US 6280987-A 111 28-AUG-2001;
FEATURES       Location/Qualifiers
               source
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Query Match      72.3%; Score 316; DB 6; Length 420;
Best Local Similarity 95.8%; Pred. No. 1.3e-93;
Matches 325; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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QY 154 CCATCTCTCGCAGGTCTAGTAAGAGTCTCTGTATTAAGAGTGGGAAGACATCTTGAATT 213
DB 111 CCATCTCTCGCAGGTCTAGTAGGAGTCTCTATATAGGGATGGGAAGACATCTTGAATT 170
QY 214 GGTTCCTGCAGACAGCAGGACATCTCCTCAGCTCCTGATGATTTGATGTCACCCGCTG 273
DB 171 GGTTCCTGCAGACAGCAGGACATCTCCTCAGCTCCTGATGATTTGATGTCACCCGCTG 230
QY 274 CATCAGAGTCTCAGACCCGCTTTAGTGGCAGTGGGTGAGCAGACAGATTTTCAACCTCGAAA 333
DB 231 CATCAGAGTCTCAGACCCGCTTTAGTGGCAGTGGGTGAGCAGACAGATTTTCAACCTCGAAA 290
QY 334 TCAGTAGAGTGAAGCTGAGGATGAGTGGTGTGATTAATCTGTCAACAACTTTAGAGTATC 393
DB 291 TCAGTAGAGTGAAGCTGAGGATGAGTGGTGTGATTAATCTGTCAACAACTTTAGAGTATC 350
QY 394 CATTCAGTTCGGCTCGGGACAAAGTTGGAATAAAACG 433
DB 351 CATTCAGTTCGGCTCGGGACAAAGTTGGAATAAAACG 390

RESULT 14
AX935403
LOCUS          AX935403              744 bp      DNA      linear      PAT 05-JAN-2004
DEFINITION     Sequence 7 from Patent WO03089475.
ACCESSION      AX935403
VERSION        AX935403.1 GI:40642176
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Peschen, D., Fischer, R., Schillberg, S., Liao, Y.C. and Dorfmueller, S.
TITLE          Antibodies, recombinant antibodies, recombinant antibody fragments
               and fusions mediated plant disease resistance against fungi
JOURNAL        Patent: WO 03089475-A 7 30-OCT-2003;
               Fraunhofer-Gesellschaft zur Foerderung der angewandten Forschung
               e.V. (DE)
FEATURES       Location/Qualifiers
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               /note="Description of Artificial Sequence: scFv VDM1 with
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Query Match      71.7%; Score 313.2; DB 6; Length 744;
Best Local Similarity 93.4%; Pred. No. 1.1e-92;
Matches 327; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 84 GAGTCACTGGGGATATTGTGATTAACCCAGGATGAATCTTCAATCTCTGTCACTTCTGGA 143
DB 391 GCGCGGGTCTGATATTGTGATGACCCAAATGAGCTCTCTATCTCTGTCACTTCTGGA 450
QY 144 GAATCAGTTTCCATCTCCTGCAAGTCTAGTAGAGTCTCCTGTATTAAGATGGGAAGACA 203
DB 451 GAATCAGTTTCCATCTCCTGCAAGTCTAGTAGAGTCTCCTGTATTAAGATGGGAAGACA 510
QY 204 TACTTGAATTGGTTTCTGCAGAGACGAGCAATCTCCTCAGCTCCTGATGATTTGATG 263
DB 511 TACTTGAATTGGTTTCTGCAGAGACGAGCAATCTCCTCAGCTCCTGATGATTTGATG 570
QY 264 TCCACCCGTCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTC 323
DB 571 TCCACCCGTCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTC 630
QY 324 ACCCTGGAAATCAGTAGAGTGAAGCTGAGGATGTTGGGTGTGTATTAATCTGTCAACACTT 383
DB 631 ACCCTGGAAATCAGTAGAGTGAAGCTGAGGATGTTGGGTGTGTATTAATCTGTCAACACTT 690
QY 384 GTAGAGTATCCATTCACGTTCCGCTCGGGACAAAGTTGGAATAAAACG 433
DB 691 GTAGAGTATCCGCTCACGTTCCGCTCGGGACAAAGTTGGAATAAAACG 740

RESULT 15
AX935454
LOCUS          AX935454              951 bp      DNA      linear      PAT 05-JAN-2004
DEFINITION     Sequence 58 from Patent WO03089475.
ACCESSION      AX935454
VERSION        AX935454.1 GI:40642202
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Peschen, D., Fischer, R., Schillberg, S., Liao, Y.C. and Dorfmueller, S.
TITLE          Antibodies, recombinant antibodies, recombinant antibody fragments
               and fusions mediated plant disease resistance against fungi
JOURNAL        Patent: WO 03089475-A 58 30-OCT-2003;
               Fraunhofer-Gesellschaft zur Foerderung der angewandten Forschung
               e.V. (DE)
FEATURES       Location/Qualifiers
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ORIGIN
Query Match      71.7%; Score 313.2; DB 6; Length 951;
Best Local Similarity 93.4%; Pred. No. 1.2e-92;
Matches 327; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 84 GAGTCACTGGGGATATTGTGATTAACCCAGGATGAATCTTCAATCTCTGTCACTTCTGGA 143
DB 598 GCGCGGGTCTGATATTGTGATGACCCAAATGAGCTCTCTATCTCTGTCACTTCTGGA 657
QY 144 GAATCAGTTTCCATCTCCTGCAAGTCTAGTAGAGTCTCCTGTATTAAGATGGGAAGACA 203
DB 658 GAATCAGTTTCCATCTCCTGCAAGTCTAGTAGAGTCTCCTGTATTAAGATGGGAAGACA 717
QY 204 TACTTGAATTGGTTTCTGCAGAGACGAGCAATCTCCTCAGCTCCTGATGATTTGATG 263
DB 718 TACTTGAATTGGTTTCTGCAGAGACGAGCAATCTCCTCAGCTCCTGATGATTTGATG 777
QY 264 TCCACCCGTCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTC 323
DB 778 TCCACCCGTCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGACAGATTTC 837
QY 324 ACCCTGGAAATCAGTAGAGTGAAGCTGAGGATGTTGGGTGTGTATTAATCTGTCAACACTT 383

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Db	838	ACCTGGAATCAGTAGAGTGAAGGCTGAGGATGTGGTGTGTATTACTGTCAACACTT	897
Qy	384	GTAGAGTATCCATTACAGTTTCGGCTCGGGGACAAAGTTGGAATATAAAG	433
Db	898	GTAGAGTATCGGCTCACGTTTCGGTGTGGACCAAGTTGGAGCTGAAAG	947

Search completed: April 18, 2005, 14:42:36
 Job time : 1944.07 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 1714.9 Seconds
(without alignments)
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Title: US-09-674-716B-2

Perfect score: 437

Sequence: 1 aagcttacagttactcagc.....agttggaataaaacgtacg 437

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
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4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	318.8	73.0	343	2	BF023001 ux02c02.y
2	311.4	71.3	351	2	BB870732 BB870732
3	305.2	69.8	353	5	BY220367 BY220367
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6	281.2	64.3	400	2	AW912881 uf46b05.y
7	266.8	61.1	313	5	BY220511 BY220511
8	259.8	59.5	524	6	CD700306 EST16830
9	258.2	59.1	597	6	CD689298 EST5820.h
10	258.2	59.1	771	6	CB956254 AGENCOURT
11	256.6	58.7	475	6	CD699289 EST15812
12	256.6	58.7	498	6	CD699812 EST16336
13	256.6	58.7	743	6	CB987308 AGENCOURT
14	256.6	58.7	757	6	CB985283 AGENCOURT
15	256.6	58.7	817	6	CB957285 AGENCOURT
16	256	58.6	725	4	EG963055 602828068
17	255	58.4	583	6	CD684087 EST607.hu
18	255	58.4	600	6	CD700169 EST16693
19	255	58.4	739	6	CB986287 AGENCOURT
20	253.4	58.0	634	4	BM783161 K-EST0061
21	253.4	58.0	791	6	CB955891 AGENCOURT
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23	251.8	57.6	522	4	BM511309 i146b08.y
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ALIGNMENTS

RESULT 1

BF023001

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF023001 343 bp mRNA linear EST 10-OCT-2000
ux02c02.y1 Soares_thymus_2NDMT Mus musculus cDNA clone
IMAGE:3470306 5' similar to SW:KV2B MOUSE P01627 IG KAPPA CHAIN
V-II REGION VKAPPA167 PRECURSOR. ; mRNA sequence.
BF023001
BF023001.1 GI:10754334
EST.
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGi:138966

FEATURES

source

Trace considered overall poor quality
Seq primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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TGTTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento

ORIGIN		Soares and M.Fatima Bonaldo."	
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DB	125	CAATCTCTGTCACCTCTGGAGATCACTTCCATCTCTCGAGTCCTAGTAAGAGTCTCT	184
	73	CAATCTCTGTCACCTCTGGAGATCACTTCCATCTCTCGAGTCCTAGTAAGAGTCTCT	132
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	133	ATATAGGATGGGAGACATACCTGTAATGGTTCTTCGAGAGACACGAGCAATCTCTCA	192
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	193	GTCCTGATGTTATGATGTCACCCGTCAGTCAGAGTCCTAGACCGTTAGTGGCAG	252
QY	305	TGGGTACGACAGATTTTCCCTCGGAATCAGTAGAGTGAAGCTGAGGATGGGTGT	364
	253	TGGGTACGACAGATTTTCCCTCGGAATCAGTAGAGTGAAGCTGAGGATGGGTGT	312
QY	365	GTATTACTGTCAACAACCTGTAGAGTATCC	394
	313	GTATTACTGTCAACAACCTGTAGAGTATCC	342
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Best Local Similarity		96.7%; Pred. No. 1.7e-84;	
Matches 318; Conservative		0; Mismatches 11; Indels 0; Gaps 0;	
QY	24	CAGGACCTCACCATGAGGTTCTCTGTTCCAGTTTCTGGGGTGCTTATGTTCTGATCTCT	83
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DB	84	GGAGTCAGTGGGATATTGTGATACCCAGATGAATCTCAATCTCTCACTCTCGGA	143
	83	GGAGTCAGTGGGATATTGTGATACCCAGATGAATCTCAATCTCTCACTCTCGGA	142
QY	144	GAATCAGTTTCCATCTCTCGAGGTCCTAGTAAGAGTCTCTGATAAGAGTGGGAAGACA	203
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QY	264	TCCACCCGTCATCAGGAGTCTCAGACCGTTTGTAGTGCAGTGGGTGAGGACAGATTTC	323
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LOCUS		BY220367	
DEFINITION		RIKEN full-length enriched, activated spleen Mus musculus	
ACCESSION		BY220367	
VERSION		BY220367.1	
KEYWORDS		EST	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 351)	
AUTHORS		Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hirose, T., Imoto, T., Imoto, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toyota, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	
TITLE		RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)	
JOURNAL		Unpublished (2001)	
COMMENT		Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/ Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.	

and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-Format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES
source
Location/Qualifiers
1..351
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/mol_type="mRNA"
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ORIGIN
Query Match 71.3%; Score 311.4; DB 2; Length 351;
Best Local Similarity 96.7%; Pred. No. 1.7e-84;
Matches 318; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 24 CAGGACCTCACCATGAGGTTCTCTGTTCCAGTTTCTGGGGTGCTTATGTTCTGATCTCT 83
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DB 23 CAAGTTCTCAGATGAGGTTCTCTTTCAGTTTCTGGGGTGCTTATGTTCTGATCTCT 82
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QY 84 GGAGTCAGTGGGATATTGTGATACCCAGATGAATCTCAATCTCTCACTCTCGGA 143
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DB 143 GAATCAGTTTCCATCTCTCGAGGTCCTAGTAAGAGTCTCTGATAAGAGTGGGAAGACA 202
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RESULT 3
BY220367
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

MEDLINE
PUBMED
COMMENT

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Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Inotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ono, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES

source
1. .342
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F830038M23"
/tissue="activated spleen"
/clone_lib="RIKEN full-length enriched, activated spleen"

ORIGIN

Query Match 67.0%; Score 292.6; DB 5; Length 342;
Best Local Similarity 94.1%; Pred. No. 1e-78;
Matches 304; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 24 CAGGACCTCACATGAGGTTCTCTGTTTCAGTTTCTGGGGTGTCTTATGTTCTGGATCTCT 83
DB 20 CAAGTTCTCAGATGAGTGCTCTCTTTCAGTTTCTGGGGTGTCTTATGTTCTGGATCTCT 79
QY 84 GGAGTCAGTGGGATATGTTGATTAACCCAGAGTAACTCTCCAATCCTGTCACCTTCTGGA 143
DB 80 GGAGTCAGTGGGATATGTTGATTAACCCAGAGTAACTCTCCAATCCTGTCACCTTCTGGA 139
QY 144 GAATCAGTTTCCATCTCTCTGAGGCTAGTAAAGAGTCTCTCTGTATAGGATGGGAAGACA 203
DB 140 GAATCAGTTTCCATCTCTCTGAGGCTAGTAAAGAGTCTCTCTGTATAGGATGGGAAGACA 199
QY 204 TACTTGAATGGTTTCTGACAGACACAGGACAATCTCTCTGAGTCTCTGATGTTATTTGATG 263
DB 200 TACTTGAATGGTTTCTGACAGACACAGGACAAGGCTCTCTGAGTCTCTGATGTTATTTGATG 259
QY 264 TCCACCCGTGATCAGGAGTCTCAGACCGGTTTGTAGTGGAGTGGTTCAGGCACAGATTTTC 323
DB 260 TCCACCCGTGATCAGGAGTCTCAGACCGGTTTGTAGTGGAGTGGTTCAGGCACAGATTTTC 319

QY 324 ACCCTGGAATCAGTACAGTGAA 346
DB 320 AACTGGAATCAGTACAGTGAA 342
RESULT 5
BF785914
LOCUS 602112548F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4240762
DEFINITION 5', mRNA sequence.
ACCESSION BF785914
VERSION BF785914.1 GI:12090950
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 906)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9855 row: p column: 11
High quality sequence stop: 718.

FEATURES

source
1. .906
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4240762"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Kid14"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"

ORIGIN

Query Match 66.4%; Score 290; DB 2; Length 906;
Best Local Similarity 81.7%; Pred. No. 8.5e-78;
Matches 335; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
QY 24 CAGGACCTCACATGAGGTTCTCTGTTTCAGTTTCTGGGGTGTCTTATGTTCTGGATCTCT 83
DB 3 CAAGTTCTCAGATGAGTGCTCTCTTTCAGTTTCTGGGGTGTCTTATGTTCTGGATCTCT 62
QY 84 GGAGTCAGTGGGATATGTTGATTAACCCAGAGTAACTCTCCAATCCTGTCACCTTCTGGA 143
DB 63 GGAGTCAGTGGGATATGTTGATTAACCCAGAGTAACTCTCCAATCCTGTCACCTTCTGGA 122
QY 144 GAATCAGTTTCCATCTCTCTGAGGCTAGTAAAGAGTCTCTCTGTATAGGATGGGAAGACA 203
DB 123 GAGTCAGTATCCATCTCTCTGAGGCTAGTAAAGAGTCTCTCTGTATAGGATGGGAAGACA 182
QY 204 TACTTGAATGGTTTCTGACAGACACAGGACAATCTCTCTGAGTCTCTGATGTTATTTGATG 263
DB 183 GACTTGTATTTGTTCTCTACAGAGGCCAGCCAGTCTCTCAGTCTCTGATATATCGGATG 242
QY 264 TCCACCCGTGATCAGGAGTCTCAGACCGGTTTGTAGTGGAGTGGTTCAGGCACAGATTTTC 323
DB 243 TCCACCTTGGCTCAGGAGTCCAGACAGGTTTCAGTGGCAGTGGGTTCAGGAATCTGTTTC 302
QY 324 ACCCTGGAATCAGTACAGTGAAAGCTGAGGATGTTGGGTGTGTATTTACTGTCAACACTTT 383

Db	303	ACACTGAGATCAGTAGAGTGAGGCTGAGAGTGGTGTATTTACTTCTTTGACACAT	362
Qy	384	GTAGAGTATCAATTCAGCTTCGGCTCGGACAAAGTTGGAATAAAACG	433
Db	363	CTAGATATCCGTACACGTTCCGAGGGGGGACCAAGCTGGAATAAAACG	412
RESULT 6			
AW912881		400 bp mRNA linear EST 25-MAY-2000	
LOCUS		uf46b05.y1 Soares mammary gland NMLMG Mus musculus cDNA clone	
DEFINITION		IMAGE:1514385 5' similar to gb:J00560 mouse ig kappa mRNA from	
		WPC21 & other myeloma mra 3' (MOUSE);, mRNA sequence.	
ACCESSION		AW912881	
VERSION		AW912881.1	GI:8078508
KEYWORDS		EST.	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
TITLE		NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.	
JOURNAL		National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
COMMENT		Tumor Gene Index	
		Unpublished (1997)	
		Contact: Robert Strausberg, Ph.D.	
		Email: cgapsb-r@mail.nih.gov	
		This clone is available royalty-free through LLNL; contact the	
		IMAGE Consortium (info@image.llnl.gov) for further information.	
		MGI:941237	
FEATURES		Seq primer: -40RP from Gibco.	
source		Location/Qualifiers	
		1..400	
		/organism="Mus musculus"	
		/mol_type="mRNA"	
		/db_xref="taxon:10090"	
		/clone="IMAGE:1514385"	
		/sex="female (lactating)"	
		/tissue_type="mammary gland"	
		/lab_host="DH10B"	
		/clone_lib="Soares mammary gland NMLMG"	
		/note="Vector: p773D-Pac (Pharmacia) with a modified	
		polylinker; 1st strand cDNA was prepared from mammary	
		gland tissue from a lactating female, and was then primed	
		with a Not I - oligo(dT) primer. Double-stranded cDNA was	
		ligated to Eco RI adaptors (Pharmacia), digested with Not	
		I and cloned into the Not I and Eco RI sites of the	
		modified p773 vector. Library is normalized. Library	
		was constructed by Bento Soares and M. Fatima Bonaldo."	
ORIGIN			
Query Match		64.3%; Score 281.2; DB 2; Length 400;	
Best Local Similarity		81.7%; Pred.No. 3.5e-75;	
Matches		325; Conservative 0; Mismatches 73; Indels 0; Gaps 0;	
Qy	36	ATGAGGTTCTCTGTTCAGTTCTCTGGGGTCTTATGTTCTGAGTCTCTGGAGTCAGTGGG	95
Db	2	ATTCGGTACGAGGCTGTTTTCTGGGGCTCTTGTCTCTGGATCTCTGGAGCATTGGG	61
Qy	96	GATATTGTGTATACCCAGGATGAATCTTCAATCTCTGTCATCTTCTGGAGATCAGTTTCC	155
Db	62	GATATTGTGTATGACTCAGGCTGCACCCCTCTGTACCTCTCACTCTCGAGAGTCAGTATCC	121
Qy	156	ATCTCTCGAGGCTCTAGTAGTCTCTCTGTATAGGATGGGAGACATCTTGAATTGG	215
Db	122	ATCTCTCGAGGCTCTAGTAAAGTCTCTGATATTGATGTCGATCTTATTTATTTGG	181
Qy	216	TTTCTGACAGACAGGACCAATCTCTCAGCTCTCTGATGTATTGTGTCACCCCGTGA	275
Db	182	TTCTGACAGAGCCAGGCGAGTCTCTCAGCTCTCTGATATATCGGATGTCACCTTGC	241
Qy	276	TCAGGAGTCTCAGCCGGTTTATGGCAGTGGGTCTAGGACAGATTTCACCCCTGGAATC	335

Db	242	TCAGGAGTCCAGACAGGTTTCACTGCGAGTGGGTCAAGAACTCTTTTCACACTGAGATC	301
Qy	336	AGTAGAGTGAAGGCTGAGGATGTGGTGTGTATTACTGTCAACAACTGTGAGATATCCA	395
Db	302	AGTAGAGTGAAGGCTGAGGATGTGGTGTGTATTACTGTATGCAACATCTAGAAATCCG	361
Qy	396	TTCACTGCTGGCTCGGGGACAAAGTTGGAAATAAAACG	433
Db	362	TACACGTTCCGAGGGGGGACCAAGCTGGAATAAAACG	399
RESULT 7			
BY220511		313 bp mRNA linear EST 10-DEC-2002	
LOCUS		BY220511 RIKEN full-length enriched, activated spleen Mus musculus	
DEFINITION		cDNA clone F830212P03 5', mRNA sequence.	
ACCESSION		BY220511	
VERSION		BY220511.1	GI:26401613
KEYWORDS		EST.	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
TITLE		1 (bases 1 to 313)	
JOURNAL		Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,	
COMMENT		Nikaido, I., Oato, N., Saito, R., Suzuki, H., Yamanaka, I.,	
		Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,	
		Schönbach, C., Gojohori, T., Baldarelli, R., Hill, D. P., Bult, C.,	
		Hume, D. A., Quackenbush, J., Schreiml, L. M., Kanapin, A., Matsuda, H.,	
		Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,	
		Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,	
		Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,	
		Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,	
		Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,	
		Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,	
		Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,	
		Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,	
		Nemata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,	
		Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,	
		Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,	
		Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,	
		Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,	
		Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,	
		Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,	
		Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,	
		Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,	
		Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,	
		Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,	
		Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,	
		Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,	
		Rogers, J., Birney, E. and Hayashizaki, Y.	
		Analysis of the mouse transcriptome based on functional annotation	
		of 60,770 full-length cDNAs	
		Nature 420, 563-573 (2002)	
JOURNAL		12466851	
MEDLINE		22354683	
PUBMED			
COMMENT		Contact: Yoshihide Hayashizaki	
		Laboratory for Genome Exploration Research Group, RIKEN Genomic	
		Sciences Center (GSC), Yokohama Institute	
		The Institute of Physical and Chemical Research (RIKEN)	
		1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan	
		Tel: 81-45-503-9222	
		Fax: 81-45-503-9216	
		Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/	
		Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,	
		Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,	
		Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,	
		Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,	
		Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and	
		Hayashizaki, Y. Direct Submission	
		Computational Analysis of Full-Length Mouse cDNAs Compared with	
		Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)	
		Normalization and subtraction of cap-trapper-selected cDNAs to	

prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedias: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC Building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

Location/Qualifiers
 source
 1. .313
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="NOD"
 /db_xref="taxon:10090"
 /clone="F830212P03"
 /tissue_type="activated spleen"
 /clone_lib="RIKEN full-length enriched, activated spleen"

ORIGIN

Query Match 61.1%; Score 266.8; DB 5; Length 313;
 Best Local Similarity 94.2%; Pred. No. 9e-71; Indels 0; Gaps 0;
 Matches 277; Conservative 0; Mismatches 17;
 QY 24 CAGGACCTCACCATGAGTTCTCTGTTTCAGTTTCTGGGGTGGTATGTTCTGGATCTCT 83
 Db 20 CAAATTCTCAGATGAGTGTCTCTTCAGTTCTTGGGGATGCTATGTTCTGGATCTCT 79
 QY 84 GGAGTCAGTGGGATATTGTGATAACCCAGGATGAATCTCCATCTCTGATCTCTGGA 143
 Db 80 GGAGTCAGTGGGATATTGTGATAACCCAGGATGAATCTCCATCTCTGATCTCTGGA 139
 QY 144 GAATCAGTTTCCATCTCTGAGTCTAGTAGAGTCTCTGTATAGGATGGGAGACA 203
 Db 140 GAATCAGTTTCCATCTCTGAGTCTAGTAGAGTCTCTGTATAGGATGGGAGACA 199
 QY 204 TACTTGAATGTTTCTCAGAGACCAGGACAAATCTCTCAGCTCTGATGTTTGTATG 263
 Db 200 TACTTGAATGTTTCTCAGAGGCCAGGACAGTCTCTCAGCTCTGATGTTTGTATG 259
 QY 264 TCCACCCGTGCATCAGAGTCTCAGACCGTTTGTAGTGGGATGGGTCAGGCACA 317
 Db 260 TCACCCGTGCATCAGAGTCTCAGACCGTTTGTAGTGGGATGGGTCAGGCACA 313

RESULT 8

CD700306
 LOCUS EST16830 human nasopharynx Homo sapiens cDNA, mRNA linear EST 25-JUN-2003
 DEFINITION
 ACCESSION CD700306
 VERSION CD700306.1 GI:32230410
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 524)
 AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
 TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
 JOURNAL Unpublished (2003)
 COMMENT Contact: Yixin Zeng
 Cancer Center

Sun Yat-sen University
 651 Dongfeng Road East, Guangzhou 510060, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzeng@gzsums.edu.cn

FEATURES

Location/Qualifiers
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 1. .524
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="normal nasopharynx"
 /clone_lib="human nasopharynx"
 /note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 59.5%; Score 259.8; DB 6; Length 524;
 Best Local Similarity 77.4%; Pred. No. 1.5e-68;
 Matches 315; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
 QY 30 CTCACATGAGTTCTCTGTTTCAGTTTCTGGGGTGGTATGTTCTGGATCTCTGGATCT 89
 Db 50 CTCACATGAGGCTCCCTGCTCAGCTCCTGGGGTGGTATGTTCTGGATCTCTGGATCT 109
 QY 90 AGTGGGGATATTGTGATAACCCAGGATGAATCTCCATCTCTGATCTCTGGAGATCA 149
 Db 110 AGTGGGGATATTGTGATAACCCAGGATCTCCATCTCTGCTGCCGTCACCCCTGGAGCGG 169
 QY 150 GTTTCATCTCTCTCAGGCTCTAGTAGAGTCTCTGTATAGGATGGGAGACATACCTTG 209
 Db 170 GCTCCATCTCTCTCAGGCTCTAGTCAGAGCTCTCTTTATAGTATAGGATACACCTATTG 229
 QY 210 AATGTTTCTCAGAGACCAGGACAAATCTCTCAGCTCTGATGTTTGTATGTTGCCACC 269
 Db 230 GATTGTTACCTCAGAGGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTGACGTCTAAT 289
 QY 270 CTGTCATCAGAGTCTCAGACCGTTTGTAGTGGTGGTCTCAGGTCAGGACAGATTTTCCACCTG 329
 Db 290 CGGGCTCTGGGGTCCCTGACAGTTCTAGTGGAGTGGATCAGGACAGATTTTACATG 349
 QY 330 GAAATCAGTAGAGTGAAGGCTGAGGATGGGTGTGTATTACTGTCTCAACAATCTGTAGAG 389
 Db 350 ACAATCAGCAGAGTGGAGGCTGAAGATGTGGGATTATTACTGTCATGCAAGCTGTACAG 409
 QY 390 TATCCATTCAGTTCTGGCTCGGGACAAAGTTGGAAATTAACGCTAC 436
 Db 410 ACTCCCTCACTTTCGGCGAGGGACCAAGGTGGAAATCAACGAAC 456

RESULT 9

CD689298
 LOCUS EST5820 human nasopharynx Homo sapiens cDNA, mRNA linear EST 25-JUN-2003
 DEFINITION
 ACCESSION CD689298
 VERSION CD689298.1 GI:32208911
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 597)
 AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
 TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
 JOURNAL Unpublished (2003)
 COMMENT Contact: Yixin Zeng
 Cancer Center
 Sun Yat-sen University
 651 Dongfeng Road East, Guangzhou 510060, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzeng@gzsums.edu.cn

/clone="IMAGE:30228074"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC 184"
/notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
Sfil (ggccattatgcc); Site_2: Sfil (ggcgcctcgcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 58.7%; Score 256.6; DB 6; Length 743;
Best Local Similarity 76.9%; Pred. No. 1.6e-67;
Matches 313; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
QY 30 CTCACCATGAGTTCTCTGTTTCTGGGGTCTTATGTTCTGGATCTCTGGAGTC 89
DB 28 CTCACATGAGGCTCCCTGCTCAGCTCTGGGGTCTTAATGCTCTGGGTCTCTGGATCC 87
QY 90 AGTGGGATATTGTGATAACCCAGGATGAATCTTCCAACTCTGTCATCTCTGGAGATCA 149
DB 88 AGTGGGATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGCTCACCCCTGGAGCCG 147
QY 150 GTTTCATCTCTCAGGCTAGTAAGAGTCTCTCTGTATAGGATGGAGACATCTTG 209
DB 148 GCCTCCATCTCTCAGGCTAGTTCAGAGGCTCTCTGTATAGTATGATACACCTATTG 207
QY 210 AATTGGTTCTGCAGAGCAGGACAAATCTCCAGCTCTCTGATGTTATGATGTCACC 269
DB 208 GATTGGTACCTGCAGAGCAGGAGCTCTCCAGCTCTCTGATCTATTTGGCTTCTAAT 267
QY 270 CGTGCATCAGAGTCTCAGACCGGTTTGTGGCAGTGGGTCAGGCACAGATTTACCCCTG 329
DB 268 CGGCGCTCCGGGTCCTGACAGGTTTGTGGCAGTGGATGATCAGGCACAGATTTACACTG 327
QY 330 GAATCAGTATGATGAAGGCTGAGGATGTTGGTGTATTAATCTCAACAACTTTAGAG 389
DB 328 AAATCAGCAGAGTGAGGCTGAGGATGTTGGGTTTATTAATCTCATGCTCAAGCTCTACAA 387
QY 390 TATCCATTACGTTCCGCTCGGGACAAAGTTGGAATAAAGCTAC 436
DB 388 ACCCGCTCACTTTCCGGCGGAGGACCAAGTGGAGATCAACGAAC 434

RESULT 14
CB985283 757 bp mRNA linear EST 01-MAY-2003
LOCUS
DEFINITION
AGENCOURT 13650893 NIH_MGC 184 Homo sapiens cDNA clone
IMAGE:30329896 5', mRNA sequence.
CB985283
ACCESSION
VERSION
CB985283.1 GI:30279807
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 757)
AUTHORS
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDCM142 row: n column: 17
High quality sequence stop: 512.
Location/Qualifiers

FEATURES
source

1. .757
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30329896"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC 184"
/notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
Sfil (ggccattatgcc); Site_2: Sfil (ggcgcctcgcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 58.7%; Score 256.6; DB 6; Length 757;
Best Local Similarity 76.9%; Pred. No. 1.6e-67;
Matches 313; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
QY 30 CTCACCATGAGTTCTCTGTTTCTGGGGTCTTATGTTCTGGATCTCTGGAGTC 89
DB 28 CTCACATGAGGCTCCCTGCTCAGCTCTGGGGTCTTAATGCTCTGGGTCTCTGGATCC 87
QY 90 AGTGGGATATTGTGATAACCCAGGATGAATCTTCCAACTCTCTGATGTTATGATGTCACC 149
DB 88 AGTGGGATATTGTGATGACTCAGTCTCCAGCTCTCCCTGCCGCTCACCCCTGGAGCCG 147
QY 150 GTTTCATCTCTCAGGCTAGTATGATGTTCTCTGATGTTATGATGTCACC 209
DB 148 GCCTCCATCTCTCAGGCTAGTTCAGAGGCTCTGATGATGTTATGATGTCACC 207
QY 210 AATTGGTTCTGCAGAGCAGGACAAATCTCTCAGCTCTCTGATGTTATGATGTCACC 269
DB 208 GATTGGTACCTGCAGAGCAGGAGCTCTCCAGCTCTCTGATCTATTTGGGTTCTAAT 267
QY 270 CGTGCATCAGGAGTCTCAGACCGGTTTGTGGCAGTGGGTCAGGCACAGATTTACCCCTG 329
DB 268 CGGCGCTCCGGGTCCTGACAGGTTTCAAGTGGATCAGGCACAGATTTTACACTG 327
QY 330 GAATCAGTATGATGAAGGCTGAGGATGTTGGTGTATTAATCTCAACAACTTTAGAG 389
DB 328 AAATCAGTATGATGAGGTTGAGGATGTTGGGGTTTATTAATGATGCAACCTCTACAA 387
QY 390 TATCCATTACGTTCCGCTCGGGACAAAGTTTGGAAATAAAGCTAC 436
DB 388 ACTCCATTCACTTTCCGGCCCTGGGACCAAGTGGATATCAACGAAC 434

RESULT 15
CB957285
LOCUS
DEFINITION
AGENCOURT 13666811 NIH_MGC 184 Homo sapiens cDNA clone
IMAGE:30354094 5', mRNA sequence.
CB957285
ACCESSION
VERSION
CB957285.1 GI:30213402
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 817)
 NIH-MGC http://mgc.ncbi.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDCM155 row: n column: 23
 High quality sequence stop: 534.

FEATURES
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 1..817
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30354094"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 184"
 /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: SfiI (ggcgcctggcc); Site_2: SfiI (ggcgcctggcc); Library is oligo-dT primed and directionally cloned. cDNA Library was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGCCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGCGCGGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 58.7%; Score 256.6; DB 6; Length 817;
 Best Local Similarity 76.9%; Pred. No. 1.e-67;
 Matches 313; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
 QY 30 CTCACCATGAGTCTCTGTTTCAGTTCTGGGGTGGCTTATGTTCTGGATCTCTGGAGTC 89
 Db 30 CTCACATGAGGCTCCCTGCTCAGCTCTGGGGTGGCTTATGTTCTGGATCTCTGGATCC 89
 QY 90 AGTGGGATATTGTGATAACCCAGGATGAATCTCCAACTCTGCTACTTCTGGAGATCA 149
 Db 90 AGTGGGATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCAACCTGGAGAGCCG 149
 QY 150 GTTTCATCTCTGAGGCTCTAGTAAGAGTCTCTGTATAGGATGGAGACATCTTG 209
 Db 150 GCCTCCATCTCTGAGGCTCTAGTCAGAGCCTCTGCTATAGTCACTATTTGGTCTAAT 209
 QY 210 AATTGGTTCTGACAGACAGGACAACTCTCTCAGCTCTCTGATGATTTGATGTCACC 269
 Db 210 GATTGGTACCTGACAGACAGGAGGCTCTCCAGCTCTCTGATCTATTTGGTCTAAT 269
 QY 270 CGTGATCAGGAGTCTCAGACCGGTTTGTAGTGGAGTGGGTGAGGACAGATTTACCCCTG 329
 Db 270 CGGGCTCCGGGTCCTGACAGGTTTCACTGGCAGTGGATCAGGCACAGATTTTACGCTG 329
 QY 330 GAAATCAGTACAGGCTGAGGATGTTGGTGTGTTATTACTGTCAACACTTGTAGAG 389
 Db 330 AAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGATGCAAGCTCTACAA 389
 QY 390 TATCCATTACGCTTCGGGTCGGGGACAAAGTTGGAATAAAGACGAC 436
 Db 390 ACTCCACTCATTTCGGCGGAGGACCAAGGTGGAGATCAACGAAC 436

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 245.823 Seconds
(without alignments)
10523.523 Million cell updates/sec

Title: US-09-674-716B-2
Perfect score: 437
Sequence: 1 agctttacagttactcagc.....agttggaataaaacgtacg 437

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	437	100.0	437	3	Aaz34746 Mouse ant
2	366.4	83.8	429	2	Aaz34746 Sequence
3	366.4	83.8	429	2	Aaz34746 Sequence
4	317.2	72.6	340	2	Aav09791 DNA encod
5	317.2	72.6	368	2	Aav09789 DNA encod
6	316	72.3	420	2	Aav09802 DNA encod
7	313.2	71.7	744	10	ADG322298 Mouse scf
8	313.2	71.7	951	10	ADG32349 DNA encod
9	309.2	70.8	368	2	Aav09793 DNA encod
10	294	67.3	399	12	Ado43548 Nucleotid
11	293.2	67.1	464	2	Aaz34746 C242:11 M
12	293.2	67.1	464	2	Aaz34746 C242 kapp
13	289.2	66.2	399	12	Ado43552 Nucleotid
14	287.4	65.8	773	10	ACF36530 Anti-huma
15	286.8	65.6	720	12	Adm72038 ChimERIC
16	286.8	65.6	961	2	Aaz34746 Anti-toba
17	284.4	65.1	426	10	ACF36518 Anti-huma
18	284.4	64.2	825	10	Adm25795 Binding d
19	280.4	64.2	1536	10	ADD25796 Binding d
20	280.4	64.2	1696	10	ADD25797 Binding d

21	280.4	64.2	1696	10	ADG322298
22	280.4	64.2	1696	12	ADG322298
23	278	63.6	399	10	ADG322298
24	277.2	63.4	441	2	Aaz34746
25	277.2	63.4	441	2	Aaz34746
26	277.2	63.4	441	2	Aaz34746
27	277.2	63.4	441	8	ABX79221
28	276.4	63.2	399	2	Aaz34746
29	276.4	63.2	399	2	Aaz34746
30	276.4	63.2	399	3	Aaz34746
31	273	62.5	720	11	ADL23132
32	271.4	62.1	720	11	ADL23132
33	260.2	59.5	720	11	ADL23132
34	258.6	59.2	720	11	ADL23132
35	257.2	58.9	348	3	Aaz34746
36	257	58.8	720	11	ADL23132
37	257	58.8	720	11	ADL23132
38	255.6	58.5	720	3	AAAL3924
39	255.4	58.4	720	10	ADG322298
40	255.4	58.4	720	11	ADL23132
41	255	58.3	772	2	Aaz34746
42	254.6	58.3	720	3	AAAL3927
43	253.8	58.1	720	11	ADL23132
44	253.4	58.0	1081	6	ABX51811
45	253	57.9	720	3	AAAL3926

ALIGNMENTS

RESULT 1

Aaz34746

ID AAZ34746 standard; cDNA; 437 BP.

AC AAZ34746;

XX 15-FEB-2000 (first entry)

XX Mouse anti-CD23 MAb C11 light chain variable region cDNA.

XX CD23: FCER2; IgE receptor; monoclonal antibody; C11; mouse;

XX monoclonal antibody; chimeric antibody; humanised antibody;

XX complementarity determining region; CDR; autoimmune disease;

XX inflammation; arthritis; lupus erythematosus; multiple sclerosis;

XX Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

XX urticaria; nephrotic syndrome; glomerulonephritis;

XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;

XX Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;

XX graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;

XX therapy; ds.

XX Mus musculus.

XX Key Location/Qualifiers

XX CDS 3..413

XX /*tag= a

XX WO9558679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAX) GLAXO GROUP LTD.

XX Bonneyfey JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WFI; 2000-053101/04.

XX P-PSDB; AAY32261.

XX Cell receptor specific antibodies useful for treating e.g. arthritis,

XX PT

PT diabetes, multiple sclerosis and psoriasis.

XX Claim 16; Fig 2; 81pp; English.

XX This DNA sequence encodes the light chain variable region (VL) of murine
CC anti-CD23 (FCERII) monoclonal antibody C11. The invention provides
CC altered antibodies, such as chimeric or humanised antibodies (see
CC AAZ34747 and AAZ34748), which comprise sufficient of the amino acid
CC sequences of the C11 light and heavy chain complementarity determining
CC regions (see AAY32254-59) to render them capable of binding to the CD23
CC type II molecule expressed on haematopoietic cells. The antibodies are
CC used to block soluble CD23 formation in human therapy, for the treatment
CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
CC malignancies (claimed). They are also useful for studying interactions
CC between CD23 and various ligands and determining the binding agents

XX SQ Sequence 437 BP; 108 A; 93 C; 114 G; 122 T; 0 U; 0 Other;

Query Match 100.0%; Score 437; DB 3; Length 437;

Best Local Similarity 100.0%; Pred. No. 6.3e-124;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTTACAGTTACTCAGCACAGAGACCTCACCATGAGGTTCTCTGTTCAAGTTCTGG 60

DB 1 AAGCTTACAGTTACTCAGCACAGAGACCTCACCATGAGGTTCTCTGTTCAAGTTCTGG 60

QY 61 GGGTGTCTTATGTTCTGGATCTCTGGAGTCAGTGGGATATTGTGATAACCCAGGATGAAC 120

DB 61 GGGTGTCTTATGTTCTGGATCTCTGGAGTCAGTGGGATATTGTGATAACCCAGGATGAAC 120

QY 121 TCTCCAACTCTGTCACTCTGGAGATCAAGTTTCCATCTCTGAGGTCAGTAAGATGTC 180

DB 121 TCTCCAACTCTGTCACTCTGGAGATCAAGTTTCCATCTCTGAGGTCAGTAAGATGTC 180

QY 181 TCTGTATTAAGATGGAGACATCTGATTTGATTTCTGAGGATCTGAGACACAGGACATCTC 240

DB 181 TCTGTATTAAGATGGAGACATCTGATTTGATTTCTGAGGATCTGAGACACAGGACATCTC 240

QY 241 CTCAGTCTCTGATGATTTGATCTCCACCGTCATCAGAGTCTCAGACCGGTTTAGTG 300

DB 241 CTCAGTCTCTGATGATTTGATCTCCACCGTCATCAGAGTCTCAGACCGGTTTAGTG 300

QY 301 GCAGTGGGTCAGGCACAGATTTTCCACCTGGAATCAGTAGAGTGAAGGCTGAGGATGTGG 360

DB 301 GCAGTGGGTCAGGCACAGATTTTCCACCTGGAATCAGTAGAGTGAAGGCTGAGGATGTGG 360

QY 361 GTGTGTATTACTGTCAACACTTGTAGATATCCATTACGTTCCGCTCGGGACAAAGT 420

DB 361 GTGTGTATTACTGTCAACACTTGTAGATATCCATTACGTTCCGCTCGGGACAAAGT 420

QY 421 TGGAAATAAAACCTACG 437

DB 421 TGGAAATAAAACCTACG 437

RESULT 2

AAQ12056

ID AAQ12056 standard; DNA; 429 BP.

XX AAQ12056;

AC AAQ12056;

XX 25-MAR-2003 (revised)

DT 15-AUG-1991 (first entry)

XX Sequence encoding light (kappa) chain variable region of murine 2E12

DE immunoglobulin.

XX

KW Chimeric antibodies; immunoconjugates; HIV; AIDS; ss.

XX Mus musculus.

XX Key Location/Qualifiers

OS 34.429

FT /*tag= a

FT /product= "mouse Mab 2E12 L(kappa)-chain variable region"

XX WO9107493-A.

XX 30-MAY-1991.

XX 13-NOV-1989; 89US-00433730.

XX 13-NOV-1989; 89US-00433730.

XX (XOMA) XOMA CORP.

XX (GREG) GREEN CROSS CORP.

XX Better MD, Horwitz AH, Ghoshdasti P, Robinson R;

XX WPI; 1991-178105/24.

XX P-PSDB; AAR12354.

XX New chimeric mouse-human antibodies - used to detect, kill and remove HIV

XX -1 antigen from sample.

XX Disclosure; Fig 1; 107pp; English.

XX This sequence encodes the light (kappa)- chain variable (V) region of a
CC mouse monoclonal antibody (Mab), 2E12, specific for an HIV-1 viral
CC antigen. It is used in the construction of a chimeric Mab comprising
CC heavy and light chains having murine V regions and human C regions. The
CC chimeric Mabs are more effective than murine Mab 2E12 since they have an
CC increased compatibility in humans. The heavy and light chain V-regions
CC are joined by manipulating their respective joining (J) regions, to
CC generate restriction enzyme recognition sites. The chimeric Mabs can be
CC used as immuno- conjugates, in association with e.g. toxins for HIV
CC treatment. They can also be used in diagnosis of HIV. See also AAQ12057-
CC 63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003
CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)

XX SQ Sequence 429 BP; 103 A; 92 C; 120 G; 114 T; 0 U; 0 Other;

Query Match 83.8%; Score 366.4; DB 2; Length 429;

Best Local Similarity 93.6%; Pred. No. 3.2e-102;

Matches 382; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 24 CAGGACCTCACCATCAGGTTCTCTGTTCAAGTTTCTGGGGTCTTATGTTCTGGATCTCT 83

DB 22 CAAGTTCTCAGATCAGGTTCTCTCTCAGTTTCTGGGGTCTTATGTTCTGGATCTCT 81

QY 84 GGAGTCAGTGGGATATTGTGATACCCAGAGTAACTCTCAATCTCTCTCACTTCTGA 143

DB 82 GGAGTCAGTGGGATATTGTGATACCCAGAGTAACTCTCAATCTCTCTCACTTCTGA 141

QY 144 GAATCAGTTTCCATCTCTGTCAGGTCCTAGTAGAGTCTCTCTATATAAGATGGAGACA 203

DB 142 GAATCAGTTTCTCTCTGTCAGGTCCTAGTAGAGTCTCTCTATATAAGATGGAGACA 201

QY 204 TACTTGAATTGGTTTCTGCAGAGACAGGACAACTCTCTCAGCTCTCTGATGTTTATGATG 263

DB 202 TACTTGAATTGGTTTCTGCAGAGACAGGACAACTCTCTCAGCTCTCTGATGTTTATGATG 261

QY 264 TCCACCCCGTCATCAGGAGTCTCAGACCGGTTTATGTCAGTGGGTGAGGCACAGATTTC 323

DB 262 TCCACCCCGTCATCAGGAGTCTCAGACCGGTTTATGTCAGTGGGTGAGGCACAGATTTC 321

QY 324 ACCCTGGAAATCAGTAGAGTGAAGCTCAGGATGTCGTTTACTGTCTCAACACTT 383

DB 322 ACCCTGGAAATCAGTAGAGTGAAGCTCAGGATGTCGTTTACTGTCTCAACACTT 381

QY 384 GTAGAGTATCCATTACAGTTCGGCTCGGGGACAAAGTTGGAATAAAA 431
 Db 382 GTAGAGTATCCGTACACATTTCGGAGGGGGACCAAGCTGGAATAAAA 429

RESULT 3

AAQ12012
 ID AAQ12012 standard; DNA; 429 BP.

XX AC AAQ12012;
 XX 25-MAR-2003 (revised)
 DT 19-AUG-1991 (first entry)

XX Sequence encoding mouse MAb 2E12 L chain V region.
 DE HIV-1; chimera; ds.
 KW Mus sp.

XX Key Location/Qualifiers
 FH CDS 34..429
 FT /*tag= a
 FT /*tag= a

XX WO9107494-A.

XX 30-MAY-1991.

XX 13-NOV-1989; 89US-00433703.

XX 13-NOV-1989; 89US-00433703.

XX (XOMA) XOMA CORP.

PA (GREG) GREEN CROSS CORP.

PA (ZOMA-) ZOMA CORP.

PI Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;

XX WPI; 1991-178106/24.

DR P-PSDB; AAR12232.

XX New chimeric mouse human antibodies - used in treatment, diagnosis and prophylaxis of HIV infections.

XX Disclosure; Fig 1; 108pp; English.

XX The mouse VL gene product may be used to produce chimeric mouse- human Abs against HIV-1 comprising human Ig constant regions and murine variable regions. These novel sequence are useful in treatment, diagnosis and prophylaxis of HIV infections, and may be produced by a bacterial, yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 429 BP; 103 A; 92 C; 120 G; 114 T; 0 U; 0 Other;

Query Match 83.8%; Score 366.4; DB 2; Length 429;
 Best Local Similarity 93.6%; Pred. No. 3.2e-102;
 Matches 382; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 24 CAGGACTCACATGAGGTCTCTGTTTCAGTTCTGGGGTGCTTATGTTCTGGATCTCT 83

Db 22 CAAGTTCTCAGAATGAGGTCTCTCTTCAGTTCTGGGGTGCTTATGTTCTGGATCTCT 81

QY 84 GGAGTCAGTGGGATATTGGATAACCCAGGATGAACTCTCCAACTCTGTCACCTCTGGA 143

Db 82 GGAGTCAGTGGGAGATTGGATAACCCAGGATGAACTCTCCAACTCTGTCACCTCTGGA 141

QY 144 GAATCAGTTCCATCTCTCAGGTCTAGTAAGAGTCTCTCTGTAAGGATGGGAAGACA 203

Db 142 GAATCAGTTCTCTCTCAGGTCTAGTAAGAGTCTCTCTGTAAGGATGGGAAGACA 201

QY 204 TACTTGAATGGTTTCTGCAGACACCAAGGACAATCTCCTCAGTCTCTGATGTTTGTG 263

|||||

Db 202 TACTTGAGTTGGTTTCTGCAGAGACCAGGACAATCTCCGAGTCTCTGATCTATCTGATG 261
 QY 264 TCCACCCGTCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTCAGGCACAGATTTC 323
 Db 262 TCCACCCGTTATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTCAGGAACAGATTTC 321
 QY 324 ACCCTGGAATCAGTAGAGTGAAAGGCTGAGGATGTGGGTGTGTATTACTCTCAACAATT 383
 Db 322 ACCCTGGAATCAGTGGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTCTCAACAATT 381
 QY 384 GTAGAGTATCCATTACAGTTCGGCTCGGGGACAAAGTTGGAATAAAA 431
 Db 382 GTAGAGTATCCGTACACATTTCGGAGGGGGACCAAGCTGGAATAAAA 429

RESULT 4

AAV09791
 ID AAV09791 standard; cDNA; 340 BP.

XX AC AAV09791;
 XX 16-JUN-1998 (first entry)

XX DNA encoding the light chain of the catalytic antibody 3B9.

XX Variable domain; lambda light chain; catalytic antibody; degradation; cocaine; cocaine transition state analogue; TSA; benzoic acid;

XX phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment; overdose; addiction; ss.

XX Mus sp.

XX Key Location/Qualifiers
 FH CDS 1..340
 FT /*tag= a
 FT /*tag= a

XX WO9749800-A1.
 XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US010965.

XX 25-JUN-1996; 96US-00672345.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

XX P-PSDB; AAW39801.

XX New catalytic antibodies able to decompose cocaine, single-chain analogues - used to treat cocaine overdose and addiction, required in far smaller doses than antibodies that antagonise cocaine by simply binding.

XX Disclosure; Fig 17; 147pp; English.

XX The present sequence encodes the light chain of a catalytic antibody which is capable of degrading cocaine. A series of cocaine transition state analogues (TSAs) were prepared and used to immunise mice for production of hybridomas. Catalytic antibodies were identified by their capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The antibodies reduce the concentration of cocaine in a subject, and are used particularly for the treatment of an overdose. They are also used for treating addiction (by reducing the in vivo concentration that can be achieved)

XX Sequence 340 BP; 86 A; 72 C; 88 G; 93 T; 0 U; 1 Other;

Query Match 72.6%; Score 317.2; DB 2; Length 340;
 Best Local Similarity 96.2%; Pred. NO. 4e-87;
 Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required in far
PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX
XX
PS Disclosure; Fig 23; 147pp; English.
XX

CC The present sequence encodes the light chain of a catalytic antibody
CC which is capable of degrading cocaine. A series of cocaine transition
CC state analogues (TSAs) were prepared and used to immunise mice for
CC production of hybridomas. Catalytic antibodies were identified by their
CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
CC antibodies reduce the concentration of cocaine in a subject, and are used
CC particularly for the treatment of an overdose. They are also used for
CC treating addiction (by reducing the in vivo concentration that can be
CC achieved)

XX Sequence 420 BP; 98 A; 95 C; 115 G; 108 T; 0 U; 4 Other;

Query Match 72.3%; Score 316; DB 2; Length 420;
Best Local Similarity 95.6%; Pred. No. 1e-86;
Matches 325; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 94 GGGATATTGTATAACCCAGGATGAACCTCTCCAACTCTGTCACTTCTGGAGAATCAGTTT 153
DB 51 GCGATATGGTGTATGACGCGAGGATGAACCTCTCCAACTCTGTCACTTCTGGAGAATCAGTTT 110
QY 154 CCATCTCTCCAGGCTCTAGTAACAGTCTCTGTATTAAGGATGGGAACATACCTCAATT 213
DB 111 CCATCTCTCCAGGCTCTAGTAACAGTCTCTGTATTAAGGATGGGAACATACCTCAATT 170
QY 214 GGTTCCTGCAGACAGCAGAGCAATCTCTCAGCTCTCTGATGTATTTGATGTCACCCGCTG 273
DB 171 GGTTCCTGCAGACAGCAGAGCAATCTCTCAGCTCTCTGATGTATTTGATGTCACCCGCTG 230
QY 274 CATCAGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGCAAGATTTTCACTTGAAAA 333
DB 231 CATCAGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGCAAGATTTTCACTTGAAAA 290
QY 334 TCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATC 393
DB 291 TCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATC 350
QY 394 CATTCAGTTTCGGCTCGGGGACAAAGTTGGAATAAAACG 433
DB 351 CATTCAGTTTCGGCTCGGGGACAAAGTTGGAATAAAACG 390

RESULT 7
ADG32298
ID ADG32298 standard; cDNA; 744 BP.

XX AC ADG32298;

XX 26-FEB-2004 (first entry)

XX Mouse scFV VDM1 antibody cDNA targeted against V_dahliae SeqID 7.
XX mouse; murine; scFV; gene; ss; anti-fungal peptide; AFP; scFV;
XX disease resistant; transgenic; plant; fungal infection; antibody;
XX pathogen-specific antibody; fungicidal; agriculture.
XX Mus sp.

XX WO2003089475-A2.

XX 30-OCT-2003.

XX 14-APR-2003; 2003WO-EP003852.

XX 22-APR-2002; 2002EP-00008929.

XX 28-MAY-2002; 2002EP-00011807.

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(FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

Peschchen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;

WPI: 2003-854088/79.

P-FSDB; ADG32323.

XX New fusion protein comprising an anti-fungal protein or peptide and an
XX antibody fragment, useful in agriculture and horticulture for producing
XX Ascomyceta-resistant transgenic plants, plant cells or plant tissues.

XX Claim 25; SEQ ID NO 7; 47pp; English.

XX This invention relates to a novel fusion protein comprising an anti-
XX fungal protein or peptide (AFP) and an antibody fragment (scFV).

XX Specifically, it refers to AFPs recognizing an epitope of an Ascomyceta
XX and a cellular targeting sequence, which can be used to generate disease
XX resistant transgenic plants that are protected against fungal infection.

XX Accordingly, a method is described for antibody based resistance in
XX plants such that the undesirable and expensive chemical controls often
XX used in agriculture are not required. The present invention provides
XX antibodies, recombinant antibodies and fragments thereof, as well as
XX fusion proteins that can be used as pathogen-specific antibodies targeted

XX to different plant cell compartments. As such, these fungicidal agents
XX confer a broad spectrum of disease resistance in both economically
XX important crops and ornamental plants. This polynucleotide is a cDNA
XX sequence encoding an antibody of the invention.

XX Sequence 744 BP; 181 A; 165 C; 218 G; 180 T; 0 U; 0 Other;

Query Match 71.7%; Score 313.2; DB 10; Length 744;
Best Local Similarity 93.4%; Pred. No. 9.2e-86;
Matches 327; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 84 GGAGTCAGTGGGGATATTGTGATTAACCCAGGATGAACCTCTCCAACTCTGTCACTTCTGGA 143
DB 391 GCGCGCGGTTCTGATATTGTGATGACCCCAAAATGAGCTCTCTATCTGTCACTTCTGGA 450

QY 144 GAATCAGTTTCCATCTCTCCAGGCTCTAGTAAGAGTCTCTGTATAAGGATGGGAAGACA 203
DB 451 GAATCAGTTTCCATCTCTCCAGGCTCTAGTAAGAGTCTCTATATAAGGATGGGAAGACA 510

QY 204 TACTTGAATTGGTTTCTGCAGAGACAGGACAATCTCTCAGCTCTCTGATGTATTTGATG 263
DB 511 TACTTGAATTGGTTTCTGCAGAGACAGGACAATCTCTCAGCTCTCTGATGTATTTGATG 570

QY 264 TCCACCCGTGCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTC 323
DB 571 TCCACCCGTGCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTC 630

QY 324 ACCCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTT 383
DB 631 ACCCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTT 690

QY 384 GTAGAGTATCCATTACAGTTTCGGCTCGGGGACAAAGTTGGAATAAAACG 433
DB 691 GTAGAGTATCCGCTCAGGTTCCGCTGCGGACCAAGTTGGAGCTGAAACG 740

RESULT 8
ADG32349
ID ADG32349 standard; DNA; 951 BP.

XX AC ADG32349;

XX 26-FEB-2004 (first entry)

XX DNA encoding the precursor fusion protein of AFP AG-scFV VDM1 SeqID 58.

XX scFV; ds; anti-fungal peptide; AFP; scFV; disease resistant; transgenic;

XX plant; fungal infection; antibody; pathogen-specific antibody;

XX fungicidal; agriculture; mouse; chimeric; murine; gene.

OS Chimeric.
OS Synthetic.
OS Aspergillus giganteus.
OS Mus musculus.

XX WO2003089475-A2.

XX 30-OCT-2003.

XX 14-APR-2003; 2003WO-EP003852.

XX 22-APR-2002; 2002EP-00008929.

XX 28-MAY-2002; 2002EP-00011807.

XX (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

XX Peschen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;

XX WPI; 2003-854088/79.

XX P-PSDB; ADG32360.

XX New fusion protein comprising an anti-fungal protein or peptide and an antibody fragment, useful in agriculture and horticulture for producing Ascomyceta-resistant transgenic plants, plant cells or plant tissues.

XX Example 15; SEQ ID NO 58; 47pp; English.

XX This invention relates to a novel fusion protein comprising an anti-fungal protein or peptide (AFP) and an antibody fragment (scFv). Specifically, it refers to AFPs recognizing an epitope of an Ascomyceta and a cellular targeting sequence, which can be used to generate disease resistant transgenic plants that are protected against fungal infection. Accordingly, a method is described for antibody based resistance in plants such that the undesirable and expensive chemical controls often used in agriculture are not required. The present invention provides antibodies, recombinant antibodies and fragments thereof, as well as fusion proteins that can be used as pathogen-specific antibodies targeted to different plant cell compartments. As such, these fungicidal agents confer a broad spectrum of disease resistance in both economically important crops and ornamental plants. This polynucleotide is a DNA sequence encoding a precursor fusion protein of the order [AFP - linker - antibody fragment] of the invention.

XX Sequence 951 BP; 236 A; 221 C; 287 G; 207 T; 0 U; 0 Other;

Query Match 71.7%; Score 313.2; DB 10; Length 951;
Best Local Similarity 93.4%; Pred. No. 1e-85; Indels 0; Gaps 0;
Matches 327; Conservative 0; Mismatches 23;

QY 84 GGAGTCAGTGGGATATTGTGATACCCAGGATGAACCTCCAACTCTGTCTCACTTCTGGA 143

DB 598 GCGCGGGTCTGATATTGTGATGACCCAAATGAGCTCTCTATCTCTGCTCACTTCTGGA 657

QY 144 GAATCAGTTTCCATCTCCCTGCGAGGTCTAGTAGAGTCTCTGTATAGGATGGGAGACA 203

DB 658 GAATCAGTTTCCATCTCCCTGCGAGGTCTAGTAGAGTCTCTGTATAGGATGGGAGACA 717

QY 204 TACTTGAATTGGTTTCTGAGAGACCCAGGACAACTCTCCAGCTCTCTGATGTATTGTATG 263

DB 718 TACTTGAATTGGTTTCTGAGAGACCCAGGACAACTCTCCAGCTCTCTGATGTATTGTATG 777

QY 264 TCCACCCGTCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTC 323

DB 778 TCCACCCGTCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTC 837

QY 324 ACCCTGGAATCAGTAGAGTGAAGCTGAGGATGGGTGTGTATTACTGTCAACAACCTT 383

DB 838 ACCCTGGAATCAGTAGAGTGAAGCTGAGGATGGGTGTGTATTACTGTCAACAACCTT 897

QY 384 GTAGAGTATCCATTACGTTTCGGCTCGGGGACAAAGTTTGGAAATAAAACG 433

DB 898 GTAGAGTATCCGCTACGTTTCGGCTCGGGGACAAAGTTTGGAGCTGAACG 947

RESULT 9

AAV09793

XX ID AAV09793 standard; cDNA; 368 BP.

XX AC AAV09793;

XX DT 18-JUN-1998 (first entry)

XX DE DNA encoding the light chain of the catalytic antibody 6A12.

XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction; ss.

XX OS Mus sp.

XX FH Key Location/Qualifiers

XX FT 1..339

XX FT /*tag= a

XX FT /note= "no stop codon given"

XX PN WO9749800-A1.

XX PD 31-DEC-1997.

XX PP 25-JUN-1997; 97WO-US010965.

XX PR 25-JUN-1996; 96US-00672345.

XX PA (UYCO) UNIV COLUMBIA NEW YORK.

XX PI Landry DW;

XX WPI; 1998-077166/07.

XX P-PSDB; AAW39886.

XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required in far
PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX Disclosure; Fig 19; 147pp; English.

XX The present sequence encodes the light chain of a catalytic antibody
CC which is capable of degrading cocaine. A series of cocaine transition
CC state analogues (TSAs) were prepared and used to immunise mice for
CC production of hybridomas. Catalytic antibodies were identified by their
CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
CC antibodies reduce the concentration of cocaine in a subject, and are used
CC particularly for the treatment of an overdose. They are also used for
CC treating addiction (by reducing the in vivo concentration that can be
CC achieved)

XX Sequence 368 BP; 95 A; 80 C; 93 G; 100 T; 0 U; 0 Other;

Query Match 70.8%; Score 309.2; DB 2; Length 368;
Best Local Similarity 94.7%; Pred. No. 1.2e-84; Indels 0; Gaps 0;
Matches 320; Conservative 0; Mismatches 18;

QY 96 GATATTGTGATAACCCAGGATGAACCTCTCCAACTCTGTCACTCTCTGGAGAAATCAGTTTCC 155

DB 1 GATATTGTGATGATGCGAAGATGAACCTCTCCAACTCTGTCACTCTCTGGAGAAATCAGTTTCC 60

QY 156 ATCTCTCCAGTCTAGTAAGAGTCTCTGTATAGGATGGGAGACATCTTGAATTGG 215

DB 61 ATCTCTCCAGTCTAGTAGGAGTCTCTATATAGGATGGGAGACATCTTGAATTGG 120

QY 216 TTCTTCGACAGACACAGGACAACTCTCTCAGCTCTCTGATGTATTTGATCTCCACCCGTGCA 275

DB 121 TTTCTGACAGACACAGGACAACTCTCTCAGCTCTCTGATGTATTTGATCTCCACCCGTGCA 180

QY 276 TCAGAGTCTCAGACCCGGTTTGTAGTGGCAGTGGGTTCAGGCACAGATTTTCCCTGGAAATC 335

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Db      181  TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTCACCTCGGAATC 240
QY      336  AGTAGAGTGAAGCTCAGGAGTGGGTGCTATTACTGTCAACAACCTGTGAGAGTATCCA 395
Db      241  AGTAGAGTGAAGCTCAGGAGTGGGTGCTATTACTGTCAACAACCTGTGAGAGTATCCA 300
QY      396  TTCACGTTCCGCTCGGGGACAAAAGTTGGAAATAAAACG 433
Db      301  TTCACGTTCCGCTCGGGGACAAAATTGGAGATAAAACG 338

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RESULT 10

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AD043548
ID      AD043548 standard; DNA; 399 BP.
XX
AC      AD043548;
XX
DT      29-JUL-2004 (first entry)
XX
DE      Nucleotide sequence of murine A34 variable light chain clone 209-970.
XX
KW      human; A34 protein; A33-like 3 protein; A33/JAM family; chromosome X;
KW      chromosome 1; cancer; oesophageal cancer; ovarian cancer; stomach cancer;
KW      gene; ss; antibody.
XX
OS      Mus musculus.
XX
FH      Key
FT      CDS

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Location/Qualifiers

```

FT      1..399
FT      /tag= a
FT      /partial
FT      /product= "A34 variable light chain"
XX

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WO2004037999-A2.

06-MAY-2004.

23-OCT-2003; 2003WO-US033707.

23-OCT-2002; 2002US-0420285P.

(LUDW-) LUDWIG INST CANCER RES.

Scanlan M, Ritter G, Old L, Jungbluth A;

WPI; 2004-365509/34.

P-PSDB; AD043549.

New pure immunoglobulin molecule that binds specifically to A34 antigen, useful in preparing a composition for diagnosing or treating cancer.

Example 4; Fig 21; 99pp; English.

The present sequence encodes a murine A34 variable light chain. The specification describes A34 and A33-like 3 proteins, and immunoglobulin molecules that bind specifically to their antigens. A34 and A33-like 3 proteins are members of the A33/JAM family. The A34 gene is mapped to chromosome X, and the A33-like 3 gene is mapped to chromosome 1. Immunoglobulin molecules of the invention useful in preparing a composition for diagnosing or treating cancer, especially oesophageal, ovarian and stomach cancers.

Sequence 399 BP; 87 A; 94 C; 109 G; 109 T; 0 U; 0 Other;

Query Match 67.3%; Score 294; DB 12; Length 399;

Best Local Similarity 83.7%; Pred. No. 5.8e-80;

Matches 333; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 36 ATGAGTTCCTCTCAGTTTCGGGGTGGCTTATGTTCTGGATCTCTGAGTCAGTGGG 95

1 ATGAGTGGCTTGTTCAGTTTCGGGGCTGCTTGTCTCTGGATCCTCGAGCCATTGGG 60

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QY      96  GATATTGTGATAACCCAGGATGAACCTCTCAATCTCTGTCACTTCTGGAGAAATCAGTTTCC 155
Db      61  GATATTGTGATGACTCAGGCTGCACCTCTGTCCCTGTCACTCTGGAGAGTCAGTATCC 120
QY      156  ATCTCTCTGAGCTCTAGTAAGAGTCTCCCTGTATAAGGATGGGAGACATACCTTGAATTGG 215
Db      121  ATCTCTCTGAGGCTCTAGTACGAGTCTCTCTGCATAGTAATGGCAACACTTACTTTGTATTGG 180
QY      216  TTTCTGCAGAGACCCAGGACAAATCTCTCAGCTCCTGATGTATTGTGATGTCACCCCGTGCA 275
Db      181  TTTCTGCAGAGCCAGGCGCAGTCTCTCAGCTCCTGATATATCGGATGTCACACTTGGC 240
QY      276  TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTCAACCTTGGAAATC 335
Db      241  TCAGGAGTCCAGACAGAGTTTCAGTGGCAGTGGGTGAGGACCAACTGGAAATAAAACG 300
QY      336  AGTAGAGTGAAGCTCAGGATGTTGGGTGTTACTGTCAACAACCTTGTAGAGTATCCA 395
Db      301  AGTAGAGTGGAGCTGAGGATGTTGGGTATTTATTACTGTATGCAACATCTAGAATATCCT 360
QY      396  TTCACGTTCCGCTCGGGGACAAAAGTTGGAAATAAAACG 433
Db      361  TTCACGTTCCGAGGGGGGACCAAACTGGAAATAAAACG 398

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RESULT 11

AAQ33097

ID AAQ33097 standard; DNA; 464 BP.

AC AAQ33097;

DT 25-MAR-2003 (revised)

DT 06-MAY-1993 (first entry)

DE C242:11 MAB kappa chain variable region coding sequence.

Kappa; chain; heavy; MAB; monoclonal antibody; C242:11; murine; IgG; hybridoma; cell line; spleen; human; colonic; adenocarcinoma; myeloma; Sp2/0; antigen; endocytosis; ss.

OS Synthetic.

Key

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FH      Key
FT      CDS
FT      /tag= a
FT      misc_RNA
FT      /tag= b
FT      /note= "Kappa variable region, VK"
FT      misc_RNA
FT      /tag= c
FT      /note= "Start of kappa constant region, CK"
XX

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EP521842-A2.

07-JAN-1993.

03-JUL-1992; 92EP-00850166.

03-JUL-1991; 91SE-00002074.

(KABI) KABI PHARMACIA AB.

(PHAA) PHARMACIA & UPJOHN AB.

Lindholm L, Holmgren J, Lind P;

WPI; 1993-002345/01.

P-PSDB; AAR30454.

Monoclonal antibody reacting with CA-242 antigen - obtd. by culturing hybridoma cell line C242:11 or mutants, useful for diagnosis and therapy of pancreatic or colorectal cancers.

Disclosure; Fig 3; 15pp; English.

Tue Apr 19 06:15:00 2005

us-09-674-716b-2.rng

XX The sequence given encodes the kappa chain variable region of the
CC monoclonal antibody (MAB), C242:II. C242:II is a monoclonal murine Ab of
CC IgG class produced when culturing in an appropriate medium a hybridoma
CC cell line obtained by fusing spleen cells from a mouse, which has been
CC immunised with a human colonic adenocarcinoma cell line, with the murine
CC myeloma cell line Sp2/0. C242:II when bound to a cell surface antigen is
CC capable of being endocytosed or internalised into cells. See also
CC AAR30448-53. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25
CC -MAR-2003 to correct PA field.)
XX
SQ Sequence 464 BP; 98 A; 109 C; 130 G; 127 T; 0 U; 0 Other;

Query Match 67.1%; Score 293.2; DB 2; Length 464;
Best Local Similarity 82.2%; Pred. No. 1.1e-79;
Matches 337; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 24 CAGGACCTCACCATGAGTCTCTGTTTCAGTTCTTGGGGTCTTATGTTCTGGATCTCT 83
DB 30 CAAAGTTCTCAGAAATGAGTGCCTAGCTGAGTTCTCTGGGCTCTTGTCTGGATCCCT 89
QY 84 GGAGTCAGTGGGATATTGTGATAACCCAGGATGAATCTTCCAAATCCTGTCTCACTTCTGGA 143
DB 90 GGAGCCATTGGGATATTGTGATGACTCAGGCTGCACCTCTGTACCTGTCACTCTGGA 149
QY 144 GAATCAGTTTCCATCTCCTGCAGGCTCTAGTAAGAGTCTCTGTATAAGGATGGGAACA 203
DB 150 GAGTCAGTATCCATCTCTGCAGGCTCTAGTAAGAGTCTCTGTATAAGGATGGGAACA 209
QY 204 TACTTGAATTTGTTCTGCAGACACGAGGATCTCTCAGCTCTCTGATGATTGATG 263
DB 210 TACTTGAATTTGTTCTGCAGACACGAGGATCTCTCAGCTCTCTGATGATTGATG 269
QY 264 TCCACCGTGCATCAGGAGTCTCAGACCGGTTTGTAGTGGAGTGGGTGAGGACAGATTTC 323
DB 270 TCCACCGTGCATCAGGAGTCTCAGACCGGTTTGTAGTGGAGTGGGTGAGGACAGATTTC 329
QY 324 ACCCTGGAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTATTACTGTCAACAATT 383
DB 330 ACAGTGAATTCAGTAGAGTGGAGGCTGAGGATGTGGGTGTATTACTGTCAACAATT 389
QY 384 GTAGATATCCATTACAGTTCCGCTCGGGACAAAGTTGGAATAAAGC 433
DB 390 CTAGATATCCGTTACAGTTCCGCTCGGGACAAAGTTGGAATAAAGC 439

RESULT 12
ID AAR36950 standard; cDNA; 464 BP.
AC AAR36950;
XX
XX 10-JUN-1993 (first entry)
DE C242 kappa chain variable region coding sequence.
XX
XX C242:II; kappa; variable; region; complementarity determining region;
KW hybridoma; CDR; grafting; cytotoxic; conjugate; gastrointestinal; chain;
KW tumour; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
CDS 42..464
FT /*tag= a
FT 102..353
FT /*tag= b
FT /*note= "Vk"
FT 171..218
FT /*tag= c
FT /*label= CDR1
FT /*note= "Claim 9"
FT 264..284
FT misc_feature

FT /*tag= d
FT /*label= CDR2
FT /*note= "Claim 9"
FT 354..464
FT /*tag= f
FT /*note= "Ck"
FT 381..407
FT /*tag= e
FT /*label= CDR3
FT /*note= "Claim 9"
XX
XX AU9219430-A.
XX
XX 07-JAN-1993.
XX
XX 03-JUL-1992; 92AU-00019430.
XX
XX 03-JUL-1991; 91GB-00014399.
XX
XX (ICIL) IMPERIAL CHEM IND PLC.
XX (KABI) KABI PHARMACIA AB.
XX
XX Fitton JE, Wright AF, Blakey DC, Lindholm L, Lind P, Holmgren J;
XX WPI; 1993-059205/08.
XX P-PSDB; AAR32541.
XX
XX Immuno-toxin conjugates of e.g. C242 antibody and ricin A - for treating
XX gastrointestinal tumours, e.g. colorectal tumours.
XX
XX Disclosure; Fig 18; 120pp; English.
XX
XX This sequence encodes the C242:II kappa chain variable region derived
XX from the C242:II hybridoma. The complementarity determining regions
XX (CDRs) from this sequence may be used in CDR grafting in the production
XX of a cytotoxic conjugate which is targeted to gastrointestinal tumours.
XX These conjugates are useful in reducing tumour size
XX
XX Sequence 464 BP; 98 A; 109 C; 130 G; 127 T; 0 U; 0 Other;

Query Match 67.1%; Score 293.2; DB 2; Length 464;
Best Local Similarity 82.2%; Pred. No. 1.1e-79;
Matches 337; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 24 CAGGACCTCACCATGAGTCTCTGTTTCAGTTCTTGGGGTCTTATGTTCTGGATCTCT 83
DB 30 CAAAGTTCTCAGAAATGAGTGCCTAGCTGAGTTCTCTGGGCTCTTGTCTGGATCCCT 89
QY 84 GGAGTCAGTGGGATATTGTGATAACCCAGGATGAATCTTCCAAATCCTGTCTCACTTCTGGA 143
DB 90 GGAGCCATTGGGATATTGTGATGACTCAGGCTGCACCTCTGTACCTGTCACTCTGGA 149
QY 144 GAATCAGTTTCCATCTCCTGCAGGCTCTAGTAAGAGTCTCTGTATAAGGATGGGAACA 203
DB 150 GAGTCAGTATCCATCTCTGCAGGCTCTAGTAAGAGTCTCTGTATAAGGATGGGAACA 209
QY 204 TACTTGAATTTGTTCTGCAGACACGAGGATCTCTCAGCTCTCTGATGATTGATG 263
DB 210 TACTTGAATTTGTTCTGCAGACACGAGGATCTCTCAGCTCTCTGATGATTGATG 269
QY 264 TCCACCGTGCATCAGGAGTCTCAGACCGGTTTGTAGTGGAGTGGGTGAGGACAGATTTC 323
DB 270 TCCACCGTGCATCAGGAGTCTCAGACCGGTTTGTAGTGGAGTGGGTGAGGACAGATTTC 329
QY 324 ACCCTGGAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTATTACTGTCAACAATT 383
DB 330 ACAGTGAATTCAGTAGAGTGGAGGCTGAGGATGTGGGTGTATTACTGTCAACAATT 389
QY 384 GTAGATATCCATTACAGTTCCGCTCGGGACAAAGTTGGAATAAAGC 433
DB 390 CTAGATATCCGTTACAGTTCCGCTCGGGACAAAGTTGGAATAAAGC 439

RESULT 13
 ADO43552 standard; DNA; 399 BP.
 XX
 AC ADO43552;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Nucleotide sequence of murine A34 variable light chain clone 209-564.
 XX
 KW human; A34 protein; A33-like 3 protein; A33/JAM family; chromosome X;
 KW chromosome 1; cancer; oesophageal cancer; ovarian cancer; stomach cancer;
 KW gene; ss; antibody.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..399
 FT /tag= a
 FT /partial
 FT /product= "A34 variable light chain"
 XX
 PN WO2004037999-A2.
 XX
 PD 06-MAY-2004.
 XX
 PF 23-OCT-2003; 2003WO-US033707.
 XX
 PR 23-OCT-2002; 2002US-0420285P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Scanlan M, Ritter G, Old L, Jungbluth A;
 XX
 DR WPI; 2004-365509/34.
 DR P-PSDB; ADO43553.
 XX
 PT New pure immunoglobulin molecule that binds specifically to A34 antigen,
 PT useful in preparing a composition for diagnosing or treating cancer.
 XX
 PS Example 4; Fig 22; 99pp; English.
 XX
 CC The present sequence encodes a murine A34 variable light chain. The
 CC specification describes A34 and A33-like 3 proteins, and immunoglobulin
 CC molecules that bind specifically to their antigens. A34 and A33-like 3
 CC proteins are members of the A33/JAM family. The A34 gene is mapped to
 CC chromosome X, and the A33-like 3 gene is mapped to chromosome 1.
 CC immunoglobulin molecules of the invention useful in preparing a
 CC composition for diagnosing or treating cancer, especially oesophageal,
 CC ovarian and stomach cancers.
 XX
 SQ Sequence 399 BP; 85 A; 95 C; 112 G; 107 T; 0 U; 0 Other;
 Query Match 66.2%; Score 289.2; DB 12; Length 399;
 Best Local Similarity 82.9%; Pred. No. 1.7e-78;
 Matches 330; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
 QY 36 ATGAGGTTCTCTGTTCAAGTTCTGGGGTCTGTTATGTTCTGGATCTCTGAGTCAGTGGG 95
 DB 1 ATGAGGTCCTTGTCTAGCTCTCTGGGGCTGTTGTTCTGATCTCTGGAGCCATTGGG 60
 QY 96 GATATTGTGATAACCCAGGATGAATCTCTCAATCTCTGTCAGTCTGAGAAATCAGTTTCC 155
 DB 61 GATATTGTGATGACTCAGGCTGCACCTCTGTACCTGTCTCTCTGAGAGTCAGTATCC 120
 QY 156 ATCTCTGCAGGCTAGTAAGTCTCTCTGTATAAGGATGGGAAGACATATTGAATTGG 215
 DB 121 ATCTCTGCAGGCTAGTACGATCTCTCTGATGTTAATGCAACACTTACTTGTATTGG 180
 QY 216 TTCTGTCAGAGACGAGACAAATCTCTCAGCTCTCTGATGTTATTTGATGCCACCCGTGCA 275
 DB 181 TTCTGTCAGAGGCGAGCCAGCTCTCTCAGCTCTCTGATATATCGGATGTCCAACTTGCC 240

QY 276 TCAGGAGTCTCAGACCCGGTTTACTGGCAGTGGGTGAGGCACAGATTTCCACCTGGAATC 335
 DB 241 TCAGGAGTCCACAGACAGGTTTCAGTGGCAGTGGGTGAGGAAGTCTTTTCCACTGAGATC 300
 QY 336 AGTAGAGTGAAGCTGAGGATGTGGTGTGTATTTACTGTCAACAACCTTGTAGAGTATCCA 395
 DB 301 AGTAGAGTGGAGGCTGAGGATGTGGGTATTTTACTGTATGCGAGCATCTAGAATATCCT 360
 QY 396 TTCACGTTTCGGCTCGGGGACAAAGTTGGAAATAAAAGC 433
 DB 361 TTCACGTTTCGGAGGGGGACCAAGCTGGAATAAAAGC 398

RESULT 14

ACF36530
 ID ACF36530 standard; cDNA; 773 BP.
 XX
 AC ACF36530;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Anti-human tenascin ST2146 MAb light chain variable region (VL) cDNA.
 XX
 KW ST2146; tenascin C; monoclonal antibody; EGF; epidermal growth factor;
 KW cytostatic; antibody therapy; vaccine; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 292..718
 FT /tag= a
 FT /product= "ST2146 light chain variable region"
 FT /partial
 FT /notes= "the stop codon is not indicated"
 FT sig_peptide 292..351
 FT /tag= b
 FT mat_peptide 352..718
 FT /tag= c
 XX
 PN WO2003072608-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 20-FEB-2003; 2003WO-IT000098.
 XX
 PR 26-FEB-2002; 2002US-0359299P.
 XX
 PA (SIGT) SIGMA-TAU IND FARM RIUNITE SPA.
 XX
 PI De Santis R, Anastasi AM;
 XX
 DR WPI; 2003-679945/64.
 DR P-PSDB; ABR82929.

New anti-human tenascin ST2146 monoclonal antibody, and its proteolytic fragments that bind to an antigenic epitope within the EGF-like repeat of human tenascin C, useful for treating tumors, e. g. gliomas, cystic brain tumors.

Example 1; Fig 10; 55pp; English.

The invention relates to an anti-human tenascin ST2146 monoclonal antibody (MAb) whose light and heavy chain variable region sequences and their proteolytic fragments that bind to an antigenic epitope within the EGF (epidermal growth factor)-like repeat of human tenascin C. The antibody, its fragment, recombinant or conjugate derivatives, immunoglobulin molecule and biotinylated derivatives are useful for a diagnostic means for detecting, or preparing a medicament for treating, diseases expressing tenascin, e.g. tumor such as gliomas, mammary, cystic brain tumors, lung carcinomas, fibrosarcomas, and squamous cell carcinomas. The diagnostic means is used in vivo imaging techniques. The medicament is in the form of a kit suitable for carrying out the three-step pre-targeting method. The antibody, in combination with a

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	317.2	72.6	339	10	US-09-940-727B-99
2	317.2	72.6	368	10	US-09-940-727B-107
3	316	72.3	420	10	US-09-940-727B-111
4	309.2	70.8	368	10	US-09-940-727B-103
5	287.4	65.8	773	17	US-10-372-719-21
6	284.4	65.1	426	17	US-10-372-719-3
7	280.4	64.2	825	15	US-10-207-655-356
8	280.4	64.2	1536	15	US-10-207-655-357
9	280.4	64.2	1696	15	US-10-207-655-358
10	280.4	64.2	1696	17	US-10-107-991B-2
11	278	63.6	399	15	US-10-207-655-355

12	273	62.5	720	17	US-10-404-724-5	Sequence 5, Appli
13	273	62.5	720	19	US-10-816-276-1	Sequence 1, Appli
14	260.2	59.5	720	17	US-10-404-724-40	Sequence 40, Appli
15	260.2	59.5	720	19	US-10-816-276-36	Sequence 36, Appli
16	258.6	59.2	720	17	US-10-404-724-44	Sequence 44, Appli
17	258.6	59.2	720	19	US-10-816-276-40	Sequence 40, Appli
18	257	58.8	720	17	US-10-404-724-9	Sequence 9, Appli
19	257	58.8	720	17	US-10-404-724-48	Sequence 48, Appli
20	257	58.8	720	19	US-10-816-276-5	Sequence 5, Appli
21	257	58.8	720	19	US-10-816-276-44	Sequence 44, Appli
22	255.4	58.4	720	17	US-10-404-724-38	Sequence 38, Appli
23	255.4	58.4	720	17	US-10-292-088-39	Sequence 39, Appli
24	255.4	58.4	720	19	US-10-816-276-34	Sequence 34, Appli
25	253.8	58.1	720	17	US-10-404-724-42	Sequence 42, Appli
26	253.8	58.1	720	19	US-10-816-276-38	Sequence 38, Appli
27	253.4	58.0	1081	17	US-10-466-164-33	Sequence 33, Appli
28	252.2	57.7	720	17	US-10-404-724-11	Sequence 11, Appli
29	252.2	57.7	720	17	US-10-404-724-46	Sequence 46, Appli
30	252.2	57.7	720	19	US-10-816-276-7	Sequence 7, Appli
31	252.2	57.7	720	19	US-10-816-276-42	Sequence 42, Appli
32	251	57.4	793	18	US-10-333-235A-9	Sequence 9, Appli
33	250	57.2	1111	18	US-10-333-235A-12	Sequence 12, Appli
34	250	57.2	1402	18	US-10-333-235A-13	Sequence 13, Appli
35	249.4	57.1	478	17	US-10-393-894-32	Sequence 32, Appli
36	249.4	57.1	478	18	US-10-695-667-32	Sequence 32, Appli
37	249.4	57.1	6097	17	US-10-395-894-12	Sequence 12, Appli
38	249.4	57.1	6097	18	US-10-395-667-12	Sequence 12, Appli
39	249	57.0	720	17	US-10-292-088-15	Sequence 15, Appli
40	249	57.0	720	17	US-10-292-088-55	Sequence 55, Appli
41	248.6	56.9	1333	18	US-10-115-635-310	Sequence 310, Appli
42	247.4	56.6	720	17	US-10-292-088-63	Sequence 63, Appli
43	247	56.5	968	10	US-09-992-600A-7	Sequence 7, Appli
44	247	56.5	968	10	US-09-924-340-7	Sequence 7, Appli
45	247	56.5	968	10	US-09-992-095B-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-940-727B-99

; Sequence 99, Application US/09940727B

; Publication No. US2003007793A1

; GENERAL INFORMATION:

; APPLICANT: Landiv, Donald W

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 0575/51400-B

; CURRENT APPLICATION NUMBER: US/09/940,727B

; CURRENT FILING DATE: 2002-09-04

; PRIOR APPLICATION NUMBER: 09/214,095

; PRIOR FILING DATE: 1998-12-28

; PRIOR APPLICATION NUMBER: PCT/US97/10965

; PRIOR FILING DATE: 1997-06-25

; PRIOR APPLICATION NUMBER: 08/672,345

; PRIOR FILING DATE: 1996-06-25

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 99

; LENGTH: 339

; TYPE: DNA

; ORGANISM: mouse

US-09-940-727B-99

Query Match 72.6%; Score 317.2; DB 10; Length 339;

Best Local Similarity 96.2%; Pred. No. 5e-98;

Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 96 GATATTGTGATACCCAGGATGAACCTCTCCATCTCTGTCAGATCAGTTTCC 155

DB 1 GATATTGTGATACCCAGGATGAACCTCTCCATCTCTGTCAGATCAGTTTCC 60

QY 156 ATCTCTCGAGGTCTAGTAAGAGTCTCTGTATTAAGGAGGAGACATACCTTGAATTGG 215

APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 368
; TYPE: DNA
; ORGANISM: mouse
US-09-940-727B-103

Query Match 70.8%; Score 309.2; DB 10; Length 368;
Best Local Similarity 94.7%; Pred. No. 2.9e-95;
Matches 320; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 96 GATATTGTGATACCCAGGATGAATCTCCAATCCTGTCACTTCTCGAGAAATCAGTTCC 155
DB 1 GATATGGTGATACCGCAAGATGAATCTCCAATCCTGTCACTTCTCGAGAAATCAGTTCC 60
QY 156 ATCTCTCGAGGCTCTAGTAAGAGTCTCTGTATAAGAGTGGGAAGACATACCTTGAATTGG 215
DB 61 ATCTCTCGAGGCTCTAGTAAGAGTCTCTGTATAAGAGTGGGAAGACATACCTTGAATTGG 120
QY 216 TTTCTGAGAGACAGAGCAATCTCTCAGCTCCTGATGATTTGATGTCACCCGTGCA 275
DB 121 TTTCTGAGAGACAGAGCAATCTCTCAGCTCCTGATGATTTGATGTCACCCGTGCA 180
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTTCAGGACAGATTTTCACTTGGAAATC 335
DB 181 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTTCAGGACAGATTTTCACTTGGAAATC 240
QY 336 AGTAGAGTGAAGCTGAGGATGTTGGTGTGTATTACTGTCAACAACCTTGTAGAGTATCCA 395
DB 241 AGTAGAGTGAAGCTGAGGATGTTGGTGTGTATTACTGTCAACAACCTTGTAGAGTATCCA 300
QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAAATAAAACG 433
DB 301 TTCACGTTCCGCTCGGGGACAAAGTTGGAGATAAAACG 338

RESULT 5

US-10-372-719-21
; Sequence 21, Application US/10372719
; Publication No. US20040005643A1
; GENERAL INFORMATION:
; APPLICANT: DE SANTIS, RITA
; APPLICANT: ANASTASI, ANNA MARIA
; TITLE OF INVENTION: ANTI-HUMAN TENASCIN MONOCLONAL ANTIBODY
; FILE REFERENCE: 2818-141
; CURRENT APPLICATION NUMBER: US/10/372,719
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 60/359,299
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: ST2146 light chain variable region nucleotide sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (292)..(717)

US-10-372-719-21

Query Match 65.8%; Score 287.4; DB 17; Length 773;
Best Local Similarity 81.4%; Pred. No. 1.2e-87;
Matches 333; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
QY 25 AGGACCTCACCATGAGGTTCTCTGTTCAAGTTTCTGGGGTGCTTATGTTCTGATCTCTG 84
DB 281 AAGTTCTCAGAAATGAGTGCCTAGCTAGTTCTCTGGGGTGCTTATGTTCTGATCTCTG 340
QY 85 GAGTCAGTGGGATATTGTATAAACCAGAGTAACTCTCCAATCTCTGATCTCTGAG 144
DB 341 GAGCCATTTGGGATATTGTATGACTCAGGCTGCACCCCTCTGTACCTGTCACTCTGGAG 400
QY 145 AATCAGTTTCCATCTCTCTCAGGCTCTAGTAAGAGTCTCTGTATAAGAGTGGGAACAT 204
DB 401 AGTCAGTATCCATCTCTCTCAGGCTCTAGTAAGAGTCTCTGTATAGTATGGAACACTT 460
QY 205 ACTTGAATTTGGTTTCTGAGAGACCAAGCAATCTCTCAGCTCCTGATGATTTGATGT 264
DB 461 ACTTGTATTGGTTTCTTACAGAGCCAGGCTCTCTCAGCTCCTGATATATCGGATGT 520
QY 265 CCACCCGTCATCAGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTTCAGTGGCACTGCTTCA 324
DB 521 CCAACCTTCCCTCAGAGTCCAGACAGGTTTCACTGGCAGTGGGTTCAGTGGCACTGCTTCA 580
QY 325 CCCTGAAATCAGTACAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACCTT 384
DB 581 CACTGAGATCAGTACAGTGGAGGCTGAGGATGTGGGTGTGTATTACTGTATCAACATC 640
QY 385 TAGAGTATCCATCAGTTCCGCTCGGGGACAAAGTTGGAAATAAAACG 433
DB 641 TAGAATATCCGCTCACGTTCCGCTGGGACCAAGCTGGAGCTGAAACG 689

RESULT 6

US-10-372-719-3
; Sequence 3, Application US/10372719
; Publication No. US20040005643A1
; GENERAL INFORMATION:
; APPLICANT: DE SANTIS, RITA
; APPLICANT: ANASTASI, ANNA MARIA
; TITLE OF INVENTION: ANTI-HUMAN TENASCIN MONOCLONAL ANTIBODY
; FILE REFERENCE: 2818-141
; CURRENT APPLICATION NUMBER: US/10/372,719
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 60/359,299
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: ST2146 light chain variable region cDNA sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(426)
US-10-372-719-3

Query Match 65.1%; Score 284.4; DB 17; Length 426;
Best Local Similarity 82.2%; Pred. No. 1e-86;
Matches 327; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
QY 36 ATGAGGTTCTCTGTTCAAGTTTCTGGGGTGCTTATGTTCTGAGTCTCTGAGTCAATGGG 95
DB 1 ATGAGGTGCTAGTCTGAGTTCTCTGGGGTGCTTGTGCTCTGGATCCCTGGAGCAATGGG 60
QY 96 GATATTGTATTAACCCAGGATGAATCTCCAATCTCTGATCTCTGATGATCACTTCC 155
DB 61 GATATTGTATGACTCAGGCTGCACCCCTCTGTACCTGTCTCTGAGAGTCACTATCC 120

Query Match 63.6%; Score 278; DB 15; Length 399;
Best Local Similarity 81.2%; Pred. No. 1.5e-84;
Matches 323; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 36 ATGAGGTTCTCTGTTTCAGTTTCCTGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95
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Db 1 ATGAGGTTCTCTGTTTCAGTTTCCTGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGGG 60
|||||

QY 96 GATATTGTGATACCCAGGATGAATCTCCATCTCTGATCTCTGGAGATCAGTTTCC 155
|||||
Db 61 GATATTGTGATACCCAGGATGAATCTCCATCTCTGATCTCTGGAGATCAGTTTCC 120
|||||

QY 156 ATCTCTCGAGTCTAGTAAAGTCTCTCTGATAGGATGGGAACATACACTTGAATTGG 215
|||||
Db 121 ATCTCTCGAGTCTAGTAAAGTCTCTCTGATAGGATGGGAACATACACTTGAATTGG 180
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QY 216 TTTCTGACAGACAGGACAAATCTCTCAGCTCTCTGATGTTTATGTTGTCACCCGTCGA 275
|||||
Db 181 TATCTGACAGACAGGACAAATCTCTCAGCTCTCTGATGTTTATGTTGTCACCCGTCGA 240
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QY 276 TCAGGAGTCTCAGACCGGTTTGTGGCAGTGGGTGAGGATGGAAGACATACACTTGAATTGG 335
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Db 241 TCAGGAGTCTCAGACCGGTTTGTGGCAGTGGGTGAGGATGGAAGACATACACTTGAATTGG 300
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QY 336 AGTAGAGTGAAGGCTGAGGATGTTGGTGTGTTTACTGTCAACAACTTCTAGAGTATCCA 395
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Db 301 AGTAGAGTGAAGGCTGAGGATGTTGGTGTGTTTACTGTCAACAACTTCTAGAGTATCCA 360
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QY 396 TTCAGTTTCGGCTCGGGGACAAAGTTGGAAATATAAAACG 433
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Db 361 CTCAGTTTCGGCTCGGGGACAAAGTTGGAAATATAAAACG 398
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RESULT 12
US-10-404-724-5
; Sequence 5, Application US/10404724
; Publication No. US20030203447A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant
; FILE REFERENCE: 13698US01
; CURRENT APPLICATION NUMBER: US/10/404,724
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/368,530
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo Sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Mouse Human Chimeric Light Chain DNA and Protein
; FEATURE:
; LOCATION: (1)..(717)
; NAME/KEY: CDS
; NAME/KEY: mat_peptide
; LOCATION: (61)..()
US-10-404-724-5

Query Match 62.5%; Score 273; DB 17; Length 720;
Best Local Similarity 80.0%; Pred. No. 1e-82;
Matches 321; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 36 ATGAGGTTCTCTGTTTCAGTTTCCTGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95
|||||
Db 1 ATGAGGTTCTCTGTTTCAGTTTCCTGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGGG 60
|||||

QY 96 GATATTGTGATACCCAGGATGAATCTCCATCTCTGATCTCTGGAGATCAGTTTCC 155
|||||

Db 61 GATATTGTGATACCCAGGATGAATCTCCATCTCTGATCTCTGGAGATCAGTTTCC 120
|||||

QY 156 ATCTCTCGAGTCTAGTAAAGTCTCTCTGATAGGATGGGAACATACACTTGAATTGG 215
|||||

Db 121 ATCTCTCGAGTCTAGTAAAGTCTCTCTGATAGGATGGGAACATACACTTGAATTGG 180
|||||

QY 216 TTTCTGACAGACAGGACAAATCTCTCAGCTCTCTGATGTTTATGTTGTCACCCGTCGA 275
|||||

Db 181 TATCTGACAGACAGGACAAATCTCTCAGCTCTCTGATGTTTATGTTGTCACCCGTCGA 240
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QY 276 TCAGGAGTCTCAGACCGGTTTGTGGCAGTGGGTGAGGATGGAAGACATACACTTGAATTGG 335
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Db 241 TCAGGAGTCTCAGACCGGTTTGTGGCAGTGGGTGAGGATGGAAGACATACACTTGAATTGG 300
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QY 336 AGTAGAGTGAAGGCTGAGGATGTTGGTGTGTTTACTGTCAACAACTTCTAGAGTATCCA 395
|||||

Db 301 AGTAGAGTGAAGGCTGAGGATGTTGGTGTGTTTACTGTCAACAACTTCTAGAGTATCCA 360
|||||

QY 396 TTCAGTTTCGGCTCGGGGACAAAGTTGGAAATATAAAACG 436
|||||

Db 361 CGGAGTTTCGGTGGAGGACCCAGCTTGAGATGAAACGAAAC 401
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RESULT 13
US-10-816-276-1
; Sequence 1, Application US/10816276
; Publication No. US20050009097A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Horwitz, Arnold H.
; TITLE OF INVENTION: Human Engineered to Antibodies to Ep-CAM
; FILE REFERENCE: 14923US02
; CURRENT APPLICATION NUMBER: US/10/816,276
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: 60/459,334
; PRIOR FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo Sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Mouse Human Chimeric Light Chain DNA and Protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
; NAME/KEY: mat_peptide
; LOCATION: (61)..()
US-10-816-276-1

Query Match 62.5%; Score 273; DB 19; Length 720;
Best Local Similarity 80.0%; Pred. No. 1e-82;
Matches 321; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 36 ATGAGGTTCTCTGTTTCAGTTTCCTGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95
|||||

Db 1 ATGAGGTTCTCTGTTTCAGTTTCCTGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGGG 60
|||||

QY 96 GATATTGTGATACCCAGGATGAATCTCCATCTCTGATCTCTGGAGATCAGTTTCC 155
|||||

Db 61 GATATTGTGATACCCAGGATGAATCTCCATCTCTGATCTCTGGAGATCAGTTTCC 120
|||||

QY 156 ATCTCTCGAGTCTAGTAAAGTCTCTCTGATAGGATGGGAACATACACTTGAATTGG 215
|||||

Db 121 ATCTCTCGAGTCTAGTAAAGTCTCTCTGATAGGATGGGAACATACACTTGAATTGG 180
|||||

QY 216 TTTCTGACAGACAGGACAAATCTCTCAGCTCTCTGATGTTTATGTTGTCACCCGTCGA 275
|||||

Db 181 TATCTGACAGACAGGACAAATCTCTCAGCTCTCTGATGTTTATGTTGTCACCCGTCGA 240
|||||

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QY 276 TCAGGAGTCTCAGACCGGTTAGTGGCAGTGGGTCAAGGCACAGATTTCACCCCTGGAAATC 335
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 TCAGGAGTCCAGACAGGTTTCAGTAGCAGTGGGTCAAGAACTGATTTCACTGAGAATC 300
QY 336 ASTAGAGTGAAGCTGAGGATGGGTGCTATTAATCTGTCACAACTGTAGAGTATCCA 395
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 AGCAGAGTGGAGGCTGAGGATGGGTGTTTATTACTGTCTCAAAATCTAGAATCTCCT 360
QY 396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAATAAAACGTAC 436
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
361 CGGACGTTCCGTTGGAGCCACCAAGCTTGAGATGAAACGAAC 401

RESULT 14
US-10-404-724-40
; Sequence 40, Application US/10404724
; Publication No. US20030203447A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/10/404,724
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/368,530
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: P2=P Human Engineered (low risk) INGI light Chain with one
; OTHER INFORMATION: moderate risk proline change; proline at position 15 (P2)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
; NAME/KEY: mat peptide
; LOCATION: (61)..()
US-10-404-724-40

Query Match 59.5%; Score 260.2; DB 17; Length 720;
Best Local Similarity 78.1%; Pred. No. 2.5e-78;
Matches 313; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 36 ATGAGGTTCTCTGTTTCAGTTTCTGGGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 ATGAGGTTCTCTGCTCAGCTTCTGGGCTGCTTGTGCTCTGGATCCTCTGGATCCACTGCA 60
QY 96 GATATTGTGATACCCAGGATGAATCTCCAATCTCTGTCACTTCTCGAGAATCAGTTTCC 155
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 GACATCGTGTATGCCAGTCTGCACCTCTCCAATCCAGTCACTCTCTGGAGTCAAGTTCC 120
QY 156 ATCTCTCGCAGTCTAGTAAGAGTCTCTGTATAAGGATGGGAAGACATACCTTGAATGG 215
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 ATCTCTCGCGGTCTAGTAAGAGTCTCTTACATAGTAATGGCATCACTTATTGTATTGG 180
QY 216 TTTCTGCAGAGACCCAGGCAATCTCTCAGCTCCTGATGTTTGTATGTCACCCCTGCA 275
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 TATCTGCAGAAACCCAGGCGAGTCTCTCAGCTGCTCATCTATCAGATGTTCAACAGACC 240
QY 276 TCAGGAGTCTCAGACCGGTTTATGTCAGTGGGTCAAGGCACAGATTTTCAACCTGGAAATC 335
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 TCAGGGTCCAGACAGGTTTCAGTAGCAGTGGATCTGGGACAGATTTCACTCTCAAGATC 300
QY 336 AGTAGAGTGAAGGCTGAGGATGGGTGTTTATTCTGTCAAACAACCTGTAGAGTATCCA 395
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 AGCAGAGTGGAGGCTGAAGATGTTGGAGTTTATTACTGTGCTCAGAACCTAGAGCTTCCG 360
QY 396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAATAAAACGTAC 436
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
361 CGGACGTTCCGTTGGAGCCACCAAGCTTGAGATGAAACGAAC 401

Search completed: April 19, 2005, 00:13:28
Job time : 1190.64 secs
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Db 361 CGGACGTTCCGTTGGAGCCACCAAGCTTGAGATGAAACGAAC 401

RESULT 15
US-10-816-276-36
; Sequence 36, Application US/10816276
; Publication No. US20050009097A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Horwitz, Arnold H.
; TITLE OF INVENTION: Human Engineered to Antibodies to Ep-CAM
; FILE REFERENCE: 14923US02
; CURRENT APPLICATION NUMBER: US/10/816,276
; PRIOR FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: 60/459,334
; PRIOR FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: P2=P Human Engineered (low risk) INGI light Chain with one
; OTHER INFORMATION: moderate risk proline change; proline at position 15 (P2)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(717)
; NAME/KEY: mat peptide
; LOCATION: (61)..()
US-10-816-276-36

Query Match 59.5%; Score 260.2; DB 19; Length 720;
Best Local Similarity 78.1%; Pred. No. 2.5e-78;
Matches 313; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 36 ATGAGGTTCTCTGTTTCAGTTTCTGGGGTGCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 ATGAGGTTCTCTGCTCAGCTTCTGGGCTGCTTGTGCTCTGGATCCTCTGGATCCACTGCA 60
QY 96 GATATTGTGATACCCAGGATGAATCTCCAATCTCTGTCACTTCTCGAGAATCAGTTTCC 155
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 GACATCGTGTATGCCAGTCTGCACCTCTCCAATCCAGTCACTCTCTGGAGTCAAGTTCC 120
QY 156 ATCTCTCGCAGTCTAGTAAGAGTCTCTGTATAAGGATGGGAAGACATACCTTGAATGG 215
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 ATCTCTCGCGGTCTAGTAAGAGTCTCTTACATAGTAATGGCATCACTTATTGTATTGG 180
QY 216 TTTCTGCAGAGACCCAGGCAATCTCTCAGCTCCTGATGTTTGTATGTCACCCCTGCA 275
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 TATCTGCAGAAACCCAGGCGAGTCTCTCAGCTGCTCATCTATCAGATGTTCAACAGACC 240
QY 276 TCAGGAGTCTCAGACCGGTTTATGTCAGTGGGTCAAGGCACAGATTTTCAACCTGGAAATC 335
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 TCAGGGTCCAGACAGGTTTCAGTAGCAGTGGATCTGGGACAGATTTCACTCTCAAGATC 300
QY 336 AGTAGAGTGAAGGCTGAGGATGGGTGTTTATTCTGTCAAACAACCTGTAGAGTATCCA 395
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 AGCAGAGTGGAGGCTGAAGATGTTGGAGTTTATTACTGTGCTCAGAACCTAGAGCTTCCG 360
QY 396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAATAAAACGTAC 436
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
361 CGGACGTTCCGTTGGAGCCACCAAGCTTGAGATGAAACGAAC 401

Search completed: April 19, 2005, 00:13:28
Job time : 1190.64 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 84.297 Seconds
(without alignments)
8482.539 Million cell updates/sec

Title: US-09-674-716B-2

Perfect score: 437

Sequence: 1 aagctttacgttactcagc.....agttggaataaaacgtacg 437

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	317.2	72.6	339	2	US-08-672-345C-88
2	317.2	72.6	339	3	US-09-214-095D-99
3	317.2	72.6	368	2	US-08-672-345C-86
4	317.2	72.6	368	3	US-09-214-095D-107
5	316	72.3	420	3	US-09-214-095D-111
6	309.2	70.8	368	2	US-08-672-345C-90
7	309.2	70.8	368	3	US-09-214-095D-103
8	293.2	67.1	464	1	US-08-438-123-15
9	276.4	63.2	399	1	US-08-253-877C-9
10	276.4	63.2	399	2	US-08-452-164A-9
11	276.4	63.2	399	3	US-08-603-024-3
12	276.4	63.2	399	4	US-08-450-809-2
13	249.6	57.1	336	3	US-08-483-749A-3
14	248.4	56.8	339	3	US-09-406-532-13
15	247	56.5	968	4	US-10-000-489-7
16	241.2	55.2	954	4	US-09-479-614-19
17	241.2	55.2	954	4	US-09-479-614-21
18	240	54.9	882	1	US-08-392-419-3
19	238.4	54.6	726	4	US-09-479-614-23
20	238.4	54.6	726	4	US-09-479-614-24
21	236	54.0	373	3	US-08-732-708C-40
22	230.8	52.8	1095	3	US-08-875-811-52
23	230.8	52.8	1098	3	US-08-875-811-54
24	226.2	51.8	405	1	US-08-259-372A-11
25	226.2	51.8	405	1	US-08-468-671-11
26	223.6	51.2	427	1	US-08-053-171-8
27	221.4	50.7	325	1	US-08-468-661-4

28	221.4	50.7	325	1	US-08-466-272A-4	Sequence 4, Appli
29	221.4	50.7	325	1	US-08-478-857-4	Sequence 4, Appli
30	221.4	50.7	325	1	US-08-471-771-4	Sequence 4, Appli
31	221.4	50.7	325	3	US-09-130-783-4	Sequence 4, Appli
32	219	50.1	434	1	US-08-053-171-4	Sequence 4, Appli
33	212.8	48.7	394	1	US-08-129-930B-93	Sequence 93, Appli
34	212.8	48.7	394	3	US-08-134-346A-48	Sequence 48, Appli
35	212.8	48.7	394	3	US-08-976-288A-93	Sequence 93, Appli
36	211.6	48.4	393	4	US-09-647-468-16	Sequence 16, Appli
37	211.6	48.4	720	3	US-08-487-550-5	Sequence 5, Appli
38	211.6	48.4	720	4	US-09-526-098-5	Sequence 5, Appli
39	211.6	48.4	720	4	US-09-383-916-5	Sequence 5, Appli
40	211.2	48.3	394	1	US-07-977-696C-64	Sequence 64, Appli
41	211.2	48.3	394	3	US-08-129-930B-64	Sequence 64, Appli
42	211.2	48.3	394	3	US-08-976-288A-64	Sequence 64, Appli
43	210	48.1	409	4	US-09-254-180C-146	Sequence 146, App
44	208.4	47.7	393	4	US-09-647-468-17	Sequence 17, Appli
45	206.6	47.3	424	3	US-08-589-939-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-672-345C-88
; Sequence 88, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-672-345C-88

Query Match 72.6%; Score 317.2; DB 2; Length 339;
Best Local Similarity 96.2%; Pred. No. 1.1e-97;
Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 96 GATATTGTGATAACCCAGGATGAACCTCCAAATCTGTCTCACTTCTGGAGATCAGTTTCC 155
Db 1 GATATTGTGATGACCCAGGATGAACCTCCAAATCTGTCTCACTTCTGGAGATCAGTTTCC 60
QY 156 ATCTCTCGAGGCTCTAGTAGAGTCTCTGTATAGAGTGGGAGACATACCTTGAATGG 215

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
; LENGTH: 368
; TYPE: DNA
; ORGANISM: Murine
US-09-214-095D-107

Query Match 72.6%; Score 317.2; DB 3; Length 368;
Best Local Similarity 96.2%; Pred. No. 1.2e-97;
Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy	96	GATATTGTGATAACCCAGGATGAATCTCCAAATCCTGTCACTTCGAGAAATCAGTTTC	155
Db	1	GATATGGTGATGACGCAAGCAAGATCTCCAAATCCTGTCACTTCGAGAAATCAGTTTC	60
Qy	156	ATCTCTCGCAGGTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATATCTTCAATTTGG	215
Db	61	ATCTCTCGCAGGTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATATCTTCAATTTGG	120
Qy	216	TTTCTGCAGAGACCCAGCAATCTCTCAGCTCCTGTATTTGTATGTCCACCCGTGCA	275
Db	121	TTTCTGCAGAGACCCAGCAATCTCTCAGCTCCTGTATTTGTATGTCCACCCGTGCA	180
Qy	276	TCAGGAGTCTCAGACCCGTTTAGTGGCAGTGGGTGAGGATTTTCAACCTGGAAATC	335
Db	181	TCAGGAGTCTCAGACCCGTTTAGTGGCAGTGGGTGAGGATTTTCAACCTGGAAATC	240
Qy	336	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTTGAGAGTATCCA	395
Db	241	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTTGAGAGTATCCA	300
Qy	396	TTACGTTTCGGCTCGGGGACAAAGTTGGAATAAAACG	433
Db	301	TTACGTTTCGGCTCGGGGACAAAGTTGGAATAAGACG	338

RESULT 5

US-09-214-095D-111
; Sequence 111, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 111
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: V_segment
; LOCATION: (1)..(403)
; OTHER INFORMATION: n at any position represents any nucleotide including c.g,t,a,u
US-09-214-095D-111

Query Match 72.3%; Score 316; DB 3; Length 420;
Best Local Similarity 95.6%; Pred. No. 3.2e-97;
Matches 325; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy	94	GGGATATTGTGATAACCCAGGATGAATCTCCAAATCCTGTCACTTCGAGAAATCAGTTT	153
Db	51	GGGATATTGTGATGACCCAGAGTGAATCTCCAAATCCTGTCACTTCGAGAAATCAGTTT	110
Qy	154	CCATCTCCTGCAGTCTAGTAAGAGTCTCCTGTATAGGATGGGAAGACATATCTTGAAT	213
Db	111	CCATCTCCTGCAGTCTAGTAGGAGTCTCCTATATAGGATGGGAAGACATATCTTGAAT	170
Qy	214	GGTTTCTGCAGAGACCCAGGACATCTCTCAGCTCCTGTATTTGATGTCCACCCGTG	273
Db	171	GGTTTCTGCAGAGACCCAGGACATCTCTCAGCTCCTGTATTTGATGTCCACCCGTG	230

Qy	274	CATCAGGAGTCTCAGACCCGTTTAGTGGCAGTGGGTGAGGATTTTCAACCTGGAAA	333
Db	231	CATCAGGAGTCTCAGACCCGTTTAGTGGCAGTGGGTGAGGATTTTCAACCTGGAAA	290
Qy	334	TCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTTGAGAGTATC	393
Db	291	TCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACTTTGAGAGTATC	350
Qy	394	CATTACGTTTCGGCTCGGGGACAAAGTTGGAATAAAACG	433
Db	351	CATTACGTTTCGGCTCGGGGACAAAGTTGGAATAAAACG	390

RESULT 6

US-08-672-345C-90
; Sequence 90, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-672-345C-90

Query Match 70.8%; Score 309.2; DB 2; Length 368;
Best Local Similarity 94.7%; Pred. No. 6.2e-95;
Matches 320; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy	96	GATATTGTGATAACCCAGGATGAATCTCTCAATCTCTGTCACTTCGAGAAATCAGTTTTC	155
Db	1	GATATGGTGATGACGCAAGATGAATCTCTCAATCTCTGTCACTTCGAGAAATCAGTTTTC	60
Qy	156	ATCTCTCGCAGGTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATATCTTGAATTTGG	215
Db	61	ATCTCTCGCAGGTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATATCTTGAATTTGG	120
Qy	216	TTTCTGCAGAGACCCAGCAATCTCTCAGCTCCTGTATTTGTATGTCCACCCGTGCA	275
Db	121	TTTCTGCAGAGACCCAGCAATCTCTCAGCTCCTGTATTTGTATGTCCACCCGTGCA	180
Qy	276	TCAGGAGTCTCAGACCCGTTTAGTGGCAGTGGGTGAGGATTTTCAACCTGGAAATC	335
Db	181	TCAGGAGTCTCAGACCCGTTTAGTGGCAGTGGGTGAGGATTTTCAACCTGGAAATC	240

Qy	336	AGTAGAGTGAAGGCTGACGATGTGGGTGTGTTACTGTCAACAATTGTAGAGTATCCA	395
Db	241	AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTTACTTTTCAACACTTTGAAGACTATCCA	300
Qy	396	TTTCAGCTTCGGCTCGGGGACAAAGTTGGAAATAAAACG	433
Db	301	TTTCAGCTTCGGCTCGGGGACAAATTTGAGATAAAACG	338

RESULTS 7

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US-09-214-095D-103
; Sequence 103, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103
; LENGTH: 368
; TYPE: DNA
; ORGANISM: MURINE
US-09-214-095D-103

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Query Match	70.8%	Score	309.2;	DB 3;	Length	368;			
Best Local Similarity	94.7%	Prod. No.	6.2e-95;						
Matches	320;	Conservative	0;	Mismatches	18;	Indels	0;	Gaps	0;
QY	96	GATATTGTGATAACCCAGAGTGAACCTCTCCAAATCTGTGCACCTCTTGGAGAATCAGTTTCC	155						
Db	1	GATATGGTGATGACGAAATGAACCTCTCCAAATCTGTGCACCTCTTGGAGAATCAGTTTCC	60						
QY	156	ATCTCCTGCAGGTCTAGTAAAGAGTCTCCTGTATAGGATGGGAAGACATATCTTGAATTGG	215						
Db	61	ATCTCCTGCAGGTCTAGTAGGAGTCTCCTATATAGGATGGGAAGACATATCTTGAATTGG	120						
QY	216	TTTCTGCAGAGACACGGAACAATCTCCTCAGCTCTCTGATGTATTTCATGTCCACCCGTGCA	275						
Db	121	TTTCTGCAGAGACACGAGACGATCTCTCAACTCTCTGATCTATTTCATGTCCACCCGTGCA	180						
QY	276	TCAGAGGCTCAGACCCGGTTTATGTGGCAGTGGGTCCAGGCACAGATTTCAACCTCGAAATC	335						
Db	181	TCAGAGGCTCAGACCCGGTTTATGTGGCAGTGGGTCCAGGCACAGATTTCAACCTCGAAATC	240						
QY	336	AGTAGAGTGAAGGCTTGAGGATGTGGGTGTGTTATTACTGTCAACAACCTTGTAGAGTATCCA	395						
Db	241	AGTAGAGTGAAGGCTTGAGGATGTGGGTGTGTTATTACTTTCACACATTTTGAAGACTATCCA	300						
QY	396	TTCACGTTCCGGCTCGGGGACAAAAGTTGGAAATAAAACG	433						
Db	301	TTCACGTTCCGGCTCGGGGACAAAATTTGGAGATAAAACG	338						

RESULT 8

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US-08-253-877C-9
; Sequence 9, Application US/08253877C
; Patent No. 5773001

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NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,877C
FILING DATE: 03-JUN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..399
US-08-253-877C-9

Query Match 63.2%; Score 276.4; DB 1; Length 399;
Best Local Similarity 80.9%; Pred. No. 9.4e-84;
Matches 322; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

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QY 36 ATGAGGTTCTGTTTCAGTTTCTGGGGGTCCTATGTTCTGGATCTCTGGAGTCAGTGGG 95
DB 1 ATGAGGTGCTAGTCTGAGTTCTGGGGCTGCTTGTGCTCTGGATCTCTGGAGCCATTGGG 60
QY 96 GATATTGTGATACCCAGGATGAATCTCCAAATCTGTCTCACTTCTGGAGATCAGTTTCC 155
DB 61 GATATTGTGATGACTCAGGCTGCACCCCTCTGTTCTCTGCTACTCTGGAGATCATTTATCC 120
QY 156 ATCTCTGCAAGTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATATCTTGAATTGG 215
DB 121 ATTTCTGCAAGTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATATCTTGTATTGG 180
QY 216 TTCTGCAAGACAGGACATCTCTCAGCTCTCTGATGATTTGATGTTCCACCCCTGCA 275
DB 181 TTCTGCAAGACAGGACATCTCTCAGCTCTCTGATGATTTGATGTTCCACCCCTGCA 240
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGGCTCAGGCTCAGGACAGATTTCACTTGAATTC 335
DB 241 TCAGGAGTCTCAGACCGGTTTGTAGTGGGCTCAGGCTCAGGACAGATTTCACTTGAATTC 300
QY 336 AGTAGAGTGAAGGCTGAGGATGTTGGTGTGTTATTTACTGTCAACAACTTGTAGAGTATCCA 395
DB 301 AGTAGAGTGAAGGCTGAGGATGTTGGTGTGTTATTTACTGTATGCAACATCTAGATATCCT 360
QY 396 TTACGTTTGGCTGGGGACAAAGTTGGAATTAACG 433
DB 361 TTCACGTTTGGTGTGGGACCAAGCTGGAGCTGAAACG 398
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RESULT 10

US-08-452-164A-9
; Sequence 9, Application US/08452164A
; Patent No. 5877296

GENERAL INFORMATION:
APPLICANT: Hamann, Philip R.
APPLICANT: Hinman, Lois
APPLICANT: Hollander, Irwin
APPLICANT: Holcomb, Ryan
APPLICANT: Hallett, William
APPLICANT: Tsou, Hwei-Ru
APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methylothio Antitumor
Agents and Intermediates for Their Synthesis
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,164A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..399
US-08-452-164A-9

Query Match 63.2%; Score 276.4; DB 2; Length 399;
Best Local Similarity 80.9%; Pred. No. 9.4e-84;
Matches 322; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

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QY 36 ATGAGGTTCTGTTTCAGTTTCTGGGGGTCCTATGTTCTGGATCTCTGGAGTCAGTGGG 95
DB 1 ATGAGGTGCTAGTCTGAGTTCTGGGGCTGCTTGTGCTCTGGATCTCTGGAGCCATTGGG 60
QY 96 GATATTGTGATACCCAGGATGAATCTCCAAATCTGTCTCACTTCTGGAGATCAGTTTCC 155
DB 61 GATATTGTGATGACTCAGGCTGCACCCCTCTGTTCTCTGCTACTCTGGAGATCATTTATCC 120
QY 156 ATCTCTGCAAGTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATATCTTGAATTGG 215
DB 121 ATTTCTGCAAGTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATATCTTGTATTGG 180
QY 216 TTCTGCAAGACAGGACATCTCTCAGCTCTCTGATGATTTGATGTTCCACCCCTGCA 275
DB 181 TTCTGCAAGACAGGACATCTCTCAGCTCTCTGATGATTTGATGTTCCACCCCTGCA 240
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGGCTCAGGCTCAGGACAGATTTCACTTGAATTC 335
DB 241 TCAGGAGTCTCAGACCGGTTTGTAGTGGGCTCAGGCTCAGGACAGATTTCACTTGAATTC 300
QY 336 AGTAGAGTGAAGGCTGAGGATGTTGGTGTGTTATTTACTGTCAACAACTTGTAGAGTATCCA 395
DB 301 AGTAGAGTGAAGGCTGAGGATGTTGGTGTGTTATTTACTGTATGCAACATCTAGATATCCT 360
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QY 396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAAATAAAACG 433
Db 361 TTCACGTTCCGGCTCGGGACCAAGCTGGAGCTGAAACG 398

RESULT 11

US-08-603-024-3
; Sequence 3, Application US/08603024
; Patent No. 6015562
; GENERAL INFORMATION:
; APPLICANT: Hinman, Lois M.
; APPLICANT: Menendez, Ana T.
; APPLICANT: Hanann, Philip R.
; TITLE OF INVENTION: TARGETED FORMS OF METHYLTRITHIO
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: NJ
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/603,024
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,932-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-683-2158
; TELEFAX: 973-683-4117
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..399
US-08-603-024-3

Query Match 63.2%; Score 276.4; DB 3; Length 399;
Best Local Similarity 80.9%; Pred. No. 9.4e-84;
Matches 322; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 36 ATGAGGTTCTCTGTTTCAGTTCTCGGGGGTCATTATGTTGATCTCTGAGTCAGTGGG 95
Db 1 ATGAGGTGCTAGCTAGTTCTCGGGGGCTGTGTCTGATCCCTGGAGCCATTGGG 60
QY 96 GATATTGTGATAACCCAGGATGAATCTCCAATCTCTGATCTCTGAGAAATCAGTTTCC 155
Db 61 GATATTGTGATGACTCAGCTGCACCCCTCTGTTCTCTGATCTCTGAGAGTCATTATCC 120
QY 156 ATCTCTCGAGGCTAGTAGAGTCTCTGATATAAGGATGGGAAGACATACCTTGAATTGG 215
Db 121 ATTTCTCGAGGCTAGTAGAGTCTCTGATATAAGGATGGGAAGACATACCTTGAATTGG 180
QY 216 TTCTCTCGAGGACAGGACATCTCTCAGCTCTGATGATTTGATGTCACCCCTGCA 275
Db 181 TTCTCTCGAGGACAGGACATCTCTCAGCTCTGATGATTTGATGTCACCCCTGCA 240
QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCAACCTGGAAATC 335

Db 241 TCCGAGTCCAGACAGGTTTCAGTGGCAGTGGGTTCAGGAATGCTTTTCACACTGAGAGTC 300
QY 336 AGTAGAGTAGAGCTGAGGATGTGGGTGTATTTACTGTCAACACTTTGTAGAGTATCCA 395
Db 301 AGTAGAGTGGAGGCTGAGGATGTGGGTGTATTTACTGTATGCAACATCTAGAAATATCCT 360
QY 396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAAATAAAACG 433
Db 361 TTCACGTTCCGGTCTGGGACCAAGCTGGAGCTGAAACG 398

RESULT 12

US-08-450-809-2
; Sequence 2, Application US/08450809
; Patent No. 6506881
; GENERAL INFORMATION:
; APPLICANT: Adair et al.
; TITLE OF INVENTION: Anti-HMFG Antibodies and
; TITLE OF INVENTION: Procedures for their Production
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6506881rlis
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,809
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/948,541B
; FILING DATE: 9/22/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Joanne Longo Feeney
; REGISTRATION NUMBER: 35,134
; REFERENCE/DOCKET NUMBER: CELL-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-450-809-2

Query Match 63.2%; Score 276.4; DB 4; Length 399;
Best Local Similarity 80.9%; Pred. No. 9.4e-84;
Matches 322; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 36 ATGAGGTTCTCTGTTTCAGTTCTCGGGGGTGTATTTGATCTCTGAGTCAGTGGG 95
Db 1 ATGAGGTGCTAGCTAGTTCTCGGGGGCTGTGTCTGATCCCTGGAGCCATTGGG 60
QY 96 GATATTGTGATAACCCAGGATGAATCTCCAATCTCTGATCTCTGAGAAATCAGTTTCC 155
Db 61 GATATTGTGATGACTCAGCTGCACCCCTCTGTCTCTGATCTCTGAGAGTCATTATCC 120
QY 156 ATCTCTCGAGGCTAGTAGAGTCTCTGATATAAGGATGGGAAGACATACCTTGAATTGG 215
Db 121 ATTTCTCGAGGCTAGTAGAGTCTCTGATATAAGGATGGGAAGACATACCTTGAATTGG 180
QY 216 TTCTCTCGAGGACAGGACATCTCTCAGCTCTGATGATTTGATGTCACCCCTGCA 275

Db 181 TTCCTGCAGAGGCCAGCCAGTCTCCCTCAACTCTCTGATATATCGGATGTCCAACTTGCC 240
Qy 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTTCACTTGGAAATC 335
Db 241 TCCGAGTCCACAGACAGTTTCAGTGGCAGTGGGTTCAGGAACTGCTTTCACACTGAGATC 300
Qy 336 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTCAACAACCTTGTAGAGTATCCA 395
Db 301 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTATGCAACATCTAGAATATCCT 360
Qy 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAACA 431
Db 361 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAACA 398

RESULT 13

US-08-483-749A-3
; Sequence 3, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336

US-08-483-749A-3

Qy 96 GATATTGTGATACCCAGGATGACTCTCAATCTGTGCTACTCTCGAGNATCAGTTTCC 155
Db 1 GATATTGTGATACCCAGGATGACTCTCTGTGCTACTCTCGAGNATCAGTTTCC 60
Qy 156 ATCTCTGCTAGTAGTCTCTGTATAGGATGGGAGACATACCTTGAATTGG 215
Db 61 ATCTCTGCTAGTAGTCTCTGTATAGGATGGGAGACATACCTTGTATTGG 120
Qy 216 TTTCTGCAGAGACAGGACAACTCTCTAGCTCTCTGATGTATTTGATGTCCACCCGTGCA 275
Db 121 TTTCTGCAGAGGCGAGGCGAGTCTCTAGCTCTCTGATATATCGGATGTCCACCTTGCC 180

Query Match 57.1%; Score 249.6; DB 3; Length 336;

Best Local Similarity 83.9%; Pred. No. 1.1e-74;

Matches 282; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Qy 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTTCACTTGGAAATC 335
Db 181 TCAGGAGTCCACAGACAGTTTCAGTGGCAGTGGGTTCAGGAACTGCTTTCACACTGAGATC 240
Qy 336 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTCAACAACCTTGTAGAGTATCCA 395
Db 241 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTATGCAATATCTAGAATATCCT 300
Qy 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAACA 431
Db 301 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAACA 336

RESULT 14

US-09-406-532-13
; Sequence 13, Application US/09406532A
; Patent No. 6365154
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: TIE2 Agonist Antibodies
; FILE REFERENCE: P50843
; CURRENT APPLICATION NUMBER: US/09/406,532A
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,098
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(339)
; OTHER INFORMATION: 13H10 light chain v region
US-09-406-532-13

Query Match

56.8%; Score 248.4; DB 3; Length 339;

Best Local Similarity 83.4%; Pred. No. 2.9e-74;

Matches 282; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 96 GATATTGTGATACCCAGGATGACTCTCAATCTGTGCTACTCTCGAGNATCAGTTTCC 155
Db 1 GATATTGTGATACCCAGGATGACTCTCTGTGCTACTCTCGAGNATCAGTTTCC 60
Qy 156 ATCTCTGCTAGTAGTCTCTGTATAGGATGGGAGACATACCTTGAATTGG 215
Db 61 ATCTCTGCTAGTAGTCTCTGTATAGGATGGGAGACATACCTTGTATTGG 120
Qy 216 TTTCTGCAGAGACAGGACAACTCTCTAGCTCTCTGATGTATTTGATGTCCACCCGTGCA 275
Db 121 TTTCTGCAGAGGCGAGGCGAGTCTCTAGCTCTCTGATATATCGGATGTCCACCTTGCC 180
Qy 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGCACAGATTTTCACTTGGAAATC 335
Db 181 TCAGGAGTCCACAGACAGTTTCAGTGGCAGTGGGTTCAGGAACTGCTTTCACACTGAGATC 240
Qy 336 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTCAACAACCTTGTAGAGTATCCA 395
Db 241 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTTACTGTATGCAACCTCTAGAATATCCT 300
Qy 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAACA 433
Db 301 TTCACGTTCCGAGGGGGGACCAAGCTGGAAATAAACA 338

RESULT 15

US-10-000-489-7
; Sequence 7, Application US/10000489
; Patent No. 6794363

GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US6.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO: 7
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..31
; NAME/KEY: CDS
; LOCATION: 32..748
; NAME/KEY: 3'UTR
; LOCATION: 749..968
; NAME/KEY: polyA signal
; LOCATION: 928..933
; NAME/KEY: polyA site
; LOCATION: 953..968
US-10-000-489-7

Query Match 56.5%; Score 247; DB 4; Length 968;
Best Local Similarity 75.4%; Pred. No. 1.5e-73;
Matches 307; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
QY 30 CTCACCATGAGGTTCCTGTTCTAGTTTCTGGGGTGCCTTATGTTCTGGATCTCTGGAGTC 89
Db 26 CTCACAATGAGGCTCCCTGCTCAGCTCTGGGCTGCTAATGCTCTGGGTCTCTGGATCC 85
QY 90 AGTGGGGATATTGTGATACCCAGGATGAACCTCCAACTCCTGTCTACTTCTGGAGATCA 149
Db 86 AGTGGGGATATTGTGATGACTCAGTCTCCACTCTTCTGCCCGTCACTCCCTGGAGAGCCG 145
QY 150 GTTTTCATCTCTGCAGGCTCTAGTAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTG 209
Db 146 GCCTCATCTCTGCAAGTCTAGTCAGGCTCTGCGTCTGATGTTCAAGGTCCTCACTATTG 205
QY 210 AATTGGTTTCTGCAGAGACAGGACAATCTCTCAGTCTCTGATGTTGATGTTCCACC 269
Db 206 GATTGTGATCACCAGGAAGCCAGGGCAGTCTCCACAACCTCTGATATCTTGGGTCTTAAT 265
QY 270 CGTGCATCAGGAGTCTCAGACCGGTTTGTGGCAGTGGGTGAGGACAGATTTCAACCTG 329
Db 266 CGGGCCCTCCGGGTCTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCAAGATTTCACTG 325
QY 330 GAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACAACCTGTAGAG 389
Db 326 AAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTATTACTGTCAAGCTCAAGCTCTACA 385
QY 390 TATCCATTACGTTCCGCTCGGGACAAAGTTTGGAAATAAAACGTAC 436
Db 386 ACTCCATTACTTTCCGCCCTGGGACCAAGATGGATATCAAGCGAAC 432

Search completed: April 18, 2005, 21:13:06
Job time : 85.297 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:59:59 ; Search time 13.8372 Seconds
(without alignments)
48.674 Million cell updates/sec

Title: US-09-674-716B-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	31	100.0	74	2	Ig kappa chain V r
2	31	100.0	112	2	Ig kappa chain V r
3	31	100.0	113	1	Ig kappa chain V r
4	31	100.0	120	1	Ig kappa chain pre
5	27	87.1	104	2	conserved hypother
6	27	87.1	234	2	hypothetical prote
7	27	87.1	342	2	flagellar motor sw
8	27	87.1	409	2	probable beta-keto
9	27	87.1	409	2	probable beta-keto
10	27	87.1	760	2	minichromosome mai
11	27	87.1	842	2	hypothetical prote
12	27	87.1	845	1	replication licens
13	27	87.1	1401	2	MAP kinase kinase
14	26	87.1	112	2	hypothetical prote
15	26	83.9	313	2	probable transcrip
16	26	83.9	341	1	NADH2 dehydrogenas
17	26	83.9	810	2	probable pona, pro
18	26	83.9	1453	2	collagen alpha 1(I
19	26	83.9	1464	1	collagen alpha 1(I
20	25	80.6	177	2	hypothetical prote
21	25	80.6	212	2	agglutinin isolect
22	25	80.6	212	2	agglutinin isolect
23	25	80.6	326	2	hypothetical prote
24	25	80.6	341	2	WD repeat protein
25	25	80.6	390	2	protein T22H9.4 [i
26	25	80.6	511	2	dopamine receptor
27	25	80.6	532	2	malate synthase (E
28	25	80.6	565	2	probable type II D
29	25	80.6	627	2	conserved hypother

30	25	80.6	664	1	OXHOAP	alcohol oxidase (E
31	25	80.6	778	2	S56293	probable membrane
32	25	80.6	887	2	T38885	probable ATP-depen
33	25	80.6	5069	2	T17464	rifamycin polyketi
34	24	77.4	82	2	I36903	gene MHC DQ-beta 1
35	24	77.4	144	2	G90913	hypothetical prote
36	24	77.4	152	2	T44544	conserved hypother
37	24	77.4	164	2	T01726	hypothetical prote
38	24	77.4	171	2	H96833	hypothetical prote
39	24	77.4	171	2	G71422	IB198-4 protein [i
40	24	77.4	176	2	T10331	hypothetical prote
41	24	77.4	190	4	A43860	cytolysin II opero
42	24	77.4	229	2	A56122	emopamil-binding p
43	24	77.4	250	2	AB3319	periplasmic immuno
44	24	77.4	270	2	G97904	conserved hypother
45	24	77.4	270	2	G95033	Cof family protein

ALIGNMENTS

RESULT 1

G30538
IG kappa chain V region (253.15E2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
C;Accession: G30538

R;Claflin, J.L.; Berry, J.

J. Immunol. 141, 4012-4019, 1988

A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pne

A;Reference number: A30534; MUID:89035545; PMID:3141511

A;Accession: G30538

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr

A;Molecule type: mRNA

A;Residues: 1-74 <CUA>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.78; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

Db 24 LMSTRAS 30

RESULT 2

KVMS16

IG kappa chain V region (M167) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004

C;Accession: A01908

R;Rudikoff, S.; Potter, M.

Biochemistry 17, 2703-2707, 1978

A;Title: Kappa-Chain variable region from M167, a phosphorylcholine binding myeloma pro

A;Reference number: A01908; MUID:79000273; PMID:95160

A;Accession: A01908

A;Molecule type: protein

A;Residues: 1-112 <RUD>

A;Cross-references: UNIPROT:P01626

C;Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-95/Domain: immunoglobulin homology <IMM>

F;23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 112;

Best Local Similarity 100.0%; Pred. No. 1.2;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|||||||
Db 55 LMSTRAS 61

RESULT 3
KWS51
Ig kappa chain V region (M511) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C:Accession: A01910
R:Appella, E.
Mol. Immunol. 17, 711-718, 1980
A:Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcholine
A:Reference number: A01910; MUID:81052016; PMID:6776396
A:Accession: A01910
A:Molecule type: protein
A:Residues: 1-113 <APP>
A:Cross-references: UNIPROT:P01628
C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|||||||
Db 55 LMSTRAS 61

RESULT 4
KWS67
Ig kappa chain precursor V region (VK167) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C:Accession: A01909
R:Selsing, E.; Storb, U.
Cell 25, 47-58, 1981
A:Title: Somatic mutation of immunoglobulin light-chain variable-region genes.
A:Reference number: A01909; MUID:82002223; PMID:6791832
A:Accession: A01909
A:Molecule type: DNA
A:Residues: 1-120 <SEL>
A:Cross-references: UNIPROT:P01627
A:Note: the sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>
F:43-113/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|||||||
Db 75 LMSTRAS 81

RESULT 5
E69832

conserved hypothetical protein yhgB - Bacillus subtilis
N:Alternate names: hypothetical protein y (pbpf 5' region)
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E69832; C40614
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ser
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrata, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: E69832
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-104 <KUN>
A:Cross-references: UNIPROT:P38048; GB:Z99109; NID:G2633260; PIDN:CAB12849;
A:Experimental source: strain 168
R:Popham, D.L.; Setlow, P.
J. Bacteriol. 175, 4870-4876, 1993
A:Title: Cloning, nucleotide sequence, and regulation of the Bacillus subtilis pbpf gene
A:Reference number: A40614; MUID:93328693; PMID:8335642
A:Accession: C40614
A:Molecule type: DNA
A:Residues: 1-67 <POP>
A:Cross-references: GB:L10630
C:Genetics:
A:Gene: yhgB

Query Match 87.1%; Score 27; DB 2; Length 104;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|||||||
Db 38 LMSTRAS 44

RESULT 6
S50468
hypothetical protein YER010c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C:Accession: S50468
R:Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lambda
A:Reference number: S50433
A:Accession: S50468
A:Molecule type: DNA
A:Residues: 1-234 <DIE>
A:Cross-references: UNIPROT:P40011; EMBL:U18778; NID:G603592; PID:G603602; GSPDB:GN00005
C:Genetics:
A:Gene: MIPS:YER010c
A:Cross-references: SGD:S0000812
A:Map position: 5R

Query Match 87.1%; Score 27; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 6
|||||||
Db 102 LMSTRAS 107


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RESULT 7
C81451
flagellar motor switch protein Cj0319 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: C81451
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillingworth, D.; Whitehead, P.; Barrell, A.;
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: C81451
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-342 <PAR>
A:Cross-references: UNIPROT:Q9PII0; GB:AL139074; GB:AL111168; MID:g6967505; PIDN:CAB7278
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: fliG; Cj0319
C:Superfamily: flagellar switch protein fliG

Query Match      87.1%; Score 27; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 MSTRAS 7
      |||||
Db      289 MSTRAS 294

RESULT 8
E86017
probable beta-ketoacyl-ACP synthase Z4866 [imported] - Escherichia coli (strain O157:H7,
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: E86017
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11208551
A:Accession: E86017
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <STO>
A:Cross-references: UNIPROT:Q8XSU5; GB:AE005174; MID:g12518154; PIDN:AGS58601.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z4866
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prot

Query Match      87.1%; Score 27; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 MSTRAS 7
      |||||
Db      77 MSTRAS 82

RESULT 9
E91171
probable beta-ketoacyl-ACP synthase Z4866 [imported] - Escherichia coli (strain O157:H7,
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: E91171
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A99629; MUID:21156231; PMID:11258796

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A:Accession: E91171
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <HAY>
A:Cross-references: UNIPROT:Q8XSU5; GB:BA000007; PIDN:BA837764.1; PID:g13363815; GSPDB:
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: EC6341
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-pro

Query Match      87.1%; Score 27; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 MSTRAS 7
      |||||
Db      77 MSTRAS 82

RESULT 10
T39991
manichromosome maintenance protein mcm7p [imported] - fission yeast (Schizosaccharomyce
N:Alternate names: cell division control protein 47 homolog
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39991; T45282
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Whithead, S.; Chillingworth, T.; Churcher,
submitted to the EMBL Data Library, July 1998
A:Reference number: Z21897
A:Accession: T39991
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-760 <LYN>
A:Cross-references: UNIPROT:O75001; EMBL:AL031158; PIDN:CAA20099.1; GSPDB:GN00067; SPDB
A:Experimental source: strain 972h-; cosmid c25D12
R:Liang, D.T.; Forsburg, S.L.
submitted to the EMBL Data Library, June 1998
A:Description: Fission yeast mcm7+ is an essential gene required for normal DNA replica
A:Reference number: Z22955
A:Accession: T45282
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-760 <LIA>
A:Cross-references: EMBL:AF070481; PIDN:AAC23693.1
A:Experimental source: strain Sp.011
C:Genetics:
A:Gene: SPBC25D12.03c; mcm7
C:Map position: 2
C:Function:
A:Description: essential replication factor
C:Superfamily: replication licensing factor MCM7; MCM homology
F:170-662/Domain: MCM homology <MCM>

Query Match      87.1%; Score 27; DB 2; Length 760;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 MSTRAS 7
      |||||
Db      243 MSTRAS 248

RESULT 11
T16198
hypothetical protein F28B4.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16198
R:Leimbach, D.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid F28B4.
A:Reference number: Z18475
A:Accession: T16198

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A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-842 <LEI>
A;Cross-references: UNIPROT:Q19852; EMBL:U42834; NID:g1125756; PID:g1125758; PIDN:AAA839
C;Genetics:
A;Gene: CBSP:F28B4.2
A;Introns: 17/3; 59/3; 93/2; 116/2; 229/3; 333/2; 510/2; 659/3; 738/3; 803/2
F;212-481/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>
Query Match 87.1%; Score 27; DB 2; Length 842;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 MSTRAS 7
DB 650 MSTRAS 655
RESULT 12
S34027
replication licensing factor MCM7 [validated] - yeast (Saccharomyces cerevisiae)
N;Alternate names: cell division control protein CDC47; protein YBR1441; protein YBR202W
C;Species: Saccharomyces cerevisiae
C;Date: 13-Aug-1999 #sequence revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: S34027; S46074; S34925; S56049
R;Jacquet, M.
submitted to the EMBL Data Library, January 1993
A;Reference number: S34022
A;Accession: S34027
A;Molecule type: DNA
A;Residues: 1-845 <JAC>
A;Cross-references: UNIPROT:P38132; EMBL:Z21487; NID:g311665; PIDN:CAA79689.1; PID:g3116
R;Bussereau, F.; Demollis, N.; Jacquet, M.; Mallet, L.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S46054
A;Accession: S46074
A;Molecule type: DNA
A;Residues: 1-845 <BUS>
A;Cross-references: EMBL:Z36071; NID:g536576; PIDN:CAA85166.1; PID:g536577; GSPDB:GN0000
R;Bussereau, F.; Mallet, L.; Gaillon, L.; Jacquet, M.
Yeast 9, 797-806, 1993
A;Title: Yeast Sequencing Reports. A 12.8 kb segment, on the right arm of chromosome II
A;Reference number: S34925; MUID:93377417; PMID:8368014
A;Accession: S34925
A;Molecule type: DNA
A;Residues: 407-620 <BU2>
A;Cross-references: EMBL:Z21487
R;Dalton, S.
submitted to the EMBL Data Library, September 1994
A;Description: Cdc47 and Cdc54 belong to a family of proteins essential for initiation o
A;Reference number: S56049
A;Accession: S56049
A;Molecule type: DNA
A;Residues: 1-551, 'G', 553-555, 'TLN', 559-573, 'Y', 575-845 <DAL>
A;Cross-references: EMBL:U14730; NID:g608168; PIDN:AAA86309.1; PID:g608169
C;Comment: The complex of six MCM proteins is one of several proteins that must be bound
phosphorylated and dissociate from the chromatin.
C;Genetics:
A;Gene: SGD:CDG47; MIPS:YBR202w
A;Cross-references: SGD:S0000406; MIPS:YBR202w
A;Map position: 2R
C;Complex: The predominant form is a heterohexamer of MCM2 (PIR:S45757), MCM3 (PIR:A3637
component of replication licensing factor.
C;Function:
A;Description: MCM7 is a component of the replication licensing factor that permits DNA
C;Superfamily: replication licensing factor MCM7; MCM homology
C;Keywords: cell cycle control; DNA replication initiation; heterohexamer; nucleus; phos
F;227-719/Domain: MCM homology <MCM>
Query Match 87.1%; Score 27; DB 1; Length 845;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTRAS 7
DB 300 MSTRAS 305
RESULT 13
T39225
MAP kinase kinase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
C;Accession: T39225
R;Churcher, C.M.; Gentles, S.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z21837
A;Accession: T39225
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-1401 <CHU>
A;Cross-references: UNIPROT:O14299; EMBL:Z98763; PIDN:CAB11500.1; GSPDB:GN000066; SPDB:SP
A;Experimental source: strain 972h-; cosmid c9G1
C;Genetics:
A;Gene: SPDB:SPAC9G1.02
A;Map position: 1
C;Superfamily: protein kinase homology
Query Match 87.1%; Score 27; DB 2; Length 1401;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LMSTRAS 7
DB 81 LMSTRAS 87
RESULT 14
E95905
hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSymB
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: E95905
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: E95905
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-112 <KUR>
A;Cross-references: UNIPROT:Q92W36; GB:AL591985; PIDN:CAC48909.1; PID:g15140382; GSPDB:G
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.,
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: Smb20530
A;Genome: plasmid
Query Match 83.9%; Score 26; DB 2; Length 112;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMSTRAS 7
DB 5 LMSTRAS 11
RESULT 15

D96028

Probable transcription activator of the pca operon, LysR family protein [imported] - Sinorhizobium meliloti
 C;Species: Sinorhizobium meliloti
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C;Accession: D96028
 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
 A;Reference number: A95842; MUID:21396508; PMID:11481431
 A;Accession: D96028
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-313 <KUR>
 A;Cross-references: UNIPROT:Q92TL9; GB:AL591985; PIDN:CAC49892.1; FID:g15141380; GSPDB:Q
 A;Experimental source: strain 1021, megaplasmid pSymB
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barlov-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 A;Contents: annotation
 C;Genetics:
 A;Gene: pcaQ; SM520580
 A;Genome: plasmid

Query Match 83.9%; Score 26; DB 2; Length 313;

Best Local Similarity 85.7%; Pred. No. 64;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

Db 199 LMPTRAS 205

Search completed: April 18, 2005, 14:23:23

Job time : 15.8372 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:57:43 ; Search time 63.6512 Seconds
(without alignments)
56.316 Million cell updates/sec

Title: US-09-674-716B-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: +
1: uniprot_sprot: +
2: uniprot_trembl: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	112	1	KV2A MOUSE
2	31	100.0	113	1	KV2C MOUSE
3	31	100.0	120	1	KV2B MOUSE
4	28	90.3	177	2	O63ME2 burkholderi
5	28	90.3	301	2	O6C0S1
6	28	90.3	847	2	O7UWT5
7	27	87.1	104	1	YHGB BACSU
8	27	87.1	124	2	O8EEB9
9	27	87.1	226	2	O7SHG3
10	27	87.1	226	2	O7MHJ0
11	27	87.1	234	1	YEK0 YEAST
12	27	87.1	235	2	O6CQX7
13	27	87.1	238	2	O75AA2
14	27	87.1	255	2	O6BWC8
15	27	87.1	342	2	O9P1I0
16	27	87.1	409	2	O6KDF2
17	27	87.1	409	2	O8FJL5
18	27	87.1	409	2	O8X5U5
19	27	87.1	454	2	O6BRF6
20	27	87.1	505	2	O7UOP6
21	27	87.1	541	2	O868T1
22	27	87.1	544	2	O8BX14
23	27	87.1	558	2	O63P50
24	27	87.1	579	2	O7YF69
25	27	87.1	657	2	O8BLC8
26	27	87.1	760	1	NCM7 SCHPO
27	27	87.1	803	2	O6BWN6
28	27	87.1	812	2	O6FJL2
29	27	87.1	813	2	O75A77
30	27	87.1	825	2	O7QTK8
31	27	87.1	826	2	O6CM41

32	27	87.1	845	1	CC47 YEAST
33	27	87.1	860	2	Q19852
34	27	87.1	981	2	O7NFT8
35	27	87.1	1024	2	O9EST5
36	27	87.1	1031	2	O6DID0
37	27	87.1	1049	2	O9XBP6
38	27	87.1	1141	2	O8LJJ7
39	27	87.1	1401	1	WIS4 SCHPO
40	26	83.9	82	2	O6H2X9
41	26	83.9	112	2	O92W36
42	26	83.9	114	2	O862S4
43	26	83.9	174	2	O6GV12
44	26	83.9	193	1	RS3A SULTO
45	26	83.9	212	2	Q862R9

P38132 saccharomyc
Q19852 caenorhabdi
O7nft8 gloeobacter
Q9es15 mus musculu
O6di10 mus musculu
Q9xbp6 myxococcus
O8ljj7 oryza sativ
O14299 schizosacch
O6h2x9 sus scrofa
Q92w36 rhizobium m
O862s4 bos taurus
Q8gv12 oryctolagus
Q975f8 sulfolobus
Q862r9 bos taurus

ALIGNMENTS

RESULT 1
KV2A MOUSE
ID KV2A MOUSE STANDARD; PRT; 112 AA.
AC P01626;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region MOPC 167.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79000273; PubMed=99160;
RA Rudikoff S., Potter M.;
RT "Kappa Chain variable region from M167, a phosphorylcholine binding myeloma protein.";
RL Biochemistry 17:2703-2707(1978).
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein that binds phosphorylcholine. The sequence of the V region of the heavy chain has also been determined.
CC PIR; A01908; KVM516.
DR HSSP; Q8KOF8; 1KN2.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|||||
Db 55 LMSTRAS 61

RESULT 2
KV2C MOUSE STANDARD; PRT; 113 AA.
ID KV2C MOUSE
AC P01628;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region MOPC 511.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81052016; PubMed=6776396; DOI=10.1016/0161-5890(80)90140-6;
RA Appella E.;
RT "Amino acid sequence of the light chain variable region of M511, a
RT phosphorylcholine-binding murine myeloma protein.";
RL Mol. Immunol. 17:711-718(1980).
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds phosphorylcholine.
DR PIR: A01910; KVM51.
DR HSP; Q8K0F8; IKN2.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin V region.
KW DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 123 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 55 LMSTRAS 61

RESULT 3
KV2B MOUSE STANDARD; PRT; 120 AA.
AC P01627;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region VKappa167 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82002223; PubMed=6791832; DOI=10.1016/0092-8674(81)90230-0;
RA Selsing E.; Storb U.;
RT "Somatic mutation of immunoglobulin light-chain variable-region
RT genes.";
RL Cell 25:47-58(1981).
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DR EMBL; J00562; AAA39032.1; -.
DR EMBL; X02415; AAA39051.1; -.
DR PIR; A01909; KVM567.
DR HSP; P01751; INOB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 120 Ig kappa chain V-II region VKappa167.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 59 Complementarity-determining-1.
FT DOMAIN 60 74 Framework-2.
FT DOMAIN 75 81 Complementarity-determining-2.
FT DOMAIN 82 113 Framework-3.
FT DOMAIN 114 120 Complementarity-determining-3.
FT DISULFID 43 113 By similarity.
SQ SEQUENCE 120 AA; 13280 MW; 63BB571F0B4DE3E8 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 75 LMSTRAS 81

RESULT 4
Q63ME2 PRELIMINARY; PRT; 177 AA.
AC Q63ME2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative exported protein.
GN ORFName=BPSS0715;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K96243;
RX PubMed=15377794;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosset B., Davis P., Deshazer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinovitch E., Rutherford K., Sanders M., Simmonds M.,
RA Songisvilas S., Stevens K., Tumapa S., Vesaratchavee M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR EMBL; BX571966; CAH38175.1; -.
SQ SEQUENCE 177 AA; 18847 MW; 1F6B18829392ADD5 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 177;
Best Local Similarity 85.7%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 126 LMSTRAS 132

RESULT 5
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O6COS1
ID Q6COS1 PRELIMINARY; PRT; 301 AA.
AC Q6COS1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similarities with sp|P40011 Saccharomyces cerevisiae YER010c.
GN ORFNames=YAL10F22209g;
OS Yarrowia lipolytica ClIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Barnay S., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Boistrame A., Boyer J., Beckerich J.M., Beyne E., Bleykasten C.,
RA Despons L., Fabre J., Fathallah C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicraud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.B.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=CLIB99;
RC Genoscops;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR382132; CAG78552.1; -
DR InterPro; IPR005493; Methyltransf 6.
DR Pfam; PF03737; Methyltransf 6; 1_-
SQ SEQUENCE 301 AA; 32405 MW; 85580D97B610B3E5 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 301;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 159 LMSTRAN 165

RESULT 6
O7UWTS PRELIMINARY; PRT; 847 AA.
ID Q7UWTS
AC Q7UWTS;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RB1802;
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
OS Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlensner H., Anann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
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RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294135; CAD72277.1; -
DR InterPro; IPR011445; DUF1550.
DR Pfam; PF07584; DUF1550; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 847 AA; 89847 MW; 437BF2BCED0B2812 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 847;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 177 LMSTRAS 183

RESULT 7
YHGB BACSU STANDARD; PRT; 104 AA.
ID YHGB BACSU
AC P38078;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein yhgb.
GN Names=yhgb; OrderedLocusNames=BSU10090;
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98240224; PubMed=9579061;
RA Noback M.A., Holsappel S., Kiewiet R., Terpstra P., Wambutt R.,
RA Wedler H., Venema G., Bron S.;
RT "The 172 kb prfA-addAB region from 83 degrees to 97 degrees of the
RT Bacillus subtilis chromosome contains several dysfunctional genes, the
RT glyB marker, many genes encoding transporter proteins, and the
RT ubiquitous hit gene.";
RL Microbiology 144:859-875(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Braun M., Brignell S.C., Bron S.,
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadate Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,
RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Tognoni K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA Takenaru K., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vasearotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzenger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
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RT subtitlis";
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 1-67 FROM N.A.
RC STRAIN=168;
RX MEDLINE=93328693; PubMed=8335642;
RA Fopham D.L., Setlow P.;
RT "Cloning, nucleotide sequence, and regulation of the Bacillus subtilis
RT pbpf gene, which codes for a putative class A high-molecular-weight
RT penicillin-binding protein.";
RL J. Bacteriol. 175:4870-4876(1993).
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CC
DR EMBL; Y14083; CAA74515.1; -
DR EMBL; Z99109; CABI2849.1; -
DR EMBL; L10630; CAA71940.2; -
DR PIR; E69832; E69832.
DR Subtilisin; BGI0426; yhgB.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 104 AA; 11998 MW; 6B44CD77B52FDF968 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 104;
Best Local Similarity 85.7%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 38 LMSTRCS 44

RESULT 8
ID Q8EEB9 PRELIMINARY; PRT; 124 AA.
AC Q8EEB9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Adhesion-related protein.
GN OrderedLocusNames=SO2467;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OC NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA Brinkac L.N., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Unayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Neallson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123 (2002).
DR EMBL; AE015688; AAN55499.1; -
DR TIGR; SO2467; -
KW Complete proteome.
SQ SEQUENCE 124 AA; 13061 MW; D77E2F6F42DEF735 CRC64;

Query Match 87.1%; Score 27; DB 2; Length 124;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RT Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 1-67 FROM N.A.
RC STRAIN=168;
RX MEDLINE=93328693; PubMed=8335642;
RA Fopham D.L., Setlow P.;
RT "Cloning, nucleotide sequence, and regulation of the Bacillus subtilis
RT pbpf gene, which codes for a putative class A high-molecular-weight
RT penicillin-binding protein.";
RL J. Bacteriol. 175:4870-4876(1993).
CC -----
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CC -----
CC
DR EMBL; Y14083; CAA74515.1; -
DR EMBL; Z99109; CABI2849.1; -
DR EMBL; L10630; CAA71940.2; -
DR PIR; E69832; E69832.
DR Subtilisin; BGI0426; yhgB.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 104 AA; 11998 MW; 6B44CD77B52FDF968 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 104;
Best Local Similarity 85.7%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 38 LMSTRCS 44

RESULT 8
ID Q8EEB9 PRELIMINARY; PRT; 124 AA.
AC Q8EEB9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Adhesion-related protein.
GN OrderedLocusNames=SO2467;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OC NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA Brinkac L.N., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Unayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Neallson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123 (2002).
DR EMBL; AE015688; AAN55499.1; -
DR TIGR; SO2467; -
KW Complete proteome.
SQ SEQUENCE 124 AA; 13061 MW; D77E2F6F42DEF735 CRC64;

Query Match 87.1%; Score 27; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 6
Db 100 LMSTRAS 105

RESULT 10
ID Q7MHJ0 PRELIMINARY; PRT; 226 AA.
AC Q7MHJ0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Xanthosine triphosphate pyrophosphatase.
GN OrderedLocusNames=VW2879;
OS Vibrio vulnificus (strain VJ2016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OC NCBI_TaxID=196600;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=14656965; DOI=10.1101/gr.1295503;
RX PubMed=14656965; DOI=10.1101/gr.1295503;

```


RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
 Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
 Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
 "Comparative genome analysis of *Vibrio vulnificus*, a marine
 pathogen.";
 RL Genome Res. 13:2577-2587(2003).
 CC -I- SIMILARITY: Belongs to the HAM1 NTPase family.
 DR EMBL; AP005341; BAC95643.1; -;
 DR HSSP; P52061; IK7K.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR002637; Hamip_like.
 DR Pfam; PF01725; Hamip_like_1.
 DR TIGRfams; TIGR00042; Hamip_like_1.
 DR Complete proteome; Hydrolase.
 KW SEQUENCE 226 AA; 24762 MW; 65E34589230DBCEA CRC64;
 Query Match 87.1%; Score 27; DB 2; Length 226;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTRAS 7
 DB 1 MSTRAS 6
 RESULT 11
 YEKO YEAST STANDARD; PRT; 234 AA.
 ID YEKO YEAST STANDARD; PRT; 234 AA.
 AC P40011;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypothetical 25.6 kDa protein in NTF2-SRP1 intergenic region.
 GN OrderedLocNames=YEKO10C;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talia E.,
 Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 Boissrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
 Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 Zenit-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weisenbach J.,
 Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts.";
 RN Nature 430:35-44(2004).
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RG Genoscope;
 RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; CR382124; CAH00758.1; -;
 DR InterPro; IPR005493; Methyltransf_6.
 DR Pfam; PF03737; Methyltransf_6; 1.
 SQ SEQUENCE 235 AA; 25766 MW; A2ED50D9CC4F7057 CRC64;
 Query Match 87.1%; Score 27; DB 2; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMSTRA 6
 DB 103 LMSTRA 108
 RESULT 13
 Q75AA2 PRELIMINARY; PRT; 238 AA.
 ID Q75AA2;
 AC Q75AA2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ADRL6Cp.
 GN ORFNames=ADRL6C;
 OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10895;
 Query Match 87.1%; Score 27; DB 1; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRA 6
 DB 102 LMSTRA 107
 RESULT 12
 Q6COX7 PRELIMINARY; PRT; 235 AA.
 ID Q6COX7;
 AC Q6COX7;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to sp|P40011 Saccharomycetes cerevisiae YER010c singleton.
 GN ORFNames=KLLA0D13442G;
 OS Kluyveromyces lactis NRRL Y-1140.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=284590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talia E.,
 Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 Boissrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
 Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 Zenit-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weisenbach J.,
 Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts.";
 RN Nature 430:35-44(2004).
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RG Genoscope;
 RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; CR382124; CAH00758.1; -;
 DR InterPro; IPR005493; Methyltransf_6.
 DR Pfam; PF03737; Methyltransf_6; 1.
 SQ SEQUENCE 235 AA; 25766 MW; A2ED50D9CC4F7057 CRC64;
 Query Match 87.1%; Score 27; DB 2; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMSTRA 6
 DB 103 LMSTRA 108
 RESULT 13
 Q75AA2 PRELIMINARY; PRT; 238 AA.
 ID Q75AA2;
 AC Q75AA2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ADRL6Cp.
 GN ORFNames=ADRL6C;
 OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10895;

RA Voegeli S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,
 RA Philippsen P.;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AE016817; RA051936.1; -;
 DR AGD; ADR016C; -;
 DR InterPro; IPR005493; Methyltransf_6.
 DR Pfam; PF03737; Methyltransf_6; 1_
 SQ SEQUENCE 238 AA; 25785 MW; 2981918CF8A8761C CRC64;

Query Match 87.1%; Score 27; DB 2; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRA 6
 |||||
 Db 102 LMSTRA 107

RESULT 14

ID Q6WC8 PRELIMINARY; PRT; 255 AA.
 AC Q6WC8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to CA2357|IPF8957 Candida albicans IPF8957 unknown
 DE function.
 GN ORFNames=DEHA0B12584g;
 OS Debaryomyces hansenii CBS767.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
 OX NCBI_TaxID=284592;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CBS767;
 RG Genolevures;

RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CBS767;
 RG Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; CR382134; CAG85495.1; -;
 DR InterPro; IPR005493; Methyltransf_6.
 DR Pfam; PF03737; Methyltransf_6; 1_
 SQ SEQUENCE 255 AA; 27450 MW; C8FF0F6527033F1C CRC64;

Query Match 87.1%; Score 27; DB 2; Length 255;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRA 6
 |||||
 Db 117 LMSTRA 122

RESULT 15

Q9PI10

ID Q9PI10 PRELIMINARY; PRT; 342 AA.
 AC Q9PI10;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Flagellar motor switch protein.
 GN Name=flig; OrderedLocusNames=Cj0319;
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=197;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NCTC 11168;
 RX MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
 RA Parkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churcher C.M.,
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
 RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
 RA Whitehead S., Barrell B.G.;
 RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
 RT reveals hypervariable sequences."
 RL Nature 403:665-668(2000).
 DR EMBL; AL139074; CAB72786.1; -;
 DR PIR; C81451; C81451.
 DR HSP; Q9WY63; 1QC7.
 DR GO; GO:0009288; C:flagellum (sensu Bacteria); IEA.
 DR GO; GO:0003774; F:motor activity; IEA.
 DR GO; GO:0006935; P:chemotaxis; IEA.
 DR GO; GO:0001539; P:ciliary or flagellar motility; IEA.
 DR InterPro; IPR000090; Flg_Motor_Flig.
 DR InterPro; IPR011002; Flig_like.
 DR Pfam; PF01706; Flig_C; 1.
 DR PRINTS; PR00954; FLGMOTORFLIG.
 DR TIGRFAMs; TIGR00207; flig; 1.
 KW Complete proteome; Flagellum.
 SQ SEQUENCE 342 AA; 38429 MW; ED4D214417C1524C CRC64;

Query Match 87.1%; Score 27; DB 2; Length 342;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTRAS 7
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 Db 289 MSTRAS 294

Search completed: April 19, 2005, 14:21:52
 Job time : 66.6512 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:32:07 ; Search time 73.7442 Seconds
(without alignments)
36.712 Million cell updates/sec

Title: US-09-674-716B-5

Perfect score: 31

Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	7	2 AAW39825	Aaw39825 Light cha
2	31	100.0	7	2 AAW39822	Aaw39822 Light cha
3	31	100.0	7	2 AAW39819	Aaw39819 Light cha
4	31	100.0	7	3 AAY32255	Aay32255 Light cha
5	31	100.0	100	4 AAE06969	Aae06969 Mouse ger
6	31	100.0	100	8 ADQ89254	Adq89254 Mouse imm
7	31	100.0	113	2 AAW39803	Aaw39803 Variable
8	31	100.0	113	2 AAW39886	Aaw39886 Light cha
9	31	100.0	113	2 AAW39802	Aaw39802 Variable
10	31	100.0	113	2 AAW39882	Aaw39882 Light cha
11	31	100.0	113	2 AAW39804	Aaw39804 Variable
12	31	100.0	116	3 AAY32262	Aay32262 Humanised
13	31	100.0	145	3 AAY32261	Aay32261 Mouse ant
14	31	100.0	248	7 ADG32323	Adg32323 Mouse scf
15	31	100.0	317	7 ADG32360	Adg32360 Precursor
16	28	90.3	7	2 AAW39816	Aaw39816 Light cha
17	28	90.3	113	2 AAW39801	Aaw39801 Variable
18	28	90.3	274	2 AAW39899	Aaw39899 Single ch
19	28	90.3	407	8 ADN17638	Adn17638 Bacterial
20	28	90.3	979	7 ADB64292	Adb64292 Human pro
21	27	87.1	7	2 AAW39876	Aaw39876 Light cha
22	27	87.1	68	4 AAU64213	Aau64213 Propionib
23	27	87.1	68	6 ABM60732	Abm60732 Propionib
24	27	87.1	119	6 ABU00425	Abu00425 Human nov
25	27	87.1	123	4 AAU54742	Aau54742 Propionib

26	27	87.1	123	6	ABM51261	Abm51261 Propionib
27	27	87.1	131	2	AAR12232	Aar12232 Mouse Mab
28	27	87.1	132	2	AAR12354	Aar12354 Light (ka
29	27	87.1	140	4	AAM95756	Aam95756 Human rep
30	27	87.1	218	5	ABG77402	Abg77402 Selected
31	27	87.1	218	5	ABJ11304	Abj11304 Yeast sel
32	27	87.1	342	6	ABU26357	Abu26357 Protein e
33	27	87.1	409	4	ABBS2717	Abbs2717 Escherich
34	27	87.1	760	8	ADS44134	Ads44134 Bacterial
35	27	87.1	809	5	ABP73372	Abp73372 Candida a
36	27	87.1	845	6	ABR53640	Abr53640 Protein s
37	27	87.1	845	7	ADK64136	Adk64136 Disease t
38	27	87.1	845	8	ADN18834	Adn18834 Bacterial
39	27	87.1	1401	8	ADN19524	Adn19524 Bacterial
40	26	83.9	77	4	AAU39838	Aau39838 Propionib
41	26	83.9	77	6	ABM36357	Abm36357 Propionib
42	26	83.9	115	4	AAU14133	Aau14133 Peptide #
43	26	83.9	115	4	ABB33078	Abb33078 Peptide #
44	26	83.9	115	4	AAM26539	Aam26539 Peptide #
45	26	83.9	115	4	ABB27906	Abb27906 Human pep

ALIGNMENTS

RESULT 1

AAW39825

ID AAW39825 standard; peptide; 7 AA.

XX AC AAW39825;

XX XX

DT 16-JUN-1998 (first entry)

XX XX

DE Light chain CDR2 of catalytic antibody 12H1.

XX XX

KW Variable domain; lambda light chain; catalytic antibody; degradation;
cocaine; cocaine transition state analogue; TSA; benzoic acid;
phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
overdose; addiction.

XX XX

OS Mus sp.

XX XX

PN W09749800-A1.

XX XX

PD 31-DEC-1997.

XX XX

PF 25-JUN-1997; 97WO-US010965.

XX XX

PR 25-JUN-1996; 96US-00672345.

XX XX

PA (UYCO) UNIV COLUMBIA NEW YORK.

XX XX

PI Landry DW;

XX XX

DR WPI; 1998-077166/07.

XX XX

PT New catalytic antibodies able to decompose cocaine, single-chain

XX XX

PT analogues - used to treat cocaine overdose and addiction, required in far

XX XX

PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX XX

PS Claim 17; Page 83; 147pp; English.

XX XX

CC AAW39824-26 represent the sequences of the light chain complementarity

XX XX

CC determining regions (CDRs) of the catalytic antibody 12H1, which is able

XX XX

CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)

XX XX

CC were prepared and used to immunise mice for production of hybridomas.

XX XX

CC Catalytic antibodies were identified by their capacity to release 3H-

XX XX

CC benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was identified

XX XX

CC using TSA2, and has a per minute Kcat of 0.16. The antibodies reduce the

XX XX

CC concentration of cocaine in a subject, and are used particularly for the

XX XX

CC treatment of an overdose. They are also used for treating addiction (by

XX XX

CC reducing the in vivo concentration that can be achieved)

XX XX

```

SQ      Sequence 7 AA;
Query Match      100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
        |||||
DB      1 LMSTRAS 7

RESULT 2
AAW39822
ID      AAW39822 standard; peptide; 7 AA.
AC      AAW39822;
XX
XX
DT      16-JUN-1998 (first entry)
XX
DE      Light chain CDR2 of catalytic antibody 2A10.
XX
Variable domain; lambda light chain; catalytic antibody; degradation;
KW      cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW      phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW      overdose; addiction.
XX
OS      Mus sp.
XX
PN      WO9749800-A1.
XX
PD      31-DEC-1997.
XX
PF      25-JUN-1997; 97WO-US010965.
XX
PR      25-JUN-1997; 97WO-US010965.
XX
PA      (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI      Landry DW;
XX
DR      WPI; 1998-077166/07.
XX
PT      New catalytic antibodies able to decompose cocaine, single-chain
PT      analogues - used to treat cocaine overdose and addiction, required in far
PT      smaller doses than antibodies that antagonise cocaine by simply binding.
XX
PS      Claim 15; Page 82; 147pp; English.
XX
CC      AAW39821-23 represent the sequences of the light chain complementarity
CC      determining regions (CDRs) of the catalytic antibody 2A10, which is able
CC      to degrade cocaine. A series of cocaine transition state analogues (TSAs)
CC      were prepared and used to immunise mice for production of hybridomas.
CC      Catalytic antibodies were identified by their capacity to release 3H-
CC      benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified
CC      using TSA1, which is an immunogenic conjugate of a phosphate monoester
CC      transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.
CC      The antibodies reduce the concentration of cocaine in a subject, and are
CC      used particularly for the treatment of an overdose. They are also used
CC      for treating addiction (by reducing the in vivo concentration that can be
CC      achieved)
XX
SQ      Sequence 7 AA;
Query Match      100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
        |||||
DB      1 LMSTRAS 7

RESULT 3
AAW39822
ID      AAW39822 standard; peptide; 7 AA.
AC      AAW39822;
XX
XX
DT      16-JUN-1998 (first entry)
XX
DE      Light chain CDR2 of catalytic antibody 2A10.
XX
Variable domain; lambda light chain; catalytic antibody; degradation;
KW      cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW      phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW      overdose; addiction.
XX
OS      Mus sp.
XX
PN      WO9749800-A1.
XX
PD      31-DEC-1997.
XX
PF      25-JUN-1997; 97WO-US010965.
XX
PR      25-JUN-1997; 96US-00672345.
XX
PA      (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI      Landry DW;
XX
DR      WPI; 1998-077166/07.
XX
PT      New catalytic antibodies able to decompose cocaine, single-chain
PT      analogues - used to treat cocaine overdose and addiction, required in far
PT      smaller doses than antibodies that antagonise cocaine by simply binding.
XX
PS      Claim 15; Page 82; 147pp; English.
XX
CC      AAW39821-23 represent the sequences of the light chain complementarity
CC      determining regions (CDRs) of the catalytic antibody 2A10, which is able
CC      to degrade cocaine. A series of cocaine transition state analogues (TSAs)
CC      were prepared and used to immunise mice for production of hybridomas.
CC      Catalytic antibodies were identified by their capacity to release 3H-
CC      benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified
CC      using TSA1, which is an immunogenic conjugate of a phosphate monoester
CC      transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.
CC      The antibodies reduce the concentration of cocaine in a subject, and are
CC      used particularly for the treatment of an overdose. They are also used
CC      for treating addiction (by reducing the in vivo concentration that can be
CC      achieved)
XX
SQ      Sequence 7 AA;
Query Match      100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
        |||||
DB      1 LMSTRAS 7

RESULT 4
AAW39822
ID      AAW39822 standard; peptide; 7 AA.
AC      AAW39822;
XX
XX
DT      15-FEB-2000 (first entry)
XX
DE      Light chain CDR L2 of mouse anti-CD23 MAB C11.
XX
KW      CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;
KW      monoclonal antibody; chimeric antibody; humanised antibody;
KW      complementarity determining region; CDR; autoimmune disease;

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AAW39819
ID      AAW39819 standard; peptide; 7 AA.
XX
XX      AAW39819;
XX
DT      16-JUN-1998 (first entry)
XX
DE      Light chain CDR2 of catalytic antibody 6A12.
XX
Variable domain; lambda light chain; catalytic antibody; degradation;
KW      cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW      phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW      overdose; addiction.
XX
OS      Mus sp.
XX
PN      WO9749800-A1.
XX
PD      31-DEC-1997.
XX
PF      25-JUN-1997; 97WO-US010965.
XX
PR      25-JUN-1996; 96US-00672345.
XX
PA      (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI      Landry DW;
XX
DR      WPI; 1998-077166/07.
XX
PT      New catalytic antibodies able to decompose cocaine, single-chain
PT      analogues - used to treat cocaine overdose and addiction, required in far
PT      smaller doses than antibodies that antagonise cocaine by simply binding.
XX
PS      Claim 13; Page 81; 147pp; English.
XX
CC      AAW39818-20 represent the sequences of the light chain complementarity
CC      determining regions (CDRs) of the catalytic antibody 6A12, which is able
CC      to degrade cocaine. A series of cocaine transition state analogues (TSAs)
CC      were prepared and used to immunise mice for production of hybridomas.
CC      Catalytic antibodies were identified by their capacity to release 3H-
CC      benzoic acid from 3H-phenyl cocaine. The 6A12 antibody was identified
CC      using TSA1, which is an immunogenic conjugate of a phosphate monoester
CC      transition state analogue. Antibody 6A12 has a per minute Kcat of 0.072.
CC      The antibodies reduce the concentration of cocaine in a subject, and are
CC      used particularly for the treatment of an overdose. They are also used
CC      for treating addiction (by reducing the in vivo concentration that can be
CC      achieved)
XX
SQ      Sequence 7 AA;
Query Match      100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
        |||||
DB      1 LMSTRAS 7

RESULT 4
AAW39822
ID      AAW39822 standard; peptide; 7 AA.
XX
XX      AAW39822;
XX
XX      15-FEB-2000 (first entry)
XX
DE      Light chain CDR L2 of mouse anti-CD23 MAB C11.
XX
KW      CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;
KW      monoclonal antibody; chimeric antibody; humanised antibody;
KW      complementarity determining region; CDR; autoimmune disease;

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KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulin;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 KW therapy.

OS Mus musculus.
 XX
 XX WO9558679-A1.
 XX
 XX PD 18-NOV-1999.
 XX
 XX PF 07-MAY-1999; 99WO-GB001434.
 XX
 XX PR 09-MAY-1998; 98GB-00009839.
 XX
 XX PA (GLAX) GLAXO GROUP LTD.
 XX
 XX PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX
 XX DR WPI: 2000-053101/04.
 XX
 XX DR N-PSDB; AAZ34749.
 XX

PT Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis.
 XX

PS Claim 1; Page 40; 81pp; English.

XX This sequence represents complementarity determining region 2 (CDR L2)
 CC of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11
 CC (see also AAY32262). The invention provides altered antibodies, such as
 CC chimeric or humanised antibodies, which comprise sufficient of the amino
 CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to
 CC render them capable of binding to the CD23 type II molecule expressed on
 CC haematopoietic cells. The antibodies are used to block soluble CD23
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis.
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They
 CC are also useful for studying interactions between CD23 and various
 CC ligands and determining the binding agents

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 |||||
 Db 1 LMSTRAS 7

RESULT 5
 AAE06969
 ID AAE06969 standard; protein; 100 AA.
 XX
 XX AC AAE06969;
 XX

DT 16-OCT-2001 (first entry)

XX Mouse germline kappa light chain variable (VK) region, 167/24.

XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;

KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;
 KW inflammatory glomerulopathy; vascular intervention;
 KW neointimal hyperplasia; VK; kappa light chain variable region.

OS Mus sp.
 XX
 XX WO200157226-A1.
 XX
 XX PD 09-AUG-2001.
 XX
 XX PF 02-FEB-2001; 2001WO-US003537.
 XX
 XX PR 03-FEB-2000; 2000US-00497625.
 XX
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX
 XX PI Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
 XX
 XX DR WPI: 2001-488888/53.

PT Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
 PT disorder in a patient, comprises a binding specificity for CCR2, and a
 PT non-human antigen binding region and human immunoglobulin.

PS Disclosure; Page 151; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
 CC comprising an antigen binding region of non-human origin and at least a
 CC portion of an immunoglobulin of human origin. The humanised antibodies
 CC are useful for inhibiting the interaction of a cell expressing CCR2. They
 CC are useful for inhibiting or treating HIV infection. The proteins of the
 CC invention are useful for inhibiting leukocyte trafficking, for treating
 CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
 CC disorders such as rheumatoid arthritis and multiple sclerosis,
 CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They
 CC are useful in therapy or diagnosis, and in the manufacture of a
 CC medicament for treating CCR-2 mediated disease. They are also useful for
 CC treating allergy, anaphylaxis, malignancy, chronic and acute
 CC inflammation, histamine and IgE-mediated allergic reaction, shock,
 CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
 CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
 CC associated with vascular intervention, including angioplasty and/or stent
 CC placement in a mammal. Humanised antibodies are also useful for
 CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
 CC neointimal hyperplasia of a vessel in a mammal, preferably associated
 CC with vascular intervention. The present sequence is mouse germline kappa
 CC light chain variable (VK) region, 167/24

XX Sequence 100 AA;

Query Match 100.0%; Score 31; DB 4; Length 100;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 |||||
 Db 55 LMSTRAS 61

RESULT 6
 ADQ89254
 ID ADQ89254 standard; protein; 100 AA.
 XX
 XX AC ADQ89254;
 XX

DT 21-OCT-2004 (first entry)

XX Mouse immunoglobulin protein #14.

XX Mouse; immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2;

KW CCR2; inflammatory disease; autoimmune disorder; graft rejection;
 KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;
 KW anti-HIV; virucide; antiarteriosclerotic.
 XX Mus musculus.
 OS US2004151721-A1.
 XX
 PN
 PD 05-AUG-2004.
 XX
 XX 10-DEC-2003; 2003US-00733563.
 PF
 XX 19-OCT-2001; 2001US-0350166P.
 PR
 PR 26-JUN-2002; 2002US-0392364P.
 PR
 PR 17-OCT-2002; 2002US-00272899.
 XX
 XX (OKEE/) O'KEEFE T.
 PA (PONA/) PONATH P.
 PA
 XX O'keefe T, Ponath P;
 PI
 XX WPI; 2004-580175/56.
 DR
 XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,
 PT useful for diagnosing and/or treating inflammatory or autoimmune
 PT diseases, and HIV infection.
 PT
 XX Example 2; SEQ ID NO 32; 128pp; English.
 PS
 XX The invention relates to humanised immunoglobulin heavy and light chains
 CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an
 CC immunoglobulin or its antigen binding fragment comprising the chains. The
 CC humanised immunoglobulin or its antigen binding fragment preferably
 CC comprises two heavy chains and two light chains. The humanised
 CC immunoglobulin and its heavy and light chains are useful for the
 CC diagnosis, prevention and/or treatment of diseases or conditions
 CC associated with aberrant expression or activity of the CCR2 polypeptide,
 CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV
 CC infection and atherosclerosis. This sequence represents a mouse
 CC immunoglobulin protein of the invention.
 XX
 XX
 SQ Sequence 100 AA;
 Query Match 100.0%; Score 31; DB 8; Length 100;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 |||||
 Db 55 LMSTRAS 61
 RESULT 7
 AAW39803
 ID AAW39803 standard; protein; 113 AA.
 XX
 AC AAW39803;
 XX
 DT 16-JUN-1998 (first entry)
 XX
 DE Variable domain of the Kappa light chain of catalytic antibody 12H1.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.
 XX
 PN WO9749800-A1.
 XX
 DT 31-DEC-1997.
 XX
 DE New catalytic antibodies able to decompose cocaine, single-chain

PF 25-JUN-1997; 97WO-US010965.
 XX
 PR 25-JUN-1996; 96US-00672345.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Landry DW;
 XX
 DR WPI; 1998-077166/07.
 DR P-PSDB; AAV09802.
 XX
 XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX
 XX Claim 18; Page 73; 147pp; English.
 PS
 XX AAW39801-05 represent the amino acid sequences of the variable domain of
 CC the Kappa light chain of catalytic antibodies which are able to degrade
 CC cocaine. A series of cocaine transition state analogues (TSAs) were
 CC prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAW39808
 CC represents the heavy chain) was identified using TSA2, and has a per
 CC minute Kcat of 0.016. The antibodies reduce the concentration of cocaine
 CC in a subject, and are used particularly for the treatment of an overdose.
 CC They are also used for treating addiction (by reducing the in vivo
 CC concentration that can be achieved)
 XX
 XX
 SQ Sequence 113 AA;
 Query Match 100.0%; Score 31; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 |||||
 Db 55 LMSTRAS 61
 RESULT 8
 AAW39886
 ID AAW39886 standard; protein; 113 AA.
 XX
 AC AAW39886;
 XX
 DT 18-JUN-1998 (first entry)
 XX
 DE Light chain of the catalytic antibody 6A12.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.
 XX
 PN WO9749800-A1.
 XX
 DT 31-DEC-1997.
 XX
 DE 25-JUN-1997; 97WO-US010965.
 XX
 PF 25-JUN-1996; 96US-00672345.
 PR
 PR (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Landry DW;
 XX
 DR WPI; 1998-077166/07.
 DR N-PSDB; AAV09793.
 XX
 XX New catalytic antibodies able to decompose cocaine, single-chain

PT analogues - used to treat cocaine overdose and addiction, required in far
 XX smaller doses than antibodies that antagonise cocaine by simply binding.
 PS Disclosure; Fig 19; 147pp; English.

CC The present sequence represents the light chain of a catalytic antibody
 CC which is capable of degrading cocaine. A series of cocaine transition
 CC state analogues (TSAs) were prepared and used to immunise mice for
 CC production of hybridomas. Catalytic antibodies were identified by their
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
 CC antibodies reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used for
 CC treating addiction (by reducing the in vivo concentration that can be
 CC achieved)

XX SQ Sequence 113 AA;

Query Match 100.0%; Score 31; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
 Db 55 LMSTRAS 61

RESULT 9

AAW39802
 ID AAW39802 standard; protein; 113 AA.

XX AC AAW39802;

XX DT 16-JUN-1998 (first entry)

XX DE Variable domain of the Kappa light chain of catalytic antibody 6A12.

XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

XX OS Mus sp.

XX PN WO9749800-A1.

XX PD 31-DEC-1997.

XX PF 25-JUN-1997; 97WO-US010965.

XX PR 25-JUN-1996; 96US-00672345.

XX PA (UYCO) UNIV COLUMBIA NEW YORK.

XX PI Landry DW;

XX DR WPI; 1998-077166/07.

XX PT New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX PS Claim 14; Page 72; 147pp; English.

XX SS AAW39801-05 represent the amino acid sequences of the variable domain of
 CC the kappa light chain of catalytic antibodies which are able to degrade
 CC cocaine. A series of cocaine transition state analogues (TSAs) were
 CC prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 6A12 antibody (AAW39807
 CC represents the heavy chain) was identified using TSA1, which is an
 CC immunogenic conjugate of a phosphate monoester transition state analogue.
 CC Antibody 6A12 has a per minute Kcat of 0.072. The antibodies reduce the
 CC concentration of cocaine in a subject, and are used particularly for the

CC treatment of an overdose. They are also used for treating addiction (by
 CC reducing the in vivo concentration that can be achieved)
 XX SQ Sequence 113 AA;

Query Match 100.0%; Score 31; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
 Db 55 LMSTRAS 61

RESULT 10

AAW39882

ID AAW39882 standard; protein; 113 AA.

XX AC AAW39882;

XX DT 16-JUN-1998 (first entry)

XX DE Light chain of the catalytic antibody 2A10.

XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

XX OS Mus sp.

XX PN WO9749800-A1.

XX PD 31-DEC-1997.

XX PF 25-JUN-1997; 97WO-US010965.

XX PR 25-JUN-1996; 96US-00672345.

XX PA (UYCO) UNIV COLUMBIA NEW YORK.

XX PI Landry DW;

XX DR WPI; 1998-077166/07.

XX N-PSDB; AAV09789.

XX PT New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX PS Disclosure; Fig 21; 147pp; English.

XX SS The present sequence represents the light chain of a catalytic antibody
 CC which is capable of degrading cocaine. A series of cocaine transition
 CC state analogues (TSAs) were prepared and used to immunise mice for
 CC production of hybridomas. Catalytic antibodies were identified by their
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
 CC antibodies reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used for
 CC treating addiction (by reducing the in vivo concentration that can be
 CC achieved)

XX SQ Sequence 113 AA;

Query Match 100.0%; Score 31; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
 Db 55 LMSTRAS 61

```

Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


Qy 1 LMSTRAS 7
 Db 55 LMSTRAS 61

RESULT 13
 ID AAY32261 standard; protein; 145 AA.
 XX AC AAY32261;
 XX DT 15-FEB-2000 (first entry)
 XX DE Mouse anti-CD23 Mab C11 light chain variable region.
 XX KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 KW therapy.
 XX OS Mus musculus.

Key Location/Qualifiers
 Region 55..70
 FT /note= "CDR L1"
 Region 83..92
 FT /note= "CDR L2"
 Region 125..134
 FT /note= "CDR L3"

XX W09958679-A1.
 XX 18-NOV-1999.
 XX 07-MAY-1999; 99WO-GB001434.
 XX 09-MAY-1998; 98GB-00009839.
 XX (GLAX) GLAXO GROUP LTD.
 XX Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 WPI; 2000-053101/04.
 N-PSDB; AAZ34746.

Cell receptor specific antibodies useful for treating e.g. arthritis,
 diabetes, multiple sclerosis and psoriasis.

Claim 8; Fig 2; 8lpp; English.

This sequence represents the light chain variable region (VL) of murine
 anti-CD23 (FCERII) monoclonal antibody C11. The invention provides
 altered antibodies, such as chimeric or humanised antibodies (see
 AAY32262 and AAY32263), which comprise sufficient of the amino acid
 sequences of the C11 light and heavy chain complementarity determining
 regions (see AAY32254-59) to render them capable of binding to the CD23
 type II molecule expressed on haematopoietic cells. The antibodies are
 used to block soluble CD23 formation in human therapy, for the treatment
 of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
 sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
 intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
 versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 bronchitis) or diabetes (particularly type I diabetes), and B-cell
 malignancies (claimed). They are also useful for studying interactions

CC between CD23 and various ligands and determining the binding agents
 XX
 SQ Sequence 145 AA;
 Query Match 100.0%; Score 31; DB 3; Length 145;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
 Db 86 LMSTRAS 92

RESULT 14
 ID ADG32323 standard; protein; 248 AA.
 XX AC ADG32323;
 XX DT 26-FEB-2004 (first entry)
 XX DE Mouse scFV VDM1 antibody targeted against V_dahliae SeqID 32.
 XX mouse; murine; scFV; anti-fungal peptide; APP; scFV; disease resistant;
 KW transgenic; plant; fungal infection; antibody;
 KW pathogen-specific antibody; fungicidal; agriculture.
 XX OS Mus sp.
 XX W02003089475-A2.
 XX 30-OCT-2003.
 XX 14-APR-2003; 2003WO-BP003852.
 XX 22-APR-2002; 2002EP-00008929.
 XX 28-MAY-2002; 2002EP-00011807.
 XX (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
 XX Peschen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;
 WPI; 2003-854088/79.
 DR N-PSDB; ADG32298.

New fusion protein comprising an anti-fungal protein or peptide and an
 antibody fragment, useful in agriculture and horticulture for producing
 Ascomyceta-resistant transgenic plants, plant cells or plant tissues.

Example 13; SEQ ID NO 32; 47pp; English.

This invention relates to a novel fusion protein comprising an anti-
 fungal protein or peptide (APP) and an antibody fragment (scFV).
 Specifically, it refers to APPs recognizing an epitope of an Ascomyceta
 and a cellular targeting sequence, which can be used to generate disease
 resistant transgenic plants that are protected against fungal infection.
 Accordingly, a method is described for antibody based resistance in
 plants such that the undesirable and expensive chemical controls often
 used in agriculture are not required. The present invention provides
 antibodies, recombinant antibodies and fragments thereof, as well as
 fusion proteins that can be used as pathogen-specific antibodies targeted
 to different plant cell compartments. As such, these fungicidal agents
 confer a broad spectrum of disease resistance in both economically
 important crops and ornamental plants. This polypeptide is an antibody
 used in an exemplification of the invention.

Qy 1 LMSTRAS 7
 Db 86 LMSTRAS 92

Query Match 100.0%; Score 31; DB 7; Length 248;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Job time : 76.7442 secs

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Db      189 LMSTRAS 195
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RESULT 15
ADG32360
ID ADG32360 standard; protein; 317 AA.
XX
AC ADG32360;
XX
DT 26-FEB-2004 (first entry)
XX
DE Precursor fusion protein of AFP AG-scfv VDM1 SeqID 69.
XX
KW scfV; anti-fungal peptide; AFP; scfV; disease resistant; transgenic;
XX plant; fungal infection; antibody; pathogen-specific antibody;
XX fungicidal; agriculture; mouse; chimeric; murine.
XX
OS Chimeric.
OS Synthetic.
OS Apergillus giganteus.
OS Mus musculus.
XX
PN WO2003089475-A2.
XX
PD 30-OCT-2003.
XX
PF 14-APR-2003; 2003WO-EP003852.
XX
PR 22-APR-2002; 2002EP-00008929.
XX
PR 28-MAY-2002; 2002EP-00011807.
XX
XX (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
XX
PI Peschen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;
XX
XX WPI; 2003-854088/79.
XX
DR N-PSDB; ADG32349.
XX
XX New fusion protein comprising an anti-fungal protein or peptide and an
FT antibody fragment, useful in agriculture and horticulture for producing
FT Ascomyceta-resistant transgenic plants, plant cells or plant tissues.
XX
XX Disclosure; SEQ ID NO 69; 47pp; English.
XX
XX This invention relates to a novel fusion protein comprising an anti-
CC fungal protein or peptide (AFP) and an antibody fragment (scfV).
CC Specifically, it refers to AFPs recognizing an epitope of an Ascomyceta
CC and a cellular targeting sequence, which can be used to generate disease
CC resistant transgenic plants that are protected against fungal infection.
CC Accordingly, a method is described for antibody based resistance in
CC plants such that the undesirable and expensive chemical controls often
CC used in agriculture are not required. The present invention provides
CC antibodies, recombinant antibodies and fragments thereof, as well as
CC fusion proteins that can be used as pathogen-specific antibodies targeted
CC to different plant cell compartments. As such, these fungicidal agents
CC confer a broad spectrum of disease resistance in both economically
CC important crops and ornamental plants. This polypeptide is a precursor
CC fusion protein of the order [AFP - linker - antibody fragment] of the
CC invention.
XX
SQ Sequence 317 AA;
Query Match 100.0%; Score 31; DB 7; Length 317;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMSTRAS 7
|||||
Db 258 LMSTRAS 264
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Search completed: April 18, 2005, 14:15:14

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:22:17 ; Search time 52.907 Seconds
(without alignments)
43.975 Million cell updates/sec

Title: US-09-674-716B-5

Perfect score: 31

Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	7	10	US-09-940-727B-23
2	31	100.0	7	10	US-09-940-727B-26
3	31	100.0	7	10	US-09-940-727B-29
4	31	100.0	100	9	US-09-840-459-32
5	31	100.0	100	16	US-10-766-773-32
6	31	100.0	100	16	US-10-766-610-32
7	31	100.0	100	16	US-10-733-563-32
8	31	100.0	113	10	US-09-940-727B-6
9	31	100.0	113	10	US-09-940-727B-7
10	31	100.0	113	10	US-09-940-727B-8
11	31	100.0	113	10	US-09-940-727B-104
12	31	100.0	113	10	US-09-940-727B-108
13	31	100.0	113	10	US-09-940-727B-112

14	29	93.5	63	15	US-10-424-599-191879	Sequence 191879,
15	28	90.3	7	10	US-09-940-727B-20	Sequence 20, Appl
16	28	90.3	113	10	US-09-940-727B-5	Sequence 5, Appl
17	28	90.3	113	10	US-09-940-727B-100	Sequence 100, App
18	28	90.3	276	15	US-10-425-114-49630	Sequence 49630, A
19	28	90.3	280	10	US-09-940-727B-119	Sequence 119, App
20	28	90.3	407	15	US-10-369-493-291	Sequence 291, App
21	28	90.3	979	15	US-10-104-047-2446	Sequence 2446, Ap
22	27	87.1	7	10	US-09-940-727B-80	Sequence 80, Appl
23	27	87.1	102	15	US-10-424-599-198627	Sequence 198627,
24	27	87.1	140	10	US-09-764-891-4114	Sequence 4114, Ap
25	27	87.1	342	15	US-10-282-122A-54281	Sequence 54281, A
26	27	87.1	409	14	US-10-238-075-835	Sequence 835, App
27	27	87.1	760	15	US-10-369-493-22564	Sequence 22564, A
28	27	87.1	809	14	US-10-032-585-7209	Sequence 7209, Ap
29	27	87.1	845	15	US-10-369-493-1487	Sequence 1487, Ap
30	27	87.1	1141	16	US-10-437-963-106873	Sequence 106873,
31	27	87.1	1401	15	US-10-369-493-2177	Sequence 2177, Ap
32	26	83.9	115	9	US-09-864-761-33844	Sequence 33844, A
33	26	83.9	133	15	US-10-104-047-2464	Sequence 2464, Ap
34	26	83.9	220	15	US-10-139-794-201	Sequence 201, App
35	26	83.9	246	15	US-10-366-125-13	Sequence 13, Appl
36	26	83.9	258	15	US-10-139-794-81	Sequence 81, Appl
37	26	83.9	347	16	US-10-437-963-151641	Sequence 151641,
38	26	83.9	364	16	US-10-437-963-110408	Sequence 110408,
39	26	83.9	420	16	US-10-468-091-24	Sequence 24, Appl
40	26	83.9	441	14	US-10-106-698-6367	Sequence 6367, Ap
41	26	83.9	449	9	US-09-925-301-884	Sequence 884, App
42	26	83.9	531	16	US-10-437-963-110409	Sequence 110409,
43	26	83.9	611	15	US-10-424-599-204138	Sequence 204138,
44	26	83.9	672	15	US-10-425-114-60058	Sequence 60058, A
45	26	83.9	810	9	US-09-712-363-281	Sequence 281, App

ALIGNMENTS

RESULT 1
US-09-940-727B-23
; Sequence 23, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940, 727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-23

Query Match 100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
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Db 1 LMSTRAS 7

RESULT 2
US-09-940-727B-26
; Sequence 26, Application US/09940727B

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; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-26

Query Match      100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 3
US-09-940-727B-29
; Sequence 29, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-29

Query Match      100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 4
US-09-840-459-32
; Sequence 32, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.

; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-766-773-32

Query Match      100.0%; Score 31; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 5
US-10-766-773-32
; Sequence 32, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-766-773-32

Query Match      100.0%; Score 31; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 6
US-10-766-610-32
; Sequence 32, Application US/10766610
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Publication No. US20040132980A1
GENERAL INFORMATION:
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-029
CURRENT APPLICATION NUMBER: US/10/766,610
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: 09/840,459
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 100
TYPE: PRT
ORGANISM: Mus musculus
US-10-766-610-32

Query Match 100.0%; Score 31; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 7
US-10-733-563-32
Sequence 32, Application US/10733563
Publication No. US20040151721A1
GENERAL INFORMATION:
APPLICANT: O'Keefe, Theresa
APPLICANT: Ponath, Paul
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
METHODS OF USE THEREOF
FILE REFERENCE: 10448-213001
CURRENT APPLICATION NUMBER: US/10/733,563
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: US 10/272,899
PRIOR FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 60/392,364
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/350,166
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 100
TYPE: PRT
ORGANISM: Mus musculus
US-10-733-563-32

Query Match 100.0%; Score 31; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 8
US-09-940-727B-6
Sequence 6, Application US/09940727B
Publication No. US20030077793A1
GENERAL INFORMATION:
APPLICANT: Landry, Donald W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 0575/51400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR FILING DATE: 1997-06-25
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 113
TYPE: PRT
ORGANISM: mouse
US-09-940-727B-6

Query Match 100.0%; Score 31; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 9
US-09-940-727B-7
Sequence 7, Application US/09940727B
Publication No. US20030077793A1
GENERAL INFORMATION:
APPLICANT: Landry, Donald W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 0575/51400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR FILING DATE: 1997-06-25
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 113
TYPE: PRT
ORGANISM: mouse
US-09-940-727B-7

Query Match 100.0%; Score 31; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 10
US-09-940-727B-8
Sequence 8, Application US/09940727B
Publication No. US20030077793A1
GENERAL INFORMATION:

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; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-8

Query Match          100.0%; Score 31; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
Db      55 LMSTRAS 61

RESULT 11
US-09-940-727B-104
; Sequence 104, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-104

Query Match          100.0%; Score 31; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
Db      55 LMSTRAS 61

RESULT 12
US-09-940-727B-108
; Sequence 108, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
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; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-108

Query Match          100.0%; Score 31; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
Db      55 LMSTRAS 61

RESULT 13
US-09-940-727B-112
; Sequence 112, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 112
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-112

Query Match          100.0%; Score 31; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
Db      55 LMSTRAS 61

RESULT 14
US-10-424-599-191879
; Sequence 191879, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 191879
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Glycine max
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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_15287C.1.pep
; US-10-424-599-191879

Query Match      93.5%; Score 29; DB 15; Length 63;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
Db      24 IMSTRAS 30

RESULT 15
US-09-940-727B-20
; Sequence 20, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
; US-09-940-727B-20

Query Match      90.3%; Score 28; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMSTRAS 7
Db      1 LMSTRSS 7

Search completed: April 18, 2005, 14:54:40
Job time : 53.907 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:01:43 ; Search time 19.0465 Seconds
(without alignments)
27.435 Million cell updates/sec

Title: US-09-674-716B-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	7	2	US-08-672-345C-23
2	31	100.0	7	2	US-08-672-345C-26
3	31	100.0	7	2	US-08-672-345C-29
4	31	100.0	7	3	US-09-214-095D-23
5	31	100.0	7	3	US-09-214-095D-26
6	31	100.0	7	3	US-09-214-095D-29
7	31	100.0	100	4	US-08-840-459-32
8	31	100.0	100	4	US-09-497-625A-32
9	31	100.0	113	2	US-08-672-345C-6
10	31	100.0	113	2	US-08-672-345C-7
11	31	100.0	113	2	US-08-672-345C-8
12	31	100.0	113	2	US-08-672-345C-96
13	31	100.0	113	2	US-08-672-345C-97
14	31	100.0	113	2	US-08-672-345C-98
15	31	100.0	113	3	US-09-214-095D-6
16	31	100.0	113	3	US-09-214-095D-7
17	31	100.0	113	3	US-09-214-095D-8
18	31	100.0	113	3	US-09-214-095D-104
19	31	100.0	113	3	US-09-214-095D-108
20	31	100.0	113	3	US-09-214-095D-112
21	28	90.3	7	2	US-08-672-345C-20
22	28	90.3	7	3	US-09-214-095D-20
23	28	90.3	113	2	US-08-672-345C-5
24	28	90.3	113	2	US-08-672-345C-95
25	28	90.3	113	3	US-09-214-095D-5
26	28	90.3	113	3	US-09-214-095D-100
27	28	90.3	280	3	US-09-214-095D-119

28	27	87.1	7	2	US-08-672-345C-80	Sequence 80, Appl
29	27	87.1	7	3	US-09-214-095D-80	Sequence 80, Appl
30	27	87.1	234	4	US-09-538-092-230	Sequence 230, App
31	27	87.1	249	4	US-09-248-796A-14685	Sequence 14685, A
32	27	87.1	331	4	US-09-248-796A-18673	Sequence 18673, A
33	27	87.1	451	4	US-09-502-540-15550	Sequence 15550, A
34	26	83.9	250	3	US-09-029-348-14	Sequence 14, Appl
35	26	83.9	1341	3	US-08-963-825-18	Sequence 18, Appl
36	26	83.9	1341	3	US-09-500-811-18	Sequence 18, Appl
37	26	83.9	1341	3	US-09-570-573-18	Sequence 18, Appl
38	26	83.9	1341	3	US-09-548-608-18	Sequence 18, Appl
39	26	83.9	1461	4	US-09-585-887-9	Sequence 9, Appl
40	26	83.9	1461	4	US-09-289-578-9	Sequence 9, Appl
41	26	83.9	1464	4	US-09-331-347C-21	Sequence 21, Appl
42	25	80.6	51	4	US-09-270-767-34317	Sequence 34317, A
43	25	80.6	51	4	US-09-270-767-49534	Sequence 49534, A
44	25	80.6	130	4	US-09-252-991A-27521	Sequence 27521, A
45	25	80.6	221	4	US-09-248-796A-20200	Sequence 20200, A

ALIGNMENTS

RESULT 1
US-08-672-345C-23
; Sequence 23, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-23

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred.No. 4.1e+05; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 2

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US-08-672-345C-26
; Sequence 26, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-672-345C-26

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 3
US-08-672-345C-29
; Sequence 29, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-672-345C-26

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 4
US-09-214-095D-23
; Sequence 23, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-23

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 5
US-09-214-095D-26
; Sequence 26, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-26

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LMSTRAS 7
| | | | |
Db 1 LMSTRAS 7

RESULT 6
US-09-214-095D-29
; Sequence 29, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214, 095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-29

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
| | | | |
Db 1 LMSTRAS 7

RESULT 7
US-09-840-459-32
; Sequence 32, Application US/09840459
; Patent No. 6698550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840, 459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-32

Query Match 100.0%; Score 31; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
| | | | |
Db 55 LMSTRAS 61

RESULT 8
US-09-497-625A-32
; Sequence 32, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-497-625A-32

Query Match 100.0%; Score 31; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
| | | | |
Db 55 LMSTRAS 61

RESULT 9
US-08-672-345C-6
; Sequence 6, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-6

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|||||||
DB 55 LMSTRAS 61

RESULT 10

US-08-672-345C-7
; Sequence 7, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-672-345C-7

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
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DB 55 LMSTRAS 61

RESULT 11

US-08-672-345C-8
; Sequence 8, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas

;
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-672-345C-8

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|||||||
DB 55 LMSTRAS 61

RESULT 12

US-08-672-345C-96
; Sequence 96, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid

US-08-672-345C-96

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-96

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
| | | | |
Db 55 LMSTRAS 61

RESULT 13

US-08-672-345C-97
; Sequence 97, Application US/08672345C
; Patent No. 5948658

; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525

; INFORMATION FOR SEQ ID NO: 97:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-97

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
| | | | |
Db 55 LMSTRAS 61

RESULT 14

US-08-672-345C-98
; Sequence 98, Application US/08672345C
; Patent No. 5948658

; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper and Dunham LLP

; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525

; INFORMATION FOR SEQ ID NO: 98:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-98

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
| | | | |
Db 55 LMSTRAS 61

RESULT 15

US-09-214-095D-6

; Sequence 6, Application US/09214095D
; Patent No. 6280987

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT

; ORGANISM: Murinae gen. sp.

US-09-214-095D-6

Query Match 100.0%; Score 31; DB 3; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
| | | | |
Db 55 LMSTRAS 61

Search completed: April 18, 2005, 14:25:26

Job time : 20.0465 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 14:49:23 ; Search time 42 Seconds
(without alignments)
16.036 Million cell updates/sec

Title: US-09-674-716B-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: piri: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	45.2	3	3 I50412	gene p20K protein
2	13	41.9	6	2 A11490	pyruvate kinase (E
3	12	38.7	5	2 I40469	dnazX-like protein
4	12	38.7	6	2 I51434	H4 histone - Afric
5	12	38.7	6	2 PT0518	T-cell receptor be
6	11	35.5	5	2 B31836	20K protein - Rick
7	11	35.5	5	2 H44817	34.5K structural p
8	11	35.5	5	2 F44817	34.5K structural p
9	11	35.5	5	2 A58728	serrawettin W2 - S
10	11	35.5	7	2 S42620	aggreacan - bovine
11	10	32.3	5	2 A37114	hypoxanthine phosph
12	10	32.3	5	2 PT0295	Ig heavy chain CRD
13	10	32.3	5	2 PT0577	T-cell receptor be
14	10	32.3	5	2 PT0700	T-cell receptor be
15	10	32.3	5	2 S69237	surface protein te
16	10	32.3	5	2 PT0565	T-cell receptor be
17	10	32.3	6	2 A37765	hypothetical prote
18	10	32.3	6	2 S14159	paraspasal crystal
19	10	32.3	6	2 B26206	alpha-1,4-glucan-p
20	10	32.3	6	2 A46474	EC epsilon R11b -
21	10	32.3	7	2 A34026	acetylcholinestera
22	10	32.3	7	2 B33541	hypothetical prote
23	10	32.3	7	4 I55382	hypothetical pepti
24	9	29.0	3	3 I78890	tyrosine protein k
25	9	29.0	5	2 S70154	URF2 protein - Xan
26	9	29.0	5	2 I40702	primase - Citrobac
27	9	29.0	5	2 B37325	pap fibmbrial regul
28	9	29.0	5	2 T14910	hypothetical prote
29	9	29.0	5	2 PT0695	T-cell receptor be

30	9	29.0	5	2 PT0686	T-cell receptor be
31	9	29.0	6	2 B34835	dnAA protein - Pse
32	9	29.0	6	2 I49808	D-SP2.5 region - m
33	9	29.0	6	2 PT0643	T-cell receptor be
34	9	29.0	6	2 A41946	T-cell receptor ga
35	9	29.0	6	2 I49421	laminin B1 - weste
36	9	29.0	6	2 PC4127	hypothetical 6 pro
37	9	29.0	6	4 S15596	orf 3 rara 5'-regi
38	9	29.0	7	2 S25266	pilE protein - Esc
39	9	29.0	7	2 S38516	mabinlin II chain
40	9	29.0	7	2 E61491	seed protein wa-5
41	9	29.0	7	2 PT0520	T-cell receptor be
42	9	29.0	7	2 PN0649	pullulanase (EC 3.
43	9	29.0	7	2 S45311	microcin C7 - Esch
44	9	29.0	7	2 A28340	myomodulin - Calif
45	9	29.0	7	2 S33244	neuromodulatory pe

ALIGNMENTS

RESULT 1

I50412
Gene p20K protein - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: I50412
R:MaO, P.L.; Beauchemin, M.; Bedard, P.A.
J. Biol. Chem. 268, 8131-8139, 1993
A:Title: Quiescence-dependent activation of the p20K promoter in growth-arrested chicken
A:Reference number: A46643; MUID:93216790; PMID:8463325
A:Accession: I50412
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3 <MAO>
A:Cross-references: GB:I02537; NID:G212616; PID:G212617
C:Genetics:
A:Gene: p20K

Query Match 45.2%; Score 14; DB 3; Length 3;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MST 4
DB 1 MST 3

RESULT 2

A11490
pyruvate kinase (EC 2.7.1.40) - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 03-Mar-1995
C:Accession: A11490
R:Hjeltnquist, G.; Andersson, J.; Edlund, B.; Engstrom, L.
Biochem. Biophys. Res. Commun. 61, 559-563, 1974
A:Title: Amino acid sequence of a (32-P)phosphopeptide from pig liver pyruvate kinase p
A:Reference number: A11490; MUID:75127438; PMID:4375989
A:Accession: A11490
A:Molecule type: protein
A:Residues: 1-6 <HJE>
A:Experimental source: liver
C:Keywords: glycolysis; phosphotransferase

Query Match 41.9%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RAS 7
DB 3 RAS 5

```

RESULT 3
I40469
dnazX-like protein - Bacillus subtilis (fragment)
C:Species: Bacillus subtilis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40469
R;Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.
Mol. Gen. Genet. 215, 478-482, 1989
A:Title: Transcription and processing of Bacillus subtilis small cytoplasmic RNA.
A:Reference number: I40469; MUID:89218958; PMID:2468993
A:Accession: I40469
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: UNIPROT:P09122; EMBL:X14796; NID:g40130; PIDN:CAA32902.1; PID:g43762
C:Genetics:
A:Start codon: GTG

Query Match 38.7%; Score 12; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTR 6
|||
Db 1 MSYQA 5

RESULT 4
I51434
H4 histone - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51434
R;Woodland, H.R.; Warmington, J.R.; Ballantine, J.E.M.; Turner, P.C.
Nucleic Acids Res. 12, 4939-4958, 1984
A:Title: Are there major developmentally regulated H4 gene classes in Xenopus?
A:Reference number: I51391; MUID:84247348; PMID:6330691
A:Accession: I51434
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-6 <WO>
A:Cross-references: GB:K02304; NID:g214227; PIDN:AAA49738.1; PID:g555517

Query Match 38.7%; Score 12; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MSTR 5
|||
Db 1 MSGR 4

RESULT 5
PT0518
T-cell receptor beta chain V-D-J region (100-4B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0518
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0518
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 38.7%; Score 12; DB 2; Length 6;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 STRAS 7
|||
Db 1 ASRAT 5

RESULT 6
B31836
20K protein - Rickettsia rickettsii (fragment)
C:Species: Rickettsia rickettsii
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999
C:Accession: B31836
R;Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.
J. Bacteriol. 170, 4493-4500, 1988
A:Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii
A:Reference number: A91885; MUID:89008059; PMID:3139629
A:Accession: B31836
A:Molecule type: DNA
A:Residues: 1-5 <AND>
A:Cross-references: GB:J03371; NID:g152455; PIDN:AAD15030.1; PID:g4362874

Query Match 35.5%; Score 11; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 MSTR 6
|||
Db 1 MDTNS 5

RESULT 7
H44817
34.5K structural protein - Leuconostoc oenos phage P32 (fragment)
C:Species: Leuconostoc oenos phage P32
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: H44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: H44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Note: sequence extracted from NCBI backbone (NCBIP:70332)

Query Match 35.5%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MST 4
|||
Db 1 MAT 3

RESULT 8
F44817
34.5K structural protein - Leuconostoc oenos phage P54 (fragment)
C:Species: Leuconostoc oenos phage P54
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: F44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: F44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Note: sequence extracted from NCBI backbone (NCBIP:70335)

Query Match 35.5%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MST 4
|||

```


Db 1 MAT 3

RESULT 9

A58728 serrawettin W2 - Serratia marcescens

C;Species: Serratia marcescens

C;Date: 10-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 12-Feb-1998

C;Accession: A58728

R;Matsuyama, T.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.

J. Bacteriol. 174, 1769-1776, 1992

A;Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent and

A;Reference number: A58728; MUID:92193260; PMID:1548227

A;Accession: A58728

A;Status: unencoded polypeptide

A;Molecule type: protein

A;Residues: 1-5 <MAT>

A;Experimental source: strain NS 25

C;Comment: A surfactant lipopeptide promoting flagellum-independent surface translocation

C;Keywords: blocked amino end; blocked carboxyl end; D-amino acid; lipoprotein; unencoded

F;1/Modified site: D-leucine (Ileu) #status experimental

F;4/Modified site: D-phenylalanine (Phe) #status experimental

F;1-5/Cross-link: 3-hydroxydecanoyl amino end, ester carboxyl end (Leu-Ile) #status experimental

Query Match

Best Local Similarity 35.5%; Score 11; DB 4; Length 5;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MST 4

Db 1 LST 3

RESULT 10

S42620

aggreccan - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998

C;Accession: S42620

R;Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.

Matrix Biol. 14, 171-179, 1994

A;Title: Aggreccan in bovine tendon.

A;Reference number: S42620; MUID:94340214; PMID:7520336

A;Accession: S42620

A;Molecule type: protein

A;Residues: 1-7 <VOG>

A;Experimental source: flexor tendon

C;Keywords: cartilage

Query Match

Best Local Similarity 40.0%; Score 11; DB 2; Length 7;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTR 5

Db 3 IVSPR 7

RESULT 11

A37114

hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistosoma mansoni) (fragm

C;Species: Schistosoma mansoni

C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 23-Jun-1993

C;Accession: A37114

R;Luan, L.; Craig, S.P.; McKerrow, J.H.; Wang, C.C.

J. Biol. Chem. 265, 13528-13532, 1990

A;Title: The hypoxanthine-guanine phosphoribosyltransferase of Schistosoma mansoni. Fur

A;Reference number: A37114; MUID:90337955; PMID:2199439

A;Accession: A37114

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <YUA>

C;Keywords: glycosyltransferase; pentosyltransferase

Query Match

Best Local Similarity 32.3%; Score 10; DB 2; Length 5;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MST 4

Db 1 MSS 3

RESULT 12

PT0295

Ig heavy chain CRD3 region (clone 5-91) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0295

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0295

A;Molecule type: DNA

A;Residues: 1-5 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 32.3%; Score 10; DB 2; Length 5;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TR 5

Db 3 TR 4

RESULT 13

PT0577

T-cell receptor beta chain V-D-J region (141-IBC) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0577; PT0574

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0577

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FEE>

A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-IBC

A;Accession: PT0574

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FE2>

A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-IQ

C;Keywords: T-cell receptor

Query Match

Best Local Similarity 32.3%; Score 10; DB 2; Length 5;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STR 5

Db 2 SSR 4

RESULT 14

PT0700

T-cell receptor beta chain V-D-J region (161-2A) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0700

R;Peeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0700
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

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Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STR 5
|:
Db 2 SSR 4

RESULT 15
S69237
surface protein tetraabrachion heavy chain - Staphylothermus marinus (fragment)
C;Species: Staphylothermus marinus
C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
C;Accession: S69237
R;Peters, J.; Nitsch, M.; Kuehlmoegen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Engelh
J. Mol. Biol. 245, 385-401, 1995
A;Title: Tetraabrachion: a filamentous archaeobacterial surface protein assembly of unusua
A;Reference number: S69237; MUID:95139068; PMID:7837271
A;Accession: S69237
A;Molecule type: protein
A;Residues: 1-5 <PET>
A;Experimental source: strain F1, DSM 3639
C;Keywords: cell wall; glycoprotein; heat-stable protein

Query Match 32.3%; Score 10; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMS 3
|:
Db 3 LLS 5

Search completed: April 18, 2005, 15:02:19
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:25:50 ; Search time 182 Seconds
(without alignments)
19.695 Million cell updates/sec

Title: US-09-674-716B-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 174

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	14	45.2	7	1 GFRP MOUSE	P99025 mus musculus
2	11	35.5	5	1 BIOA CITFR	P13071 citrobacter
3	11	35.5	6	2 P82541	P82541 spinacia ol
4	11	35.5	7	1 UC24 MAIZE	P80630 zea mays (m
5	10	32.3	6	1 VP19 HHV1K	P23210 human herpe
6	10	32.3	7	2 Q65578	Q65578 bovine herp
7	9	29.0	4	1 ILME SEPOF	P83568 sepia offic
8	9	29.0	6	1 PYF1 PENNO	P84005 penaeus mon
9	9	29.0	7	1 UH11 RAT	P56576 rattus norv
10	9	29.0	7	1 WWAL_ACHFUFU	P35919 achatina fu
11	9	29.0	7	1 WWAL_ACHFUFU	P35920 achatina fu
12	9	29.0	7	1 WWAL_ACHFUFU	P35921 achatina fu
13	9	29.0	7	2 P83492	P83492 bionectria
14	9	29.0	7	2 Q8MFY6	Q8MFY6 taraxacum (
15	9	29.0	7	2 Q95945	Q95945 saccharomyc
16	9	29.0	7	2 P93233	P93233 lycopersico
17	9	29.0	7	2 P70804	P70804 azotobacter
18	9	29.0	7	2 Q8KMS3	Q8KMS3 klebsiella
19	9	29.0	7	2 Q47505	Q47505 escherichia
20	8	25.8	5	2 Q99007	Q99007 hordeum vul
21	8	25.8	7	1 CIA_ENTFA	P11932 enterococcu
22	7	22.6	4	1 TUFT_HUMAN	P01858 homo sapien
23	7	22.6	6	2 P82181	P82181 spinacia ol
24	7	22.6	6	2 P82182	P82182 spinacia ol
25	7	22.6	7	2 IGAO_DACDE	P06294 dactylium d
26	7	22.6	7	2 Q34028	Q34028 sphingomona
27	7	22.6	7	2 Q47029	Q47029 enterobacte
28	6	19.4	4	1 DCMS_PSECH	P19918 pseudomonas
29	6	19.4	4	1 FFKA_ANTEL	P58705 anthopleura
30	6	19.4	5	1 BIOB CITFR	P12997 citrobacter
31	6	19.4	5	1 PRCT_CARMA	P67857 carcinus ma

32	6	19.4	5	1 PRCT LIMPO	P67858 limulus pol
33	6	19.4	5	1 PRCT PERAM	P67859 periplaneta
34	6	19.4	5	1 PSK DAUCA	P58261 daucus caro
35	6	19.4	5	2 P83073	P83073 bacillus ce
36	6	19.4	6	1 TRPI_PSEPU	P36414 pseudomonas
37	6	19.4	6	1 UN06_CLOPA	P81351 clostridium
38	6	19.4	6	2 P83533	P83533 lactobacill
39	6	19.4	7	1 CCFL_ENTFA	P20104 enterococcu
40	6	19.4	7	1 CHOX_ALCSP	P16101 alcaligenes
41	6	19.4	7	2 Q15897	Q15897 homo sapien
42	6	19.4	7	2 Q15903	Q15903 homo sapien
43	6	19.4	7	2 Q8NH77	Q8NH77 homo sapien
44	6	19.4	7	2 Q8TAQ4	Q8TAQ4 homo sapien
45	6	19.4	7	2 Q9BRY4	Q9BRY4 homo sapien

ALIGNMENTS

RESULT 1

ID	GFRP MOUSE	STANDARD;	PRT;	7 AA.
AC	P99025;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).			
GN	Name=Gchfr; Synonyms=Gfrp;			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE			
RC	TISSUE=liver;			
RA	Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,			
RA	Hoogland C., Appel R.D., Binz P.-A., Hochrasser D.F., Cowthorne M.;			
RL	Submitted (AUG-1998) to Swiss-Prot.			
CC	-!- FUNCTION: Mediates tetrahydrobiopterin inhibition of GTP			
CC	cyclohydrolase I. This inhibition is reversed by L-phenylalanine			
CC	(By similarity).			
CC	-!- SUBUNIT: Homodimer (By similarity).			
DR	SWISS-2DPAGE; P99025; MOUSE.			
KW	Direct protein sequencing.			
FT	INIT MET 0 0			
FT	NON_TER 7 7			
SQ	SEQUENCE 7 AA; 806 MW; 71BSB057273B4700 CRC64;			

Query Match 45.2%; Score 14; DB 1; Length 7;

Best Local Similarity 75.0%; Pred. NO. 1.6e+06;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1 LMST 4
Db	4 List 7

RESULT 2

ID	BIOA CITFR	STANDARD;	PRT;	5 AA.
AC	P13071;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase			
DE	(EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA			
DE	aminotransferase) (Fragment).			
GN	Name=bioA;			
OS	Citrobacter freundii.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Citrobacter.			
OX	NCBI_TaxID=546;			
RN	[1]			

RP SEQUENCE FROM N.A.
RX MEDLINE=89006280; PubMed=2971595; DOI=10.1016/0378-1119(88)90397-6;
RA Shiuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of *Escherichia coli*,
Citrabacter freundii and *Salmonella typhimurium* biotin operons.";
RL Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-diaminononanoate.
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- PATHWAY: Biotin biosynthesis.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent aminotransferase family.
CC -----
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CC -----
CC EMBL; M21922; -; NOT_ANNOTATED_CDS.
CC PIR; I40697; I40697.
CC InterPro; IPR005814; Aminotrans 3.
CC PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
CC Amino transferase; Biotin biosynthesis; Pyridoxal phosphate;
CC Transferase.
CC NON TER 5 5
CC SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
CC
CC Query Match 35.5%; Score 11; DB 1; Length 5;
CC Best Local Similarity 66.7%; Pred. No. 1.6e+06;
CC Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 2 MST 4
CC | |
CC 1 MTT 3
CC
CC Db
CC
CC RESULT 3
CC P82541
CC ID P82541 PRELIMINARY; PRT; 6 AA.
CC AC P82541;
CC DT 01-OCT-2000 (TrEMBLrel. 15, Created)
CC DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
CC DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
CC DE Chloroplast 30S ribosomal protein S19 beta (fragment).
CC OS Spinacia oleracea (Spinach).
CC OG Chloroplast
CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
CC OC Caryophyllales; Amaranthaceae; Spinacia.
CC OX NCBI_TaxID=3562;
CC RN [1]
CC SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
CC STRAIN=cv. ALMARO; TISSUE=Leaf;
CC RX MEDLINE=20435797; PubMed=10874039; DOI=10.1074/jbc.M004350200;
CC RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
CC RT "The plastid ribosomal proteins. Identification of all the proteins in the small subunit of an organelle ribosome (chloroplast).";
CC RL J. Biol. Chem. 37:28455-28465(2000).
CC CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC CC -1- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
CC CC -1- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
CC CC -1- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PT. S19 BETA FORM IS THE MINOR BASIC FORM.
CC CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 kDa.
CC CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC GO; GO:0009507; C:chloroplast; IEA.

DR GO; GO:0019843; F:rRNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR002222; Ribosomal_S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;
CC
CC Query Match 35.5%; Score 11; DB 2; Length 6;
CC Best Local Similarity 66.7%; Pred. No. 1.6e+06;
CC Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 4 TRA 6
CC | |
CC 1 TRS 3
CC
CC Db
CC
CC RESULT 4
CC UC24_MAIZE
CC ID UC24_MAIZE STANDARD; PRT; 7 AA.
CC AC P80630;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 05-JUL-2004 (Rel. 44, Last annotation update)
CC DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 447) (fragment).
CC OS Zea mays (Maize).
CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
CC OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
CC OX NCBI_TaxID=4577;
CC RN [1]
CC SEQUENCE
CC TISSUE=Coleoptile;
CC RA Touzet P., Riccardi P., Morin C., Danervall C., Huet J.-C.,
CC RT Pernollet J.-C., Zivy M., de Vienne D.;
CC RT "The maize two dimensional gel protein database: towards an integrated genome analysis program";
CC RL Theor. Appl. Genet. 93:997-1005(1996).
CC CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 6.0, its MW is: 30.0 kDa.
CC CC Maize-2DPAGE; P80630; COLEOPTILE.
CC DR MaizeDB; 123956; -.
CC KW Direct protein sequencing.
CC FT NON TER 1
CC FT NON TER 7
CC FT NON TER 7
CC SQ SEQUENCE 7 AA; 665 MW; 6DC1B5B33DC1B5D0 CRC64;
CC
CC Query Match 35.5%; Score 11; DB 1; Length 7;
CC Best Local Similarity 60.0%; Pred. No. 1.6e+06;
CC Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CC
CC QY 3 STRAS 7
CC | |
CC 1 STAKS 5
CC
CC Db
CC
CC RESULT 5
CC VP19_HHV1K
CC ID VP19_HHV1K STANDARD; PRT; 6 AA.
CC AC P23210;
CC DT 01-NOV-1991 (Rel. 20, Created)
CC DT 01-NOV-1991 (Rel. 20, Last sequence update)
CC DT 05-JUL-2004 (Rel. 44, Last annotation update)
CC DE Capsid assembly and DNA maturation protein (Virion protein UL38) (Capped protein VP19C) (fragment).
CC OS Human herpesvirus 1 (strain KOS) (HHV-1) (Human herpes simplex virus 1).
CC OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CC OC Alphaherpesvirinae; Simplexvirus.
CC OX NCBI_TaxID=10306;
CC RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=91101287; PubMed=1846198;
RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the
RT expression of UL38, a true late gene involved in capsid assembly.";
RL J Virol. 65:769-786 (1991).
CC -!- FUNCTION: Component of the basal layer in which the capsids are
CC embedded. Binds DNA.
CC -!- SIMILARITY: Belongs to the herpesviruses VP19C family.
CC -----
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CC or send an email to license@isb-eib.ch).
CC -----
DR EMBL; M57646; AAA45830.1; -;
KW Capsid assembly; Coat protein; DNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 32.3%; Score 10; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MST 4
| | | |
Db 1 MKT 3

RESULT 6
Q65578 PRELIMINARY; PRT; 7 AA.
AC Q65578;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Bovine herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Cooper;
RX MEDLINE=95313343; PubMed=7793062;
RA Vicek C., Benes V., Lu Z., Kutish G.F., Paces V., Rock D.,
RA Letchworth G.J., Schwytzer M.;
RT "Nucleotide sequence analysis of a 30-kb region of the bovine
RT herpesvirus 1 genome which exhibits a colinear gene arrangement with
RT the UL21 to UL4 genes of herpes simplex virus.";
RL Virology 210:100-108 (1995).
DR EMBL; Z48053; CAA88130.1; -;
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 7 AA; 758 MW; 6DD33455B1F1B1C0 CRC64;

Query Match 32.3%; Score 10; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 STRA 6
| | | |
Db 4 SNKA 7

RESULT 7
ILME SEPOF
ID -ILME_SEPOF STANDARD; PRT; 4 AA.
AC P83568;

DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pheromone peptide ILME.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
RP SPECTROMETRY.
RC TISSUE=Egg;
RX MEDLINE=20403899; PubMed=10944457; DOI=10.1006/bbrc.2000.3286;
RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
RT "TIME: a waterborne pheromonal peptide released by the eggs of Sepia
RT officinalis";
RL Biochem. Biophys. Res. Commun. 275:217-222 (2000).
RN [2]
RP SEQUENCE.
RC TISSUE=Egg;
RX MEDLINE=22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;
RA Zatylny C., Marvin L., Gagnon J., Henry J.;
RT "Fertilization in Sepia officinalis: the first mollusk sperm-
RT attracting peptide";
RL Biochem. Biophys. Res. Commun. 296:1186-1193 (2002).
CC -!- FUNCTION: Has myotropic activity targeting the genital tract.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Follicle, fully grown oocyte and egg (EC2).
CC -!- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
KW Direct protein sequencing; Pheromone.
SQ SEQUENCE 4 AA; 505 MW; 6B16972030000000 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LM 2
| |
Db 2 LM 3

RESULT 8
PYFI_PENMO STANDARD; PRT; 6 AA.
ID PYFI_PENMO
AC P84005;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peptide tyrosine phenylalanine 1 (Pm-PYFI).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
RC TISSUE=Eveatalk;
RX PubMed=12431727; DOI=10.1016/S0196-9781(02)00176-6;
RA Sithigongul P., Pupum J., Krungkarn C., Longyant S., Panchan N.,
RA Chaiyuthangkura P., Sithigongul W., Petsom A.;
RT "Four novel PYFs: members of NPY/PP peptide superfamily from the
RT eyestalk of the giant tiger prawn Penaeus monodon.";
RL Peptides 23:1895-1906 (2002).
CC -!- FUNCTION: May act as a neurotransmitter, neuromodulator or
CC neurohormone.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Limited to neuronal cell bodies, neuronal
CC processes and sinus gland.
CC -!- MASS SPECTROMETRY: MW=801.5; METHOD=MALDI; RANGE=1-6; NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the NPY family.
DR InterPro; IPR001955; Pancreatic hormn.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; PARTIAL.
DR PROSITE; PS50276; PANCREATIC_HORMONE_2; PARTIAL.

KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 6 6 Phenylalanine amide (Potential).
 SQ SEQUENCE 6 AA; 802 MW; 69D417740DC46000 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RA 6
 DB 1 RA 2

RESULT 9
 UH11_RAT
 ID UH11_RAT STANDARD; PRT; 7 AA.
 AC P56576;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Unknown protein from 2D-PAGE of heart tissue (Spot P11) (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Heart;
 RA Li X.-P., Pleisner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
 RA Jungblut P.R.;
 RL Submitted (SEP-1998) to Swiss-Prot.
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 8.5, its MW is: 42 kDa.
 KW Direct protein sequencing.
 FT NON_TER 2 2 S or A.
 FT UNSURE 7 7
 SQ SEQUENCE 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 STR 5
 DB 2 SAR 4

RESULT 10
 WWA1_ACHF
 ID WWA1_ACHF STANDARD; PRT; 7 AA.
 AC P35919;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Wwamide-1.
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Ganglion;
 RX MEDLINE=93265912; PubMed=8495720; DOI=10.1016/0014-5793(93)81458-C;
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
 RT "Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from
 RT ganglia of the African giant snail, Achatina fulica.";
 RL FEBS Lett. 323:104-108(1993).
 CC -1- FUNCTION: Exhibits modulatory effects on the peripheral nervous
 CC system. Inhibits activity on a central neuron.
 DR PIR; S33245; S33245.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 7 7 Tryptophan amide.
 SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MS 3
 DB 4 MS 5

RESULT 11
 WWA2_ACHF
 ID WWA2_ACHF STANDARD; PRT; 7 AA.
 AC P35920;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Wwamide-2.
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Ganglion;
 RX MEDLINE=93265912; PubMed=8495720; DOI=10.1016/0014-5793(93)81458-C;
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
 RT "Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from
 RT ganglia of the African giant snail, Achatina fulica.";
 RL FEBS Lett. 323:104-108(1993).
 CC PIR; S33246; S33246.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 7 7 Tryptophan amide.
 SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MS 3
 DB 4 MS 5

RESULT 12
 WWA3_ACHF
 ID WWA3_ACHF STANDARD; PRT; 7 AA.
 AC P35921;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Wwamide-3.
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Ganglion;
 RX MEDLINE=93265912; PubMed=8495720; DOI=10.1016/0014-5793(93)81458-C;
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
 RT "Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from
 RT ganglia of the African giant snail, Achatina fulica.";
 RL FEBS Lett. 323:104-108(1993).
 CC PIR; S33244; S33244.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 7 7 Tryptophan amide.
 SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MS 3
 DB 4 MS 5

QY 2 MS 3
 Db 4 MS 5

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13

P83492 P83492 PRELIMINARY; PRT; 7 AA.
 ID P83492; AC Q95945; PRELIMINARY; PRT; 7 AA.
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alkaline protease Gr3 (EC 3.4.21.-) (Fragment).
 OS Bionectria ochroleuca (Gliocladium roseum).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocrymectididae; Hypocreales; Bionectriaceae; Bionectria.
 OX NCBI_TaxID=29856;
 RN [1]
 RP SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.
 RC STRAIN=Gr87;
 RA Zhao M., Zhang K.;
 RL Submitted (DEC-2002) to Swiss-Prot.
 CC -!- FUNCTION: Acts as a serine protease.
 CC -!- SUBCELLULAR LOCATION: Secreted
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR InterPro: IPR000209; Pept S8 S53.
 DR PROSITE: PS00136; SUBTILASE ASP; PARTIAL.
 DR PROSITE: PS00137; SUBTILASE HIS; PARTIAL.
 DR PROSITE: PS00138; SUBTILASE SER; PARTIAL.
 KW Hydrolase; Serine protease.
 FT NON TER 7
 SQ SEQUENCE 7 AA; 688 MW; 776DD455A6C1ADB0 CRC64;

Query Match 29.0%; Score 9; DB 2; Length 7;
 Best Local Similarity 20.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7
 Db 1 ATQSN 5

RESULT 14

Q8MEY6 Q8MEY6 PRELIMINARY; PRT; 7 AA.
 ID Q8MEY6; AC Q8MEY6; PRELIMINARY; PRT; 7 AA.
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PsaA (Fragment).
 GN Name=psaA;
 OS Taraxacum (sect. Dioszegia) sp. 4310Hnew.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae;
 OC Taraxacum; unclassified Taraxacum.
 OX NCBI_TaxID=154248;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Mes T.H.M.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY015477; AAK21591.1; -
 DR GO: GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 1
 SQ SEQUENCE 7 AA; 675 MW; 687451B5A76DDB70 CRC64;

Query Match 29.0%; Score 9; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;

RESULT 15

Q95945 Q95945 PRELIMINARY; PRT; 7 AA.
 ID Q95945; AC Q95945; PRELIMINARY; PRT; 7 AA.
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Inside intron 5 (Fragment).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OG Mitochondrion.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D273-10B;
 RX MEDLINE=81069885; PubMed=6254986;
 RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
 RT "Assembly of the mitochondrial membrane system: Structure and nucleotide sequence of the gene coding for subunit 1 of yeast cytochrome oxidase."
 RL J. Biol. Chem. 255:11927-11941(1980).
 DR EMBL; V00694; CAA24066.1; -
 DR GO: GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 1
 SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match 29.0%; Score 9; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RA 6
 Db 1 RA 2

Search completed: April 18, 2005, 15:00:45
 Job time : 185 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:23:45 ; Search time 167 Seconds
(without alignments)
16.212 Million cell updates/sec

Title: US-09-674-716B-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 121728

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	7	2 AAW39825	Aaw39825 Light cha
2	31	100.0	7	2 AAW39822	Aaw39822 Light cha
3	31	100.0	7	2 AAW39819	Aaw39819 Light cha
4	31	100.0	7	3 AAY32255	Aay32255 Light cha
5	28	90.3	7	2 AAW39816	Aaw39816 Light cha
6	27	87.1	7	2 AAW39876	Aaw39876 Light cha
7	22	71.0	7	5 AAU70329	Aau70329 Human int
8	20	64.5	7	7 ADJ32068	Adj32068 Human int
9	19	61.3	4	3 AAY81430	Aay81430 Amino aci
10	19	61.3	7	2 AAY06840	Aay06840 Peptide S
11	19	61.3	7	2 AAY05015	Aay05015 Tumour an
12	19	61.3	7	5 ABP62370	Abp62370 Human imm
13	19	61.3	7	5 ABP62382	Abp62382 Human imm
14	19	61.3	7	5 ABP62364	Abp62364 Human imm
15	19	61.3	7	7 ADC82748	Adc82748 CDR regio
16	19	61.3	7	8 ADN08646	Adn08646 Corton wi
17	19	61.3	7	8 ADP47259	Adp47259 Human pho
18	19	61.3	7	8 ADP47256	Adp47256 Human pho
19	19	61.3	7	8 ADS52415	Ads52415 Fab targe
20	18	58.1	6	4 AAB35205	Aab35205 Retrovira
21	18	58.1	7	2 AAR46961	Aar46961 Peptide f
22	18	58.1	7	2 AAR76083	Aar76083 Mab 55.1
23	18	58.1	7	2 AAW31179	Aaw31179 Hepatitis
24	18	58.1	7	2 AAY05016	Aay05016 Tumour an
25	18	58.1	7	3 AAY95223	Aay95223 Anti-plat

26	18	58.1	7	5 ABP62377	Abp62377 Human imm
27	18	58.1	7	5 ABG77536	Abg77536 Targettin
28	18	58.1	7	7 ADC82750	Adc82750 CDR regio
29	18	58.1	7	7 ADJ72439	Adj72439 VL chain
30	18	58.1	7	8 ADL93628	Adl93628 Human CD4
31	18	58.1	7	8 ADL93550	Adl93550 Human CD4
32	18	58.1	7	8 ADP47068	Adp47068 Murine li
33	18	58.1	7	8 ADP47070	Adp47070 Murine li
34	18	58.1	7	8 ADP47292	Adp47292 Human pho
35	18	58.1	7	8 ADP47253	Adp47253 Human pho
36	18	58.1	7	8 ADP47252	Adp47252 Human pho
37	18	58.1	7	8 ADS52373	Ads52373 Fab targe
38	18	58.1	7	8 ADS52403	Ads52403 Fab targe
39	17	54.8	6	2 AAW95268	Aaw95268 Anti-prog
40	17	54.8	7	2 AAR30157	Aar30157 MAb GAH v
41	17	54.8	7	2 AAR57966	Aar57966 MAb NFS2
42	17	54.8	7	2 AAR50317	Aar50317 MAb NFS2
43	17	54.8	7	2 AAR57964	Aar57964 MAb NFS2
44	17	54.8	7	2 AAR54108	Aar54108 Humanised
45	17	54.8	7	2 AAR98485	Aar98485 Anti-IL-5

ALIGNMENTS

RESULT 1
AAW39825
ID AAW39825 standard; peptide; 7 AA.
AC AAW39825;
XX
XX
DT 16-JUN-1998 (first entry)
XX
DE Light chain CDR2 of catalytic antibody 12H1.
XX
XX Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
OS Mus sp.
XX
PN WO9749800-A1.
XX
PD 31-DEC-1997.
XX
PF 25-JUN-1997; 97WO-US010965.
XX
PR 25-JUN-1996; 96US-00672345.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Landry DW;
XX
XX WPI; 1998-077166/07.
XX
DR New catalytic antibodies able to decompose cocaine, single-chain
XX
PT analogues - used to treat cocaine overdose and addiction, required in far
PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX
XX Claim 17; Page 83; 147pp; English.
XX
XX AAW39824-26 represent the sequences of the light chain complementarity
XX determining regions (CDRs) of the catalytic antibody 12H1, which is able
XX to degrade cocaine. A series of cocaine transition state analogues (TSAs)
XX were prepared and used to immunise mice for production of hybridomas.
XX Catalytic antibodies were identified by their capacity to release 3H-
XX benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was identified
XX using TSA2, and has a per minute Kcat of 0.16. The antibodies reduce the
XX concentration of cocaine in a subject, and are used particularly for the
XX treatment of an overdose. They are also used for treating addiction (by
XX reducing the in vivo concentration that can be achieved)

```

SQ Sequence 7 AA;
Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 2
AAW39822
ID AAW39822 standard; peptide; 7 AA.
AC AAW39822;
XX
XX
XX 16-JUN-1998 (first entry)
XX
XX Light chain CDR2 of catalytic antibody 2A10.
XX
XX Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
XX Mus sp.
OS
XX
XX WO9749800-A1.
XX
XX 31-DEC-1997.
XX
XX 25-JUN-1997; 97WO-US010965.
XX
XX 25-JUN-1996; 96US-00672345.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Landry DW;
XX
XX WPI; 1998-077166/07.
XX
XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required in far
PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX
XX Claim 15; Page 82; 147pp; English.
XX
XX AAW39821-23 represent the sequences of the light chain complementarity
CC determining regions (CDRs) of the catalytic antibody 2A10, which is able
CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
CC were prepared and used to immunise mice for production of hybridomas.
CC Catalytic antibodies were identified by their capacity to release 3H-
CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified
CC using TSA1, which is an immunogenic conjugate of a phosphate monoester
CC transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.
CC The antibodies reduce the concentration of cocaine in a subject, and are
CC used particularly for the treatment of an overdose. They are also used
CC for treating addiction (by reducing the in vivo concentration that can be
CC achieved)
XX
XX Sequence 7 AA;
Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 3
AAW39822
ID AAW39822 standard; peptide; 7 AA.
AC AAW39822;
XX
XX
XX 16-JUN-1998 (first entry)
XX
XX Light chain CDR2 of catalytic antibody 2A10.
XX
XX Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
XX Mus sp.
OS
XX
XX WO9749800-A1.
XX
XX 31-DEC-1997.
XX
XX 25-JUN-1997; 97WO-US010965.
XX
XX 25-JUN-1996; 96US-00672345.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Landry DW;
XX
XX WPI; 1998-077166/07.
XX
XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required in far
PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX
XX Claim 15; Page 82; 147pp; English.
XX
XX AAW39821-23 represent the sequences of the light chain complementarity
CC determining regions (CDRs) of the catalytic antibody 2A10, which is able
CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
CC were prepared and used to immunise mice for production of hybridomas.
CC Catalytic antibodies were identified by their capacity to release 3H-
CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified
CC using TSA1, which is an immunogenic conjugate of a phosphate monoester
CC transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.
CC The antibodies reduce the concentration of cocaine in a subject, and are
CC used particularly for the treatment of an overdose. They are also used
CC for treating addiction (by reducing the in vivo concentration that can be
CC achieved)
XX
XX Sequence 7 AA;
Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 4
AAW39822
ID AAW39822 standard; peptide; 7 AA.
AC AAW39822;
XX
XX
XX 15-FEB-2000 (first entry)
XX
XX Light chain CDR L2 of mouse anti-CD23 MAB C11.
XX
XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;

```

AAW39819

ID AAW39819 standard; peptide; 7 AA.

XX

AC AAW39819;

XX

XX 16-JUN-1998 (first entry)

XX

XX Light chain CDR2 of catalytic antibody 6A12.

XX

Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

XX

OS Mus sp.

XX

XX WO9749800-A1.

XX

XX 31-DEC-1997.

XX

XX 25-JUN-1997; 97WO-US010965.

XX

XX 25-JUN-1996; 96US-00672345.

XX

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX

XX Landry DW;

XX

XX WPI; 1998-077166/07.

XX

New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX

XX Claim 13; Page 81; 147pp; English.

XX

AAW39818-20 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 6A12, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
 CC were prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 6A12 antibody was identified
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester
 CC transition state analogue. Antibody 6A12 has a per minute Kcat of 0.072.
 CC The antibodies reduce the concentration of cocaine in a subject, and are
 CC used particularly for the treatment of an overdose. They are also used
 CC for treating addiction (by reducing the in vivo concentration that can be
 CC achieved)

XX

XX Sequence 7 AA;

SQ

Query Match 100.0%; Score 31; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 LMSTRAS 7

Db

1 LMSTRAS 7

XX

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XX

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 KW therapy.

XX Mus musculus.

OS

XX WO958679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAX) GLAXO GROUP LTD.

XX Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WPI; 2000-053101/04.

XX N-PSDB; AAZ34749.

XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis.

XX Claim 1; Page 40; 81pp; English.

XX This sequence represents complementarity determining region 2 (CDR L2)
 CC of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11
 CC (see also AAY32262). The invention provides altered antibodies, such as
 CC chimeric or humanised antibodies, which comprise sufficient of the amino
 CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to
 CC render them capable of binding to the CD23 type II molecule expressed on
 CC haematopoietic cells. The antibodies are used to block soluble CD23
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They
 CC are also useful for studying interactions between CD23 and various
 CC ligands and determining the binding agents

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

Db 1 LMSTRAS 7

RESULT 5

AAW39816

ID AAW39816 standard; peptide; 7 AA.

XX AAW39816;

XX 16-JUN-1998 (first entry)

XX Light chain CDR2 of catalytic antibody 3B9.

XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

XX Mus sp.

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US010965.

XX 25-JUN-1996; 96US-00672345.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX Claim 11; Page 80; 147pp; English.

XX AAW39815-17 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 3B9, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
 CC were prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester
 CC transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11.
 CC The antibodies reduce the concentration of cocaine in a subject, and are
 CC used particularly for the treatment of an overdose. They are also used
 CC for treating addiction (by reducing the in vivo concentration that can be
 CC achieved)

XX Sequence 7 AA;

Query Match 90.3%; Score 28; DB 2; Length 7;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

Db 1 LMSTRSS 7

RESULT 6

AAW39876

ID AAW39876 standard; peptide; 7 AA.

XX AAW39876;

XX 16-JUN-1998 (first entry)

XX Light chain CDR2 of a catalytic antibody capable of degrading cocaine.

XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

XX Mus sp.

XX Key Location/Qualifiers
 FT Misc-difference 6 /note= "not specified"

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US010965.

XX 25-JUN-1996; 96US-00672345.
 PR (UYCO) UNIV COLUMBIA NEW YORK.
 PA Landry DW;
 PI WPI; 1998-077166/07.
 XX
 XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 XX
 PS Claim 10; Page 5; 147pp; English.
 XX
 CC AAW39875-77 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of a catalytic antibody which is capable of
 CC degrading cocaine. A series of cocaine transition state analogues (TSAs)
 CC were prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. These antibodies were found to have
 CC CDRs of the present sequence. The antibodies reduce the concentration of
 CC cocaine in a subject, and are used particularly for the treatment of an
 CC overdose. They are also used for treating addiction (by reducing the in
 CC vivo concentration that can be achieved)
 XX
 SQ Sequence 7 AA;
 Query Match 87.1%; Score 27; DB 2; Length 7;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 DB 1 LMSTRXS 7
 RESULT 7
 AAU70329
 ID AAU70329 standard; peptide; 7 AA.
 AC AAU70329;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human Kappa II light chain CDR2.
 XX
 KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
 KW IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
 XX
 OS Homo sapiens.
 XX
 PN WO200183806-A1.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US014349.
 XX
 PR 02-MAY-2000; 2000US-00563222.
 XX
 PA (EPIC-) EPICYTE PHARM INC.
 XX
 XX Hiatt AC, Hein MB;
 PI WPI; 2002-055482/07.
 XX
 XX Preparing immunoglobulin binding protein array in plant cells by
 PT transforming the cells with different polynucleotides encoding binding
 PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array.
 XX

PS Disclosure; Page 14; 129pp; English.
 XX
 CC The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IgBP that binds to
 CC a ligand, and transformed plant cells are selected, and preparing an IgBP
 CC array in plant cells. At least one peptide sequence has at least 75%
 CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
 CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
 CC useful for preparing an immunoglobulin binding protein array, preferably
 CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
 CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
 CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
 CC discovery of e.g. screening assays of IgBPs having desired
 CC characteristics. The present sequence is a mammalian immunoglobulin
 CC derived peptide that may be incorporated into an IgBP of the invention
 XX
 SQ Sequence 7 AA;
 Query Match 71.0%; Score 22; DB 5; Length 7;
 Best Local Similarity 71.4%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 DB 1 LVSNRAS 7
 RESULT 8
 ADJ32068
 ID ADJ32068 standard; peptide; 7 AA.
 XX
 AC ADJ32068;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human interferon-gamma antibody light chain CDR2 peptide SeqID22.
 XX
 KW antibody; antigen binding domain; interferon-gamma; INF-gamma;
 KW antagonist antibody; antiinflammatory; immunosuppressive;
 KW autoimmune disease; inflammatory condition; human;
 KW complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 XX
 PN US2003099647-A1.
 XX
 PD 29-MAY-2003.
 XX
 PF 05-OCT-2001; 2001US-00972656.
 XX
 PR 05-OCT-2001; 2001US-00972656.
 XX
 PA (DESH/) DESHPANDE R V.
 PA (TSAL/) TSAI M.
 XX
 PI Deshpande RV, Tsai M;
 XX
 XX WPI; 2003-696068/66.
 XX
 XX New antibody or antigen binding domain, or its fragment, variant or
 PT derivative, which binds to an interferon-gamma protein, useful for
 PT preparing a composition for preventing or treating inflammatory or
 PT autoimmune disorders.
 XX
 PS Claim 14; SEQ ID NO 22; 113pp; English.
 XX
 CC This invention relates to a novel antibody or antigen binding domain, or
 CC its fragment, variant or derivative, which binds to an interferon-gamma
 CC (INF-gamma) protein, and is an antagonist antibody. The invention may be
 CC useful for the development of compounds with an antiinflammatory or

CC immunosuppressive activity through action as interferon-gamma agonists. A
CC composition containing the antibody is useful for preventing or treating
CC an autoimmune disease and an inflammatory condition. The present sequence
CC is that of a peptide which represents a complementarity determining
CC region (CDR) of a human IFN-gamma antibody which may be part of the
CC invention.

[illegible]

Qy 1 LMSTRAS 7
| | | |
Db 1 LASNRAS 7

RESULT 9
AAY81430
ID AAY81430 standard; peptide; 4 AA.

AC AAY81430;

DT 19-JUN-2000 · (first entry)

DE Amino acids encoded by 5' portion of pTugAS vector SacI-HindIII region.

pTugAS vector; Cellulomonas fimi; endoglucanase C; CBD;
 cellulose binding domain; polysaccharide binding peptide; fusion protein;
 recombinant protein; cell separation; affinity phase separation.

OS Synthetic.

XX
PN
US6048715-A.

11-APR-2000.

XX
PF 24-JUL-1996; 96US-00685808.

PR 08-JUL-1988; 88US-00216794.

PK	23-OCT-1990;	300S-00803987.
PR	08-APR-1992;	92US-00865095.

FR 24-MAY-1994; 94US-00249037;
PR 24-JUL-1995; 95US-00505860.

PA (UYBR-) UNIV BRITISH COLUMBIA

PI Haynes CA, Tomme P, Kilburn

DR WPI; 2000-328038/28.

Two-phase partition affinity separa

PT a phase-separation a

PS Disclosure; Fig 3A; 46pp; English.

CC The invention relates to a novel t

separation system comprises a phase-forming oligosaccharide polymer, to which a polysaccharide binding peptide (PBP) binds, and a phase separation inducing agent. The system may be used for the separation and purification of recombinant proteins from cell cultures. The protein of interest is expressed in the host cell as a fusion protein with a polysaccharide binding peptide, and the cell lysate or fermentation broth (or other composition comprising the fusion protein) is contacted with the phase separation system. The fusion protein partitions into the oligosaccharide polymer phase, and can then be isolated e.g., via the use of a solution with a low ionic strength, high pH or containing a chaotropic agent, or by the use of chemical cleavage agents such as cyanogen bromide. If the fusion protein has been engineered such that there is a protease recognition site between the PBP and the protein of interest, the protein can be cleaved from the PBP, which remains bound to

```
Query Match          61.3%; Score 19; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7
Db 3 STRAT 7

RESULT 11
AAY05015
ID RAY05015 standard; peptide; 7 AA.
AC AAY05015;
DT 16-JUN-1999 (first entry)
DE Tumour antigen antibody light chain CDR2 clone F14.
KW Tumour antigen; antibody; CDR; complementarity determining region;
KW binding molecule identification; tumour-specific binding polypeptide;
KW cancer therapy; light chain.
XX Homo sapiens.
OS
XX WO9906834-A2.
PN
XX 11-FEB-1999.
PD
XX 04-AUG-1998; 98WO-US016280.
PF
XX 04-AUG-1997; 97US-00905825.
PR
XX (IXSY-) IXSYS INC.
PA
XX
XX Watkins JD, Huse WD, Wu H;
PI WPI; 1999-153951/13.
XX
XX Identifying binding molecules for ligands, particularly tumour antigens -
PT by selectively immobilising a population of binding molecules to a solid
PT support and screening for binding to two or more ligands.
XX
XX Claim 15; Page 57; 80pp; English.
XX
XX This sequence represents a light chain complementarity determining region
CC (CDR) from a tumour antigen specific antibody. The invention relates to a
CC method for identifying a binding molecule having selective affinity for a
CC ligand comprising: (a) selectively immobilising a diverse population of
CC binding molecules to a solid support; (b) simultaneously contacting the
CC diverse population immobilised on the solid support with 2 or more
CC ligands; and (c) determining at least one binding molecule which
CC selectively binds to one or more of the ligands. The method allows for
CC the rapid and efficient methods for the identification of binding
CC molecules which exhibit selective affinity for one or more ligands of
CC interest. They are used particularly for identifying tumour-specific
CC binding polypeptides which can be used as targeting agents for cancer
CC therapy that minimises impact on non-tumour tissues
XX
XX Sequence 7 AA;

Query Match          61.3%; Score 19; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7
Db 3 STRAT 7

RESULT 12
ABF62370
ID ABF62370 standard; peptide; 7 AA.
AC
DT
DE
KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.
XX Homo sapiens.
OS
XX WO200259340-A1.
PN
XX
```

```
XX ABP62370;
AC
XX 10-OCT-2002 (first entry)
DT
XX Human immunopeptide to HCV E2 glycoprotein light chain CDR #47.
DE
XX Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.
XX Homo sapiens.
OS
XX WO200259340-A1.
PN
XX 01-AUG-2002.
PD
XX 25-JAN-2002; 2002WO-US002303.
PF
XX 26-JAN-2001; 2001US-0264451P.
PR
XX (SCRI ) SCRIPPS RES INST.
PA
XX Maruyama T, Jones IM, Burton DR, Fox RI;
PI WPI; 2002-599801/64.
XX
XX New human immunopolypeptide with binding specificity for certain envelope
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT diagnosing or treating patients having or suspected of having HCV
PT infection.
XX
XX Claim 1; Fig 17; 308pp; English.
XX
XX The present invention relates to human immunopolypeptides, produced by a
CC phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificity for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection
XX
XX Sequence 7 AA;

Query Match          61.3%; Score 19; DB 5; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7
Db 3 STRAT 7

RESULT 13
ABP62382
ID ABP62382 standard; peptide; 7 AA.
AC
XX ABP62382;
AC
XX 10-OCT-2002 (first entry)
DT
XX Human immunopeptide to HCV E2 glycoprotein light chain CDR #59.
DE
XX Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.
XX Homo sapiens.
OS
XX WO200259340-A1.
PN
XX
```

```

PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-US002303.
XX
PR 26-JAN-2001; 2001US-0264451P.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Maruyama T, Jones IM, Burton DR, Fox RI;
XX
DR WPI; 2002-599801/64.
XX
PT New human immunopolypeptide with binding specificity for certain envelope
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT diagnosing or treating patients having or suspected of having HCV
PT infection.
XX
PS Claim 1; Fig 17; 308pp; English.
XX
CC The present invention relates to human immunopolypeptides, produced by a
CC phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificity for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection
XX
SQ Sequence 7 AA;

Query Match 61.3%; Score 19; DB 5; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7
DB ||||:
3 STRAT 7

RESULT 15
ADC82748
ID ADC82748 standard; peptide; 7 AA.
XX
AC ADC82748;
XX
DT 01-JAN-2004 (first entry)
XX
DE CDR region #13 in light chain of human Fab fragment.
XX
KW Binding molecule; selective affinity; ligand;
KW anti-immunoglobulin reagent; phage expressed antibody library;
KW tumour antigen; complementarity determining region; CDR; human disease;
KW cellular pathology; human; Fab; light chain.
XX
OS Homo sapiens.
XX
PN US2003044772-A1.
XX
PD 06-MAR-2003.
XX
PF 15-OCT-2001; 2001US-00977797.
XX
PR 04-AUG-1997; 97US-0113667P.
XX
PR 04-AUG-1998; 98US-00129026.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Watkins JD, Huse WD, Wu H;
XX
DR WPI; 2003-625402/59.
XX
DR N-PSDB; ADC82747.
XX
PT Identifying binding molecules having selective affinity for ligands for
PT discovering reagents for treating diseases, by contacting solid support
PT coated with anti-immunoglobulin reagent to a phage expressed antibody
PT library.
XX
PS Example 5; Page 15; 26pp; English.
XX
CC The present invention relates to a method for identifying a binding
CC molecule having selective affinity for a ligand. The method involves
CC providing a solid support coated with an anti-immunoglobulin reagent, and
CC a phage expressed antibody library, and contacting the solid support to
CC the phage expressed antibody library. The invention also discloses a
CC method for identifying an antibody having selective affinity for a
CC tumour, and a complementarity determining region (CDR) of an antibody
CC selective for a tumour antigen. The methods of the invention are useful

```

CC for identifying a binding molecule having selective affinity for a
CC ligand, for the discovery of specific reagents for diagnosis and
CC treatment of human diseases, for identifying binding molecules to, for
CC example tumour cells or other cellular pathologies for the selective
CC targeting of therapeutic agents, or for the identification of binding
CC molecules to normal or diseased tissues for the selective targeting of,
CC for example diagnostic agents such as imaging reagents. The methods are
CC rapid and efficient for the identification of binding molecules which
CC exhibit selective affinity for one or more ligands of interest. The
CC methods allow the simultaneous screening of multiple binding molecules
CC against multiple ligands of interest. Moreover, very little information
CC is required regarding the identity or function of either the binding
CC molecule or the ligand. For example diverse populations of binding
CC molecules can be simultaneously screened against diverse populations of
CC ligands to rapidly identify numerous molecules exhibiting a desired
CC binding specificity. The methods provide improved sensitivity and
CC specificity of detection through the selective immobilisation of the
CC binding molecule population on a solid support. The present sequence
CC represents a CDR region in the light chain of human Fab fragment.

XX
SQ

Sequence 7 AA;

Query Match 61.3%; Score 19; DB 7; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7
|||:
Db 3 STRAT 7

Search completed: April 18, 2005, 14:57:35
Job time : 169 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:00:54 ; Search time 130 Seconds
(without alignments)
17.897 Million cell updates/sec

Title: US-09-674-716B-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370693 residues

Total number of hits satisfying chosen parameters: 59827

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	7	10	US-09-940-727B-23
2	31	100.0	7	10	US-09-940-727B-26
3	31	100.0	7	10	US-09-940-727B-29
4	28	90.3	7	10	US-09-940-727B-20
5	27	87.1	7	10	US-09-940-727B-80
6	22	71.0	7	10	US-09-563-222-9
7	22	71.0	7	16	US-10-783-950-9
8	20	64.5	7	10	US-09-972-656-22
9	19	61.3	7	10	US-09-977-797A-30
10	19	61.3	7	16	US-10-396-578-66
11	19	61.3	7	17	US-10-783-311-161
12	19	61.3	7	17	US-10-783-311-185
13	19	61.3	7	17	US-10-783-311-249

14	19	61.3	7	17	US-10-783-311-329
15	19	61.3	7	17	US-10-863-729-30
16	19	61.3	7	17	US-10-869-355-6
17	19	61.3	7	17	US-10-726-332-171
18	19	61.3	7	17	US-10-726-332-174
19	18	58.1	7	10	US-09-977-797A-32
20	18	58.1	7	15	US-10-418-182-94
21	18	58.1	7	16	US-10-663-244-45
22	18	58.1	7	16	US-10-663-244-123
23	18	58.1	7	16	US-10-396-578-24
24	18	58.1	7	16	US-10-396-578-54
25	18	58.1	7	17	US-10-783-311-89
26	18	58.1	7	17	US-10-725-962-124
27	18	58.1	7	17	US-10-725-962-126
28	18	58.1	7	17	US-10-726-332-168
29	18	58.1	7	17	US-10-726-332-177
30	18	58.1	7	17	US-10-726-332-207
31	17	54.8	7	9	US-09-749-831-5
32	17	54.8	7	9	US-09-828-708-43
33	17	54.8	7	9	US-09-828-708-46
34	17	54.8	7	9	US-09-249-011A-18
35	17	54.8	7	10	US-09-563-222-15
36	17	54.8	7	10	US-09-563-222-27
37	17	54.8	7	10	US-09-972-656-15
38	17	54.8	7	10	US-09-995-529-22
39	17	54.8	7	10	US-09-995-529-22
40	17	54.8	7	11	US-09-791-551-29
41	17	54.8	7	13	US-10-146-305-10
42	17	54.8	7	14	US-10-144-644-11
43	17	54.8	7	14	US-10-071-962-19
44	17	54.8	7	14	US-10-371-404-34
45	17	54.8	7	15	US-10-156-214A-293

ALIGNMENTS

RESULT 1
US-09-940-727B-23
; Sequence 23, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940, 727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-23

Query Match 100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 2
US-09-940-727B-26
; Sequence 26, Application US/09940727B

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; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-26

Query Match          100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 3
US-09-940-727B-29
; Sequence 29, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
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; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-29

Query Match          100.0%; Score 31; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 4
US-09-940-727B-20
; Sequence 20, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-20

Query Match          90.3%; Score 28; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRSS 7

RESULT 5
US-09-940-727B-80
; Sequence 80, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: MISC.FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: any amino acid
US-09-940-727B-80

Query Match          87.1%; Score 27; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRSS 7

RESULT 6
US-09-563-222-9
; Sequence 9, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-9

Query Match 71.0%; Score 22; DB 10; Length 7;
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Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|:|||||
Db 1 LVSNRAS 7

RESULT 7

US-10-783-950-9
; Sequence 9, Application US/10783950
; Publication No. US20040199945A1
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/10/783,950
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US/09/563,222
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US/09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-783-950-9

Query Match 71.0%; Score 22; DB 16; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|:|||||
Db 1 LVSNRAS 7

RESULT 8

US-09-972-656-22
; Sequence 22, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-22

Query Match 64.5%; Score 20; DB 10; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 LMSTRAS 7
|:|||||
Db 1 LASNRAS 7

RESULT 9

US-09-977-797A-30
; Sequence 30, Application US/09977797A
; Publication No. US20030044772A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
; FILE REFERENCE: AME-06805
; CURRENT APPLICATION NUMBER: US/09/977,797A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 09/129,026
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 08/905,825
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-797A-30

Query Match 61.3%; Score 19; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7
|:|||||
Db 3 STRAT 7

RESULT 10

US-10-396-578-66
; Sequence 66, Application US/10396578
; Publication No. US20040191260A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; FILE REFERENCE: 25563
; CURRENT APPLICATION NUMBER: US/10/396,578
; CURRENT FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
; OTHER INFORMATION: specifically binding HLA-A2/Tax11-19 complex.
US-10-396-578-66

Query Match 61.3%; Score 19; DB 16; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7
|:|||||
Db 3 STRAT 7

```
RESULT 11
US-10-783-311-161
; Sequence 161, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light Chain amino acid sequence
US-10-783-311-161

Query Match      61.3%; Score 19; DB 17; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 STRAS 7
DB      3 STRAT 7

RESULT 12
US-10-783-311-185
; Sequence 185, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light Chain amino acid sequence
US-10-783-311-185

Query Match      61.3%; Score 19; DB 17; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 STRAS 7
DB      3 STRAT 7

RESULT 13
US-10-783-311-249
; Sequence 249, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/863,729
; CURRENT FILING DATE: 2004-06-07
; PRIOR APPLICATION NUMBER: 60/476,909
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/503,356
; PRIOR FILING DATE: 2003-09-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 249
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light Chain amino acid sequence
US-10-783-311-249

Query Match      61.3%; Score 19; DB 17; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 STRAS 7
DB      3 STRAT 7

RESULT 14
US-10-783-311-329
; Sequence 329, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 329
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Light Chain amino acid sequence
US-10-783-311-329

Query Match      61.3%; Score 19; DB 17; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 STRAS 7
DB      3 STRAT 7

RESULT 15
US-10-863-729-30
; Sequence 30, Application US/10863729
; Publication No. US20050013819A1
; GENERAL INFORMATION:
; APPLICANT: Carles-Kinch, Kelly
; APPLICANT: Kinch, Michael S.
; TITLE OF INVENTION: USE OF EphA4 AND MODULATOR OF EphA4 FOR CANCER
; FILE REFERENCE: 10271-117-999
; CURRENT APPLICATION NUMBER: US/10/863,729
; CURRENT FILING DATE: 2004-06-07
; PRIOR APPLICATION NUMBER: 60/476,909
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/503,356
; PRIOR FILING DATE: 2003-09-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Light Chain amino acid sequence
US-10-863-729-30

Query Match      61.3%; Score 19; DB 17; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 STRAS 7
DB      3 STRAT 7
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; SEQ ID NO 30
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CDR2 of VL region of EA44
US-10-863-729-30

Query Match      61.3%; Score 19; DB 17; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 STRAS 7
      ||||:
Db      3 STRAT 7
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Search completed: April 18, 2005, 15:13:19
Job time : 131 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:48:09 ; Search time 40 Seconds
(without alignments)
13.064 Million cell updates/sec

Title: US-09-674-716B-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 61165

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	7	2	US-08-672-345C-23
2	31	100.0	7	2	US-08-672-345C-26
3	31	100.0	7	2	US-08-672-345C-29
4	31	100.0	7	3	US-09-214-095D-23
5	31	100.0	7	3	US-09-214-095D-26
6	31	100.0	7	3	US-09-214-095D-29
7	28	90.3	7	2	US-08-672-345C-20
8	28	90.3	7	3	US-09-214-095D-20
9	27	87.1	7	2	US-08-672-345C-80
10	27	87.1	7	3	US-09-214-095D-80
11	22	71.0	7	4	US-09-563-222C-9
12	19	61.3	4	3	US-08-685-808-9
13	19	61.3	4	3	US-08-505-860C-9
14	18	58.1	7	1	US-08-353-400-31
15	17	54.8	6	4	US-09-424-712-36
16	17	54.8	7	1	US-08-264-093-25
17	17	54.8	7	1	US-08-467-420A-11
18	17	54.8	7	1	US-08-470-110A-11
19	17	54.8	7	1	US-08-360-125-20
20	17	54.8	7	1	US-08-667-769A-11
21	17	54.8	7	2	US-08-452-724A-34
22	17	54.8	7	2	US-08-450-578-20
23	17	54.8	7	2	US-08-940-371-11
24	17	54.8	7	2	US-09-017-628-20
25	17	54.8	7	2	US-09-014-880-20
26	17	54.8	7	3	US-09-100-409A-30
27	17	54.8	7	3	US-08-637-647-11

28.	17	54.8	7	3	US-07-987-264-5	Sequence 5, Appl
29	17	54.8	7	4	US-08-450-363-20	Sequence 20, Appl
30	17	54.8	7	4	US-08-453-623-34	Sequence 34, Appl
31	17	54.8	7	4	US-09-563-222C-15	Sequence 15, Appl
32	17	54.8	7	4	US-09-563-222C-27	Sequence 27, Appl
33	17	54.8	7	4	US-09-467-903-20	Sequence 20, Appl
34	17	54.8	7	4	US-09-830-748B-8	Sequence 8, Appl
35	17	54.8	7	4	US-09-627-896B-18	Sequence 18, Appl
36	17	54.8	7	5	PCT-US93-08435-24	Sequence 24, Appl
37	17	54.8	7	5	PCT-US93-08435-37	Sequence 37, Appl
38	17	54.8	7	5	PCT-US93-08435-41	Sequence 41, Appl
39	17	54.8	7	5	PCT-US95-17082A-11	Sequence 11, Appl
40	16	51.6	4	1	US-07-776-257-3	Sequence 3, Appl
41	16	51.6	4	4	US-09-509-994-6	Sequence 6, Appl
42	16	51.6	4	1	US-08-503-062-14	Sequence 14, Appl
43	16	51.6	7	2	US-08-340-283-90	Sequence 90, Appl
44	16	51.6	7	3	US-09-084-605B-8	Sequence 8, Appl
45	16	51.6	7	3	US-09-174-216-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-672-345C-23
; Sequence 23, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-23

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 2

US-08-672-345C-26
; Sequence 26, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-26

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 3
US-08-672-345C-29
; Sequence 29, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-29

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 4
US-09-214-095D-23
; Sequence 23, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 23
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-23

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 5
US-09-214-095D-26
; Sequence 26, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-26

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 6

US-09-214-095D-29
; Sequence 29, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-29

Query Match 100.0%; Score 31; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 7

US-08-672-345C-20
; Sequence 20, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-20

Query Match 90.3%; Score 28; DB 2; Length 7;

Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 8

US-09-214-095D-20
; Sequence 20, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-20

Query Match 90.3%; Score 28; DB 3; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 9

US-08-672-345C-80
; Sequence 80, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-80

US-08-672-345C-80

Query Match 87.1%; Score 27; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|||||
DB 1 LMSTRAS 7

RESULT 10

US-09-214-095D-80
; Sequence 80, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen.sp.
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (6)..(6)
; OTHER INFORMATION: X at position 6 represents any amino acid
US-09-214-095D-80

Query Match 87.1%; Score 27; DB 3; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|||||
DB 1 LMSTRAS 7

RESULT 11

US-09-563-222C-9
; Sequence 9, Application US/09563222C
; Patent No. 6896620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICHAEL B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-9

Query Match 71.0%; Score 22; DB 4; Length 7;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|:|:|:|
DB 1 LVSNRAS 7

RESULT 12

US-08-685-808-9
; Sequence 9, Application US/08685808
; Patent No. 6048715
; GENERAL INFORMATION:
; APPLICANT: HAYNES, CHARLES A., et al
; TITLE OF INVENTION: SEPARATION AND CONCENTRATION SYSTEMS BASED
; TITLE OF INVENTION: ON SOLUBLE OLIGOSACCHARIDE BINDING DOMAINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP
; STREET: 260 Sheridan Ave., Ste. 440
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,808
; FILING DATE: 24-JULY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/505,860
; FILING DATE: 24-JULY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Venter, Barbara
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CDDT.017.01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: no
US-08-685-808-9

Query Match 61.3%; Score 19; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTR 5
|||
DB 1 MSTR 4

RESULT 13

US-08-505-860C-9
; Sequence 9, Application US/08505860C
; Patent No. 6174700
; GENERAL INFORMATION:
; APPLICANT: HAYNES, CHARLES A., et al
; TITLE OF INVENTION: SEPARATION AND CONCENTRATION SYSTEMS BASED
; TITLE OF INVENTION: ON SOLUBLE OLIGOSACCHARIDE BINDING DOMAINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP
; STREET: 260 Sheridan Ave., Ste. 440
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/505,860C
;; FILING DATE: 24-JULY-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rae-Venter, Barbara
;; REGISTRATION NUMBER: 32,750
;; REFERENCE/DOCKET NUMBER: CBDDT.017.000US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 328-4400
;; TELEFAX: (650) 328-4477
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: no
;; US-08-505-860C-9

Query Match 61.3%; Score 19; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTR 5
|||
Db 1 MSTR 4

RESULT 14
US-08-353-400-31
; Sequence 31, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-353-400-31

Query Match 58.1%; Score 18; DB 1; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 STRAS 7
|||
Db 3 STRTS 7

RESULT 15
US-09-424-712-36
; Sequence 36, Application US/09424712
; Patent No. 6620587
; GENERAL INFORMATION:
; APPLICANT: TAUSSIG, Michael John
; APPLICANT: HE, Mingyue
; TITLE OF INVENTION: RIBOSOME COMPLEXES AS SELECTION PARTICLES FOR IN VITRO DISPLAY A
; TITLE OF INVENTION: EVOLUTION OF PROTEINS
; FILE REFERENCE: 37945-0017
; CURRENT APPLICATION NUMBER: US/09/424,712
; CURRENT FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/GB98/01564
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: GB 9804195.7
; PRIOR FILING DATE: 1998-02-28
; PRIOR APPLICATION NUMBER: GB 9724850.4
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: GB 9710829.4
; PRIOR FILING DATE: 1997-05-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-424-712-36

Query Match 54.8%; Score 17; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 STRAS 7
|||
Db 2 STRS 6

Search completed: April 18, 2005, 15:01:30
Job time : 41 secs

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IG kappa chain V region (253.15E2) - mouse (fragment)
G30538
C/Species: Mus musculus (house mouse)
C/Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #t
C/Accession: G30538
R/Glatlin, J.L.; Berry, J.

J. Immunol. 141, 4012-4019, 1988
 A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae
 A;Reference number: A30534; MUID:89035545; PMID:3141511
 A;Accession: G30538
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-74 <CIA>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin

Query Match 87.5%; Score 42; DB 2; Length 74;
 Best Local Similarity 88.9%; Pred. No. 0.15; Mismatches 0; Indels 1; Gaps 0;
 Matches 8; Conservative 0

QY 1 QQLVEYPT 9
 |||||
 DB 63 QQLVEYPT 71

RESULT 3
 KWS16
 Ig kappa chain V region (M167) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
 C;Accession: A01908
 R;Rudikoff, S.; Potter, M.
 Biochemistry 17, 2703-2707, 1978
 A;Title: Kappa-Chain variable region from M167, a phosphorylcholine binding myeloma protein
 A;Reference number: A01908; MUID:79000273; PMID:99160
 A;Accession: A01908
 A;Molecule type: protein
 A;Residues: 1-112 <RUD>
 A;Cross-references: UNIPROT:P01626
 C;Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer
 F;16-95/Domain: immunoglobulin homology <IMM>
 F;23-93/Disulfide bonds: #status predicted

Query Match 87.5%; Score 42; DB 1; Length 112;
 Best Local Similarity 88.9%; Pred. No. 0.23; Mismatches 0; Indels 1; Gaps 0;
 Matches 8; Conservative 0

QY 1 QQLVEYPT 9
 |||||
 DB 94 QQLVEYPT 102

RESULT 4
 KWS51
 Ig kappa chain V region (M511) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
 C;Accession: A01910
 R;Appella, E.
 Mol. Immunol. 17, 711-718, 1980
 A;Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcholine-binding myeloma protein
 A;Reference number: A01910; MUID:81052016; PMID:6776396
 A;Accession: A01910
 A;Molecule type: protein
 A;Residues: 1-113 <APP>
 A;Cross-references: UNIPROT:P01628
 C;Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer
 F;16-95/Domain: immunoglobulin homology <IMM>
 F;23-93/Disulfide bonds: #status predicted

Query Match 87.5%; Score 42; DB 1; Length 113;
 Best Local Similarity 88.9%; Pred. No. 0.23; Mismatches 0; Indels 1; Gaps 0;
 Matches 8; Conservative 0

QY 1 QQLVEYPT 9
 |||||
 DB 94 QQLVEYPT 102

RESULT 5
 KWS67
 Ig kappa chain precursor V region (VK167) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
 C;Accession: A01909
 R;Selsing, E.; Storb, U.
 Cell 25, 47-58, 1981
 A;Title: Somatic mutation of immunoglobulin light-chain variable-region genes.
 A;Reference number: A01909; MUID:82002223; PMID:6791832
 A;Accession: A01909
 A;Molecule type: DNA
 A;Residues: 1-120 <SEL>
 A;Cross-references: UNIPROT:P01627
 A;Note: the sequence was determined from the germline gene
 C;Genetics:
 A;Introns: 17/1
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger disulfide bonds.
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>
 F;36-115/Domain: immunoglobulin homology <IMM>
 F;43-113/Disulfide bonds: #status predicted

Query Match 77.1%; Score 37; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 2.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0

QY 1 QQLVEYPT 7
 |||||
 DB 114 QQLVEYPT 120

RESULT 6
 A85363
 Probable calmodulin-binding protein [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C;Accession: A85363
 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor Laboratory
 Nature 402, 769-777, 1999
 A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A;Reference number: A85001; MUID:20083488; PMID:10617198
 A;Accession: A85363
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-467 <STO>
 A;Cross-references: UNIPROT:O65550; GB:NC_001268; NID:97270002; PIDN:CAB79818.1; GSPDB:1CAB79818.1
 C;Genetics:
 A;Gene: At4g31000
 A;Map position: 4

Query Match 77.1%; Score 37; DB 2; Length 467;
 Best Local Similarity 75.0%; Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;
 Matches 6; Conservative 1

QY 1 QQLVEYPT 8
 |||||
 DB 334 QQLVEYPT 341

RESULT 7
 S36277

Ig lambda chain V region (clone alpha-FOG1-G8) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36277
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A>Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36277
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-108 <GRL>
A:Cross-references: EMBL:Z18829; NID:933417; PIDN:CAA79281.1; PID:9339910
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 36; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 3.8;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9
|||: |||
Db 89 QQLISVPLT 97

RESULT 8
T38148
phosphatidyl synthase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38148
R:Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z21774
A:Accession: T38148
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-570 <PEA>
A:Cross-references: UNIPROT:O13899; EMBL:Z99295; PIDN:CAB16578.1; GSPDB:GN00066; SPDB:SH
A:Experimental source: strain 972h-; cosmid C22A12
C:Genetics:
A:Gene: SPDB:SPAC22A12.08c
A:Map position: 1
A:Introns: 43/2; 62/2; 227/2; 483/1

Query Match 75.0%; Score 36; DB 2; Length 570;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9
|||: |||
Db 547 QQLVEYSFT 555

RESULT 9
B29775
Ig kappa chain precursor V region (mouse 24.1) - shrew mouse
C:Species: Mus pahari
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C:Accession: B29775
R:Jouvin-Marche, E.; Rudikoff, S.
Immunogenetics 24, 191-201, 1986
A>Title: Evolution of a V-kappa gene family
A:Reference number: A91751; MUID:87006895; PMID:3093373
A:Accession: B29775
A:Molecule type: DNA
A:Residues: 1-120 <JOU>
A:Cross-references: GB:M15553; NID:9197470; PIDN:AAA39037.1; PID:gl97471
A>Note: this sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region 24.1 #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 35; DB 2; Length 120;
Best Local Similarity 85.7%; Pred. No. 6.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7
|||: |||
Db 114 QQLVEYP 120

RESULT 10
A86371
hypothetical protein F508.25 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: A86371
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.W.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86371
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-480 <STO>
A:Cross-references: UNIPROT:Q9ZUC5; GB:AE005172; NID:94056452; PIDN:AAC98025.1; GSPDB:G
C:Genetics:
A:Map position: 1

Query Match 72.9%; Score 35; DB 2; Length 480;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QQLVEYPP 8
|||: |||
Db 269 QQLVEYPP 275

RESULT 11
D82100
meat protein VC2242 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: D82100
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82100
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-440 <HEI>
A:Cross-references: UNIPROT:Q9KPY0; GB:AE004296; GB:AE003852; NID:99656799; PIDN:AAF953
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2242
A:Map position: 1
C:Superfamily: Cell cycle protein MesJ

Query Match 70.8%; Score 34; DB 2; Length 440;
Best Local Similarity 75.0%; Pred. No. 45;

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Matches      6;  Conservative      0;  Mismatches      2;  Indels      0;  Gaps      0;

QY      1  QQLVEYPP 8
      ||| |||
Db      10  QQLARYPP 17

RESULT 12
D89903
hypothetical protein Sall31 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D89903
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogino,
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D89503
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-586 <KUR>
A:Cross-references: UNIPROT:Q99UI4; GB:BA0000018; PID:g13701089; PIDN:BAB42384.1; GSPDB:Q
A:Experimental source: strain N315
C:Genetics:
A:Gene: Sall31
C:Superfamily: Halobacterium halobium 2-oxoacid ferredoxin oxidoreductase; 2-oxoacid fer
Query Match      70.8%; Score 34; DB 2; Length 586;
Best Local Similarity 75.0%; Pred. No. 61;
Matches      6;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;

QY      2  QQLVEYPP 9
      ||| |||
Db      109  QQLTEPPT 116

RESULT 13
S76367
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Accession: S76367
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76367
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-722 <KAN>
A:Cross-references: UNIPROT:Q55690; EMBL:D64000; GB:AB001339; MUID:g1001484; PIDN:BAA1021
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: glycine-tRNA ligase beta chain
Query Match      70.8%; Score 34; DB 2; Length 722;
Best Local Similarity 85.7%; Pred. No. 76;
Matches      6;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1  QQLVEYPP 7
      ||| |||
Db      254  EQLVEYPP 260

RESULT 14
T01906
hypothetical protein T12H20.3 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004

```

```

C:Accession: T01906
R:Cotton, M.; Graves, T.; Sutterer, C.; Modde, T.
submitted to the EMBL Data Library, July 1998
A:Description: The sequence of A. thaliana T12H20.
A:Reference number: Z14453
A:Accession: T01906
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1074 <COT>
A:Cross-references: UNIPROT:O82491; EMBL:AF080119; MUID:g3600029; PID:g3600033
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Note: T12H20.3
Query Match      70.8%; Score 34; DB 2; Length 1074;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches      5;  Conservative      2;  Mismatches      0;  Indels      0;  Gaps      0;

QY      2  QLVVEYPP 8
      ||| |||
Db      853  ELIEYPP 859

RESULT 15
D26317
Ig kappa chain V region (H37-84) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C:Accession: D26317
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhardt, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a d
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: D26317
A:Molecule type: DNA
A:Residues: 1-112 <CAT>
A:Experimental source: strain Balb/c
A:Note: this sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>
Query Match      68.8%; Score 33; DB 2; Length 112;
Best Local Similarity 75.0%; Pred. No. 17;
Matches      6;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;

QY      2  QLVVEYPP 9
      ||| |||
Db      95  QHLEYPPT 102

Search completed: April 18, 2005, 14:23:25
Job time : 19.7907 secs

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:57:43 ; Search time 81.8372 Seconds
(without alignments)
56.316 Million cell updates/sec

Title: US-09-674-716B-7
Perfect score: 48
Sequence: 1 QQLVEVPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	89.6	383	1	CYB_APILI
2	42	87.5	112	1	KV2A MOUSE
3	42	87.5	113	1	KV2C MOUSE
4	40	83.3	349	2	Q85TH4
5	39	81.2	506	2	Q87RR4
6	38	79.2	368	2	Q6PRB0
7	38	79.2	532	2	Q6LTX1
8	37	77.1	120	1	KV2B MOUSE
9	37	77.1	278	2	Q8W454
10	37	77.1	467	2	Q6S550
11	37	77.1	609	2	Q8H816
12	36	75.0	84	2	Q9B313
13	36	75.0	247	2	Q9MPF34
14	36	75.0	330	2	Q6YAK6
15	36	75.0	331	2	Q6YAK5
16	36	75.0	352	2	Q9XNV8
17	36	75.0	371	2	Q8M293
18	36	75.0	377	2	Q9XNV0
19	36	75.0	377	2	Q9XNV5
20	36	75.0	379	1	CYB_AKQAE
21	36	75.0	379	1	CYB_AKQJE
22	36	75.0	379	1	CYB_AKQJU
23	36	75.0	379	1	CYB_AKQKU
24	36	75.0	379	1	CYB_AKQMO
25	36	75.0	379	1	CYB_AKOPU
26	36	75.0	379	1	CYB_AKOPR
27	36	75.0	379	1	CYB_AKOSI
28	36	75.0	379	1	CYB_AKOSU
29	36	75.0	379	1	CYB_AKOTB
30	36	75.0	379	1	CYB_AKOTO
31	36	75.0	379	1	CYB_MICMI

32	36	75.0	379	2	Q8LU40
33	36	75.0	379	2	Q8M290
34	36	75.0	379	2	Q8M292
35	36	75.0	379	2	Q8M294
36	36	75.0	379	2	Q8M295
37	36	75.0	379	2	Q8M296
38	36	75.0	379	2	Q8M297
39	36	75.0	379	2	Q8M299
40	36	75.0	379	2	Q8M2A0
41	36	75.0	379	2	Q84QC8
42	36	75.0	379	2	Q33641
43	36	75.0	379	2	Q33642
44	36	75.0	379	2	Q33809
45	36	75.0	379	2	Q33810

ALIGNMENTS

RESULT 1

CYB_APILI STANDARD; PRT; 383 AA.
AC P34845;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cytochrome b.
GN Name=MTCVB; Synonyms=COB, CYTB;
OS Apis mellifera ligustica (Common honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7469;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thorax;
RX MEDLINE=92261310; PubMed=1533894;
RA Crozier R.H., Crozier Y.C.;
RT "The cytochrome b and ATPase genes of honeybee mitochondrial DNA.";
RL Mol. Biol. Evol. 9:474-482(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Thorax;
RX MEDLINE=93114603; PubMed=8417993;
RA Crozier R.H., Crozier Y.C.;
RT "The mitochondrial genome of the honeybee Apis mellifera: complete sequence and genome organization.";
RL Genetics 133:97-117(1993).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential coupled to ATP synthesis (By similarity).
CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562 nm, and heme 2 (or BH or b566) is high-potential and absorbs at about 566 nm (By similarity).
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b, cytochrome c1 and the Rieske protein (By similarity).
CC -!- SIMILARITY: Belongs to the cytochrome b family.
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CC -----
CC EMBL; L06178; AAB96809.1; -;
CC EMBL; M87052; -; NOT ANNOTATED_CDS.
CC PIR; C42622; C42622.
CC InterPro; IPR005798; Cytb_b6_C.

```

DR InterPro: IPR005797; Cytb b6 N.
DR Pfam: PF00032; Cytochrom B_C7; 1.
DR Pfam: PF00033; Cytochrom B_N; 1.
DR PROSITE: PS1003; CYTB_CTER; 1.
DR PROSITE: PS1002; CYTB_NTER; 1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT METAL 85 Iron 1 (heme b562 axial ligand).
FT METAL 99 Iron 2 (heme b566 axial ligand).
FT METAL 184 Iron 1 (heme b562 axial ligand).
FT METAL 198 Iron 2 (heme b566 axial ligand).
SQ SEQUENCE 383 AA; 45256 MW; A140A05E6053C2D5 CRC64;

Query Match 89.6%; Score 43; DB 1; Length 383;
Best Local Similarity 77.8%; Pred. No. 5.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
DB 341 QQLVEYPFT 349

RESULT 2
KV2A MOUSE
ID KV2A_MOUSE STANDARD; PRT; 112 AA.
AC P01626;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region MOPC 167.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
MEDLINE=79000273; PubMed=99160;
Rudikoff S., Potter M.;
RT "Kappa Chain variable region from M167, a phosphorylcholine binding
RT myeloma protein.";
RL Biochemistry 17:2703-2707(1978).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds phosphorylcholine. The sequence of the V region of the heavy
CC chain has also been determined.
DR PIR: A01908; KWS16.
DR HSPF: Q8K0F8; IKN2.
DR InterPro: IPR007110; Ig-like.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Complementarity-determining-3.
FT DOMAIN 94 102 Complementarity-determining-4.
FT DOMAIN 103 112 By similarity.
FT DISULFID 23 93
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;

Query Match 87.5%; Score 42; DB 1; Length 112;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
DB 94 QQLVEYPFT 102

RESULT 3
KV2A MOUSE
ID KV2A_MOUSE STANDARD; PRT; 112 AA.
AC P01626;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region MOPC 167.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
MEDLINE=79000273; PubMed=99160;
Rudikoff S., Potter M.;
RT "Kappa Chain variable region from M167, a phosphorylcholine binding
RT myeloma protein.";
RL Biochemistry 17:2703-2707(1978).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds phosphorylcholine. The sequence of the V region of the heavy
CC chain has also been determined.
DR PIR: A01908; KWS16.
DR HSPF: Q8K0F8; IKN2.
DR InterPro: IPR007110; Ig-like.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Complementarity-determining-3.
FT DOMAIN 94 102 Complementarity-determining-4.
FT DOMAIN 103 112 By similarity.
FT DISULFID 23 93
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;

Query Match 87.5%; Score 42; DB 1; Length 112;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
DB 94 QQLVEYPFT 102

RESULT 4
KV2C MOUSE
ID KV2C_MOUSE STANDARD; PRT; 113 AA.
AC P01628;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region MOPC 511.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
MEDLINE=81052016; PubMed=6776396; DOI=10.1016/0161-5890(80)90140-6;
RA Appella E.;
RT "Amino acid sequence of the light chain variable region of M511, a
RT phosphorylcholine-binding murine myeloma protein.";
RL Mol. Immunol. 17:711-718(1980).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds phosphorylcholine.
DR PIR: A01910; KWS51.
DR HSPF: Q8K0F8; IKN2.
DR InterPro: IPR007110; Ig-like.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Complementarity-determining-3.
FT DOMAIN 94 102 Complementarity-determining-4.
FT DOMAIN 103 112 By similarity.
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Query Match 87.5%; Score 42; DB 1; Length 113;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
DB 94 QQLVEYPFT 102

RESULT 4
KV2C_MOUSE PRELIMINARY; PRT; 349 AA.
ID Q85TH4;
AC Q85TH4;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Cytochrome b.
GN Name=Cytb;
OS Melipona bicolor.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Melipona.
OX NCBI_TaxID=60889;
RN [1]
RP SEQUENCE FROM N.A.
RA Silvestre D., Arias M.C.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBSJ databases.
CC -1- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC complex (complex III or cytochrome b-c1 complex), which is a
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -1- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
CC b562) is low-potential and absorbs at about 562 nm, and heme 2 (or

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CC BH or b566) is high-potential and absorbs at about 566 nm (By
CC similarity).
CC -1- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).
CC -1- SIMILARITY: Belongs to the cytochrome b family.
DR EMBL: AF466146; AA018422.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005746; C: mitochondrial electron transport chain; IEA.
DR GO: GO:0005739; C: mitochondrion; IEA.
DR GO: GO:0016491; F: oxidoreductase activity; IEA.
DR GO: GO:0006118; P: electron transport; IEA.
DR GO: GO:0006810; P: transport; IEA.
DR InterPro: IPR005798; Cytb_b6_C.
DR InterPro: IPR005797; Cytb_b6_N.
DR Pfam: PF00032; Cytochrom_B_C; 1.
DR Pfam: PF00033; Cytochrom_B_N; 1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME; UNKNOWN_1.
DR PROSITE: PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane; Transport.
SQ SEQUENCE 349 AA; 41464 MW; 9B1DC3A6927DADD3 CRC64;

Query Match 83.3%; Score 40; DB 2; Length 349;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QLVVEYPPT 9
DB |||:|||||
311 QMVEYPT 318

RESULT 5
Q87RR4 PRELIMINARY; PRT; 506 AA.
AC Q87RR4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein VP0713.
GN OrderedLocustNames=VP0713;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749 (2003).
DR EMBL: AP005075; BAC58976.1; -.
DR GO: GO:0003677; F: DNA binding; IEA.
DR GO: GO:0001556; P: two-component response regulator activity; IEA.
DR GO: GO:0000160; P: two-component signal transduction system (p. . .; IEA.
DR InterPro: IPR009059; bi_resp_regltr_C.
DR InterPro: IPR001867; Trans_reg_C.
DR Pfam: PF00486; Trans_reg_C; 1.
DR ProDom: PD000329; Trans_reg_C; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 506 AA; 57784 MW; 7B566E691D449223 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 506;
Best Local Similarity 77.8%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLVVEYPPT 9
DB |||:|||||
209 QQVEYPT 217

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RESULT 6

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Q6PNB0 PRELIMINARY; PRT; 368 AA.
AC Q6PNB0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome b.
GN Name=CyTB;
OS Steineriema carpopapuae.
OG Mitochondrion.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Steinernematidae; Steinernema.
OX NCBI_TaxID=34508;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bretton;
RA Montiel R., Medeiros J., Lucena M., Simoes N.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY591323; AAT00527.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005746; C: mitochondrial electron transport chain; IEA.
DR GO: GO:0005739; C: mitochondrion; IEA.
DR GO: GO:0016491; F: oxidoreductase activity; IEA.
DR GO: GO:0006118; P: electron transport; IEA.
DR GO: GO:0006810; P: transport; IEA.
DR InterPro: IPR005798; Cytb_b6_C.
DR InterPro: IPR005797; Cytb_b6_N.
DR Pfam: PF00032; Cytochrom_B_C; 1.
DR PROSITE: PS00192; CYTOCHROME_B_HEME; UNKNOWN_1.
DR PROSITE: PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
KW Mitochondrion.
SQ SEQUENCE 368 AA; 43163 MW; 695BCB37839DBACE CRC64;

Query Match 79.2%; Score 38; DB 2; Length 368;
Best Local Similarity 77.8%; Pred. No. 48;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLVVEYPPT 9
DB |||:|||||
331 QCMVEYPT 339

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RESULT 7

```

Q6LTX1 PRELIMINARY; PRT; 532 AA.
AC Q6LTX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein VP0713.
GN Names=VP0713; OrderedLocustNames=PBPPA0841;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RC Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR378665; CAG19254.1; -.
DR GO: GO:0003677; F: DNA binding; IEA.
DR GO: GO:0001556; P: two-component response regulator activity; IEA.
DR GO: GO:0000160; P: two-component signal transduction system (p. . .; IEA.
DR InterPro: IPR009059; bi_resp_regltr_C.
DR InterPro: IPR001867; Trans_reg_C; 1.
DR Pfam: PF00486; Trans_reg_C; 1.
DR ProDom: PD000329; Trans_reg_C; 1.

```

KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 532 AA; 60884 MW; D863B4B91ED55249 CRC64;
Query Match 79.2%; Score 38; DB 2; Length 532;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 QQLVEYPT 9
DB 235 QOOIEYPT 243
RESULT 8
KV2B_MOUSE STANDARD; PRT; 120 AA.
ID KV2B_MOUSE
AC P01627;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region VKappa167 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82002223; PubMed=6791832; DOI=10.1016/0092-8674(81)90230-0;
RA Selsing E., Storb U.;
RT "Somatic mutation of immunoglobulin light-chain variable-region genes";
RL Cell 25:47-58(1981).
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CC
DR EMBL; J00562; AAA39032.1; -;
DR EMBL; K02415; AAA39051.1; -;
DR PIR; A01909; KVMS67.
DR HSP; P01751; INOB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 120
FT DOMAIN 21 43
FT DOMAIN 44 59
FT DOMAIN 60 74
FT DOMAIN 75 81
FT DOMAIN 82 113
FT DOMAIN 114 120
FT DISULFID 43 113
SQ SEQUENCE 120 AA; 13280 MW; 63BB571F0E4DE3E8 CRC64;
Query Match 77.1%; Score 37; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQLVEYPT 7
DB 114 QQLVEYPT 120
RESULT 9
Q8W454 PRELIMINARY; PRT; 278 AA.
ID Q8W454

Q8W454;
AC 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative calmodulin-binding protein.
GN Name=At4g31000;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY062856; AAL32934.1; -;
DR EMBL; AY114575; AAM47894.1; -;
SQ SEQUENCE 278 AA; 31406 MW; 398DCFB65C85A836 CRC64;
Query Match 77.1%; Score 37; DB 2; Length 278;
Best Local Similarity 75.0%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QQLVEYPT 8
DB 145 QQLVEYPT 152
RESULT 10
O65550 PRELIMINARY; PRT; 467 AA.
AC O65550;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative calmodulin-binding protein.
GN Name=F6118.90; Synonyms=AT4g31000;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Benes V., Rechmann S., Borkova D., Ansoorge W., Hoheisel J.,
RA Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Borkova D., Ansoorge W., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL022198; CA18193.1; -.
 DR EMBL; AL161578; CAB79818.1; -.
 DR PIR; A85363; A85363.
 SQ SEQUENCE 467 AA; 52831 MW; 4DB1FB318D553B3D CRC64;

Query Match 77.1%; Score 37; DB 2; Length 467;
 Best Local Similarity 75.0%; Pred. No. 96;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPP 8
 |||:||||
 Db 334 QHLEIYPP 341

RESULT 11

Q8H816 PRELIMINARY; PRT; 609 AA.
 ID Q8H816
 AC Q8H816
 DT 01-MAR-2003 (TEMBLrel. 23, Created)
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE Hypothetical protein OJ1743A09.11.
 GN Name-OJ1743A09.11;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OC NCBI_TaxID=39947;
 [1]
 RN SEQUENCE FROM N.A.
 RP Wang R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Sasaki C.,
 RA Currie J., Collura K.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC105364; AA05331.1; -.
 DR Gramene; Q8H816; -.
 DR InterPro; IPR002086; Aldehyd_dehydrog.
 DR InterPro; IPR001810; F-box.
 DR Pfam; PF00646; F-box; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CVS; UNKNOWN_1.
 DR PROSITE; PS00181; FBOX; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 609 AA; 68105 MW; AEA195731E08F07C CRC64;

Query Match 77.1%; Score 37; DB 2; Length 609;
 Best Local Similarity 77.8%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPP 9
 |||:||||
 Db 569 QQLLEIYPP 577

RESULT 12

Q9B313 PRELIMINARY; PRT; 84 AA.
 ID Q9B313
 AC Q9B313
 DT 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE Cytochrome b (Fragment).
 OS Neoceratodus forsteri (Australian lungfish).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Dipnoi; Ceratodontiformes; Ceratodontidae; Neoceratodus.
 OC NCBI_TaxID=7892;
 [1]
 RN SEQUENCE FROM N.A.
 RP Frentiu F., Ovenden J.R., Street R.;
 RA "Australian lungfish (Neoceratodus forsteri) have low genetic
 RT diversity at allozyme and mitochondrial loci: A conservation alert for
 RT a living fossil?";
 RL Conserv. Genet. 0:0-0(2001).

DR EMBL; AF344663; AAK29031.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR005798; Cytb_b6_C.
 DR Pfam; PF00032; Cytochrom_B_C; 1.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 84 AA; 9673 MW; 1E7AFAD921592DAC CRC64;

Query Match 75.0%; Score 36; DB 2; Length 84;
 Best Local Similarity 87.5%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPP 9
 |||:||||
 Db 27 QPVEYPP 34

RESULT 13

Q9MP34 PRELIMINARY; PRT; 247 AA.
 ID Q9MP34
 AC Q9MP34
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE Cytochrome b (Fragment).
 OS Bothriomyx meridionalis.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Formicidae; Dolichoderinae; Bothriomyx.
 OC NCBI_TaxID=121499;
 [1]
 RN SEQUENCE FROM N.A.
 RP Chiotis M., Jermin L.S., Crozier R.H.;
 RA Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Component of the ubiquinol-cytochrome c reductase
 CC complex (complex III or cytochrome b-c1 complex), which is a
 CC respiratory chain that generates an electrochemical potential
 CC coupled to ATP synthesis (By similarity).
 CC -1- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
 CC b562) is low-potential and absorbs at about 562 nm, and heme 2 (or
 CC BH or b566) is high-potential and absorbs at about 566 nm (By
 CC similarity).
 CC -1- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
 CC cytochrome c1 and the Rieske protein (By similarity).
 CC -1- SIMILARITY: Belongs to the cytochrome b family.
 DR EMBL; AF146714; AAF66714.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR005798; Cytb_b6_C.
 DR InterPro; IPR005797; Cytb_b6_N.
 DR Pfam; PF00032; Cytochrom_B_C; 1.
 DR Pfam; PF00033; Cytochrom_B_N; 1.
 DR PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
 KW Electron transport; Heme; Mitochondrion; Respiratory chain;
 KW Transmembrane; Transport.
 FT NON_TER 1
 SQ SEQUENCE 247 AA; 29263 MW; CC68F8BA0D065B1A CRC64;

Query Match 75.0%; Score 36; DB 2; Length 247;
 Best Local Similarity 75.0%; Pred. No. 81;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPP 9
 |||:||||
 Db 201 QSIEYPP 208

RESULT 14
 Q6YAK6 PRELIMINARY; PRT; 330 AA.
 ID Q6YAK6
 AC Q6YAK6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cytochrome b (Fragment).
 GN Name=cytb;
 OS Galerida magnirostris (large-billed lark).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Alaudidae;
 OC Spizocorys.
 OX NCBI_TaxID=215324;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22480425; PubMed=12590762; DOI=10.1098/rspb.2002.2205;
 RA Tieleman B.I., Williams J.B., Bloomer P.;
 RT "Adaptation of metabolism and evaporative water loss along an aridity
 gradient.";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 270:207-214(2003).
 CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
 CC complex (complex III or cytochrome b-c1 complex), which is a
 CC respiratory chain that generates an electrochemical potential
 CC coupled to ATP synthesis (By similarity).
 CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
 CC b562) is low-potential and absorbs at about 562 nm, and heme 2 (or
 CC BH or b566) is high-potential and absorbs at about 566 nm (By
 CC similarity).
 CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
 CC cytochrome c1 and the Rieske protein (By similarity).
 CC -!- SIMILARITY: Belongs to the cytochrome b family.
 DR EMBL; AY165170; AA060667.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR005798; Cytb_b6_C.
 DR InterPro; IPR005797; Cytb_b6_N.
 DR Pfam; PF00032; Cytochrom_B_C; 1.
 DR Pfam; PF00033; Cytochrom_B_N; 1.
 DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
 DR PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
 KW Electron transport; Heme; Mitochondrion; Respiratory chain;
 KW Transmembrane; Transport.
 FT NON_TER 1
 FT NON_TER 331
 SQ SEQUENCE 331 AA; 36761 MW; 91B07FFD83401CAF CRC64;
 Query Match 75.0%; Score 36; DB 2; Length 331;
 Best Local Similarity 87.5%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 QLYEYPPT 9
 DB 302 QPVEYPPT 309

Search completed: April 18, 2005, 14:21:54
 Job time : 83.8372 secs

RESULT 15
 Q6YAK5 PRELIMINARY; PRT; 331 AA.
 ID Q6YAK5
 AC Q6YAK5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cytochrome b (Fragment).
 GN Name=cytb;
 OS Spizocorys sclateri (Sclater's lark).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Alaudidae;
 OC Galerida.
 OX NCBI_TaxID=215324;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22480425; PubMed=12590762; DOI=10.1098/rspb.2002.2205;
 RA Tieleman B.I., Williams J.B., Bloomer P.;
 RT "Adaptation of metabolism and evaporative water loss along an aridity
 gradient.";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 270:207-214(2003).
 CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
 CC complex (complex III or cytochrome b-c1 complex), which is a
 CC respiratory chain that generates an electrochemical potential
 CC coupled to ATP synthesis (By similarity).
 CC -!- COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or
 CC b562) is low-potential and absorbs at about 562 nm, and heme 2 (or
 CC BH or b566) is high-potential and absorbs at about 566 nm (By
 CC similarity).
 CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
 CC cytochrome c1 and the Rieske protein (By similarity).
 CC -!- SIMILARITY: Belongs to the cytochrome b family.
 DR EMBL; AY165169; AA060667.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR005798; Cytb_b6_C.
 DR InterPro; IPR005797; Cytb_b6_N.
 DR Pfam; PF00032; Cytochrom_B_C; 1.
 DR Pfam; PF00033; Cytochrom_B_N; 1.
 DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
 DR PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
 KW Electron transport; Heme; Mitochondrion; Respiratory chain;
 KW Transmembrane; Transport.
 FT NON_TER 1
 FT NON_TER 330
 SQ SEQUENCE 330 AA; 36708 MW; 7F06BC73B311DD0D5 CRC64;
 Query Match 75.0%; Score 36; DB 2; Length 330;
 Best Local Similarity 87.5%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 QLYEYPPT 9
 DB 301 QPVEYPPT 308

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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:32:07 ; Search time 94.8139 Seconds
(without alignments)
36.712 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QQLVYFPFT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	3 AAY32256	Aay32256 Light cha
2	48	100.0	116	3 AAY32262	Aay32262 Humanised
3	48	100.0	145	3 AAY32261	Aay32261 Mouse ant
4	45	93.8	19	3 AAY70804	Aay70804 Murine an
5	45	93.8	122	3 AAY70790	Aay70790 Murine an
6	45	93.8	131	2 AAR12232	Aar12232 Mouse MAB
7	45	93.8	132	2 AAR12354	Aar12354 Light (ka
8	44	91.7	9	2 AAW39823	Aaw39823 Light cha
9	44	91.7	113	2 AAW39882	Aaw39882 Light cha
10	44	91.7	113	2 AAW39804	Aaw39804 Variable
11	42	87.5	248	7 ADG32323	Adg32323 Mouse scf
12	42	87.5	317	7 ADG32360	Adg32360 Precursor
13	37	77.1	100	4 AAE06969	Aae06969 Mouse ger
14	37	77.1	100	8 ADQ89254	Adq89254 Mouse imm
15	36	75.0	9	2 AAW39817	Aaw39817 Light cha
16	36	75.0	9	8 ADR38732	Adr38732 Mouse lig
17	36	75.0	107	8 ADI2109	Adi2109 Anti-plat
18	36	75.0	113	2 AAW39803	Aaw39803 Variable
19	36	75.0	113	2 AAW39801	Aaw39801 Variable
20	36	75.0	241	2 AAW24063	Aaw24063 Human WSX
21	36	75.0	241	5 AAW90948	Aaw90948 Insulin/i
22	36	75.0	241	7 ADC08951	Adc08951 Human WSX
23	36	75.0	251	5 ABP45299	Abp45299 Human Bly
24	36	75.0	251	7 ADG96126	Adg96126 Single ch
25	36	75.0	253	5 ABP44925	Abp44925 Human Bly

26	36	75.0	253	7	ADG95752	Adg95752 Single ch
27	36	75.0	274	2	AAW39899	Aaw39899 Single ch
28	36	75.0	392	3	AAI10863	Aai10863 S11-VSGF2
29	36	75.0	510	3	AAI10864	Aai10864 S11-scVEG
30	35	72.9	112	3	AAI90813	Aay90813 2G3 hybri
31	35	72.9	126	2	AAI36951	Aay36951 Protein 1
32	35	72.9	425	6	ABM69120	Abm69120 Photothab
33	35	72.9	533	3	AAI27700	Abm27700 Arabidops
34	35	72.9	536	3	AAI27699	Abm27699 Arabidops
35	35	72.9	622	3	AAI27698	Abm27698 Arabidops
36	34	70.8	9	3	AAI92171	Aay92171 Murine 13
37	34	70.8	113	3	AAI92171	Aay92171 Murine 13
38	34	70.8	146	2	AAW28154	Aaw28154 Amino aci
39	34	70.8	440	6	ABU49487	Abu49487 Protein e
40	34	70.8	531	8	ADU86167	Adu86167 Aspergill
41	34	70.8	585	5	ABP40069	Abp40069 Staphyloc
42	34	70.8	585	8	ADU4921	Adu4921 Staphyloc
43	34	70.8	601	6	ABM73103	Abm73103 Staphyloc
44	34	70.8	604	4	AAI81648	Aai81648 S. epider
45	34	70.8	1074	8	ADJ50367	Adj50367 Oil-aesoc

ALIGNMENTS

RESULT 1

AAV32256

ID AAY32256 standard; peptide; 9 AA.

XX

AC AAY32256;

XX

DT 15-FEB-2000 (first entry)

XX

DE Light chain CDR L3 of mouse anti-CD23 MAB C11.

XX

KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;

KW monoclonal antibody; chimeric antibody; humanised antibody;

KW complementarity determining region; CDR; autoimmune disease;

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;

KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

KW urticaria; nephrotic syndrome; glomerulonephritis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;

KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;

KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;

XX

OS Mus musculus.

XX

PN WO9558679-A1.

XX

PD 18-NOV-1999.

XX

PF 07-MAY-1999; 99WO-GB001434.

XX

PR 09-MAY-1998; 98GB-00009839.

XX

PA (GLAX) GLAXO GROUP LTD.

XX

PI Bonneyfoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX

DR WPI; 2000-053101/04.

XX

DR N-PSDB; AA234741.

XX

PT Cell receptor specific antibodies useful for treating e.g. arthritis,

PT diabetes, multiple sclerosis and psoriasis.

XX

PS Claim 1; Page 40; 81pp; English.

XX

CC This sequence represents complementarity determining region 3 (CDR L3)

CC of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11

CC (see also AAY32262). The invention provides altered antibodies, such as

CC chimeric or humanised antibodies, which comprise sufficient of the amino

CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on
CC haematopoietic cells. The antibodies are used to block soluble CD23
CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's
CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,
CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,
CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute
CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,
CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes
CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They
CC are also useful for studying interactions between CD23 and various
CC ligands and determining the binding agents

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
| | | | |
Db 1 QQLVEYPFT 9

RESULT 2

AAV32262

ID AAY32262 standard; protein; 116 AA.

XX AC AAY32262;

XX DT 15-FEB-2000 (first entry)

XX DE Humanised anti-CD23 Mab C11 light chain variable region.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human;
XX monoclonal antibody; chimeric antibody; humanised antibody;
XX complementarity determining region; CDR; autoimmune disease;
XX inflammation; arthritis; lupus erythematosus; multiple sclerosis;
XX Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
XX urticaria; nephrotic syndrome; glomerulonephritis;
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;
XX Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
XX graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
XX therapy.

OS Homo sapiens.
OS Synthetic.

XX FH Key Location/Qualifiers

FT Region 1. .23 /note= "framework region 1"

FT Region 24. .39 /note= "CDR 1"

FT Region 40. .54 /note= "framework region 2"

FT Region 55. .61 /note= "CDR 2"

FT Region 62. .93 /note= "framework region 3"

FT Region 94. .102 /note= "CDR 3"

FT Region 103. .113 /note= "framework region 4"

XX WO9958679-A1.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 95WO-GB001434.

XX PR 09-MAY-1998; 98GB-00009839.

XX PA (GLAX) GLAXO GROUP LTD.

XX PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
XX WPI; 2000-053101/04.
XX DR N-PSDB; AAZ34747.
XX Cell receptor specific antibodies useful for treating e.g. arthritis,
XX diabetes, multiple sclerosis and psoriasis.
XX Claim 9; Fig 3; 81pp; English.
XX This sequence represents the light chain variable region (VL) of
XX humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human
XX framework (H5IGKVII) and the light chain complementarity determining
XX regions (see AAY32254-56) of murine antibody C11. The DNA was constructed
XX by splice overlap PCR. The invention provides altered antibodies, such as
XX chimeric or humanised antibodies, which comprise sufficient of the amino
XX acid sequences of the C11 light and heavy chain complementarity
XX determining regions to render them capable of binding to the CD23 type II
XX molecule expressed on haematopoietic cells. The antibodies are used to
XX block soluble CD23 formation in human therapy, for the treatment of
XX arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
XX sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
XX syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
XX colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
XX intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
XX versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
XX bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
XX malignancies (claimed). They are also useful for studying interactions
XX between CD23 and various ligands and determining the binding agents

XX SQ Sequence 116 AA;

Query Match 100.0%; Score 48; DB 3; Length 116;

Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0;
QY 1 QQLVEYPFT 9
| | | | |
Db 94 QQLVEYPFT 102

RESULT 3

AAV32261

XX ID AAY32261 standard; protein; 145 AA.

XX AC AAY32261;

XX DT 15-FEB-2000 (first entry)

XX DE Mouse anti-CD23 Mab C11 light chain variable region.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;
XX monoclonal antibody; chimeric antibody; humanised antibody;
XX complementarity determining region; CDR; autoimmune disease;
XX inflammation; arthritis; lupus erythematosus; multiple sclerosis;
XX Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
XX urticaria; nephrotic syndrome; glomerulonephritis;
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;
XX Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
XX graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
XX therapy.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT Region 55. .70 /note= "CDR L1"

FT Region 83. .92 /note= "CDR L2"

FT Region 125. .134 /note= "CDR L3"

PN WO9958679-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-GB001434.
 XX
 PR 09-MAY-1998; 98GB-00009839.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Bonneyfo J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX
 DR WPI; 2000-053101/04.
 XX
 DR N-PSDB; AAZ34746.
 XX
 PT Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis.
 XX
 PS Claim 8; Fig 2; 8lpp; English.
 XX
 CC This sequence represents the light chain variable region (VL) of murine
 CC anti-CD23 (FCERII) monoclonal antibody C11. The invention provides
 CC altered antibodies, such as chimeric or humanised antibodies (see
 CC AAY32262 and AAY32263), which comprise sufficient of the amino acid
 CC sequences of the C11 light and heavy chain complementarity determining
 CC regions (see AAY32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies are
 CC used to block soluble CD23 formation in human therapy, for the treatment
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
 CC malignancies (claimed). They are also useful for studying interactions
 CC between CD23 and various ligands and determining the binding agents
 XX
 SQ Sequence 145 AA;
 Query Match 100.0%; Score 48; DB 3; Length 145;
 Best Local Similarity 100.0%; Pred. NO. 0.15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQLVEVPPT 9
 |||||
 DB 125 QQLVEVPPT 133
 RESULT 4
 AAY70804
 ID AAY70804 standard; peptide; 19 AA.
 XX
 AC AAY70804;
 XX
 DT 31-JUL-2000 (first entry)
 XX
 DE Murine anti-PAB-421 IDI-1 mAb light chain CDR based peptide IDI-1 L3.
 XX
 KW Murine, p53 protein; monoclonal antibody; mAb; PAB-421; IDI-1 L3;
 KW light chain variable region; VL; complementarity determining region; CDR;
 KW dermatological; immunosuppressive; antiinflammatory; autoimmune response;
 KW SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen;
 KW DNA-binding domain; anti-idiotypic antibody.
 XX
 OS Mus sp.
 XX
 PN WO200023082-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 19-OCT-1999; 99WO-US024443.
 XX
 PP
 XX

PR 19-OCT-1998; 98US-0104816P.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Cohen IR, Rotter V, Erez-Alon N, Herkel J;
 XX
 DR WPI; 2000-339512/29.
 XX
 PT Treatment of systemic lupus erythematosus by down-regulating the
 PT autoimmune response to the C-terminal DNA-binding domain of the p53
 PT protein by an active compound comprising of antibodies to p53 or
 PT fragments of p53.
 XX
 PS Claim 78; Fig 10; 87pp; English.
 XX
 CC The patent discloses a method for the treatment of systemic lupus
 CC erythematosus (SLE) by down-regulating the autoimmune response to the C-
 CC terminal DNA-binding domain of p53 protein by an active compound. The
 CC present sequence is a IDI-1 L3 peptide which comprises the
 CC complementarity determining region (CDR) of the light chain of IDI-1
 CC monoclonal antibody (mAb). The IDI-1 mAb is an anti-idiotypic
 CC antibody/Ab2 mAb specific for PAB-421 which is an Ab1 mAb specific to the
 CC C-terminal DNA-binding domain of murine p53 protein. The peptide
 CC corresponds to residues 92-110 of IDI-1 light chain variable region. It
 CC is an example of the active compound useful in the diagnosis, prevention
 CC and treatment of SLE in humans
 XX
 SQ Sequence 19 AA;
 Query Match 93.8%; Score 45; DB 3; Length 19;
 Best Local Similarity 88.9%; Pred. NO. 0.067;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQLVEVPPT 9
 |||||
 DB 6 QQLVEVPPT 14
 RESULT 5
 AAY70790
 ID AAY70790 standard; protein; 122 AA.
 XX
 AC AAY70790;
 XX
 DT 31-JUL-2000 (first entry)
 XX
 DE Murine anti-PAB-421 IDI-1 mAb light chain variable region.
 XX
 KW Murine, p53 protein; PAB-421; monoclonal antibody; mAb; IDI-1;
 KW anti-idiotypic antibody; DNA-binding domain; dermatological;
 KW immunosuppressive; antiinflammatory; autoimmune response; SLE;
 KW systemic lupus erythematosus; diagnosis; treatment; autoantigen;
 KW light chain variable region; VL; complementarity determining region; CDR.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 27..42
 FT /label= CDR
 FT /note= "Complementarity determining region"
 FT Region 58..64
 FT /label= CDR
 FT /note= "Complementarity determining region"
 FT Region 97..105
 FT /label= CDR
 FT /note= "Complementarity determining region"
 PN WO200023082-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 19-OCT-1999; 99WO-US024443.
 XX
 PP
 XX

PR 19-OCT-1998; 98US-0104816P.
 XX (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Cohen IR, Rotter V, Erez-Alon N, Herkel J;
 DR WPI; 2000-339512/29.
 XX
 XX Treatment of systemic lupus erythematosus by down-regulating the
 PT autoimmune response to the C-terminal DNA-binding domain of the p53
 PT protein by an active compound comprising of antibodies to p53 or
 PT fragments of p53.
 XX
 XX Claim 78; Fig 9; 87pp; English.
 XX
 CC The patent discloses a method for the treatment of systemic lupus
 CC erythematosus (SLE) by down-regulating the autoimmune response to the C-
 CC terminal DNA-binding domain of p53 protein by an active compound. The
 CC present sequence is a light chain variable region of IDI-1 an anti-
 CC idiotype antibody/Ab2 monoclonal antibody (mAb) specific for PAb-421
 CC which is an Ab1 mAb specific to the C-terminal DNA-binding domain of
 CC murine p53 protein. The Ab1 and Ab2 mAbs and peptides based on
 CC complementarity determining regions of light and heavy chain variable
 CC regions of these antibodies, are examples of active compounds useful in
 CC the diagnosis, prevention and treatment of SLE in humans
 XX
 XX Sequence 122 AA;
 SQ
 Query Match 93.8%; Score 45; DB 3; Length 122;
 Best Local Similarity 88.9%; Pred. NO. 0.49;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQLVEYPPT 9
 DB 97 QQLVEYPPT 105
 RESULT 6
 AAR12232
 ID AAR12232 standard; protein; 131 AA.
 XX AC AAR12232;
 XX AC
 XX 25-MAR-2003 (revised)
 DT 19-AUG-1991 (first entry)
 XX
 XX Mouse MAB 2E12 L chain V region.
 DE
 XX HIV-1; chimera.
 KW
 XX Mus sp.
 OS
 XX WO9107494-A.
 PN
 XX 30-MAY-1991.
 PD
 XX 13-NOV-1989; 89US-00433703.
 PP
 XX 13-NOV-1989; 89US-00433703.
 PR
 XX (XOMA) XOMA CORP.
 PA (GREG) GREEN CROSS CORP.
 PA (ZOMA-) ZOMA CORP.
 XX
 XX Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;
 PI WPI; 1991-178106/24.
 XX N-PSDB; AAQ12012.
 DR
 XX
 XX New chimeric mouse human antibodies - used in treatment, diagnosis and
 PT prophylaxis of HIV infections.
 PT
 XX Disclosure; Fig 1; 108pp; English.

XX The mouse VL gene product may be used to produce chimeric mouse-human
 CC Abs against HIV-1 comprising human Ig constant regions and murine
 CC variable regions. These novel sequence are useful in treatment, diagnosis
 CC and prophylaxis of HIV infections, and may be produced by a bacterial,
 CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct
 CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 131 AA;
 Query Match 93.8%; Score 45; DB 2; Length 131;
 Best Local Similarity 88.9%; Pred. NO. 0.53;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQLVEYPPT 9
 DB 114 QQLVEYPPT 122
 RESULT 7
 AAR12354
 ID AAR12354 standard; protein; 132 AA.
 XX AC AAR12354;
 XX 25-MAR-2003 (revised)
 DT 15-AUG-1991 (first entry)
 XX
 XX Light (kappa) chain variable region of murine 2E12 immunoglobulin.
 DE
 XX Chimeric antibodies; immunoconjugates; HIV; AIDS.
 KW
 XX Mus musculus.
 OS
 XX WO9107493-A.
 PN
 XX 30-MAY-1991.
 PD
 XX 13-NOV-1989; 89US-00433730.
 PP
 XX 13-NOV-1989; 89US-00433730.
 PR
 XX (XOMA) XOMA CORP.
 PA (GREG) GREEN CROSS CORP.
 XX
 XX Better MD, Horwitz AH, Ghoshdasti P, Robinson R;
 PI WPI; 1991-178105/24.
 XX N-PSDB; AAQ12056.
 DR
 XX New chimeric mouse-human antibodies - used to detect, kill and remove HIV
 PT -1 antigen from sample.
 PT
 XX Disclosure; Fig 1; 107pp; English.
 PS
 XX This is the light (kappa)- chain variable (V) region of a mouse
 CC monoclonal antibody (MAB), 2E12, and is specific for an HIV-1 viral
 CC antigen. It is used in the construction of a chimeric MAB comprising
 CC heavy and light chains having murine V regions and human C regions. The
 CC chimeric MABs are more effective than murine MAB 2E12 since they have an
 CC increased compatibility in humans. The heavy and light chain V-regions
 CC are joined by manipulating their respective joining (J) regions, to
 CC generate restriction enzyme recognition sites. The chimeric MABs can be
 CC used as immuno- conjugates, in association with e.g. toxins for HIV
 CC treatment. They can also be used in diagnosis of HIV. See also AAQ12057-
 CC 63. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003
 CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)
 XX
 XX Sequence 132 AA;
 Query Match 93.8%; Score 45; DB 2; Length 132;
 Best Local Similarity 88.9%; Pred. NO. 0.54;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 DB 114 QQLVEYPFT 122

RESULT 8

AAW39823
 ID AAW39823 standard; peptide; 9 AA.

XX AC AAW39823;

DT 16-JUN-1998 (first entry)

DE Light chain CDR3 of catalytic antibody 2A10.

XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

XX OS Mus sp.

XX PN WO9749800-A1.

XX PD 31-DEC-1997.

XX PF 25-JUN-1997; 97WO-US010965.

XX PR 25-JUN-1996; 96US-00672345.

XX PA (UYCO) UNIV COLUMBIA NEW YORK.

XX PI Landry DW;

XX DR WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

PS Claim 15; Page 82; 147pp; English.

CC AAW39821-23 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 2A10, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
 CC were prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester
 CC transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.
 CC The antibodies reduce the concentration of cocaine in a subject, and are
 CC used particularly for the treatment of an overdose. They are also used
 CC for treating addiction (by reducing the in vivo concentration that can be
 CC achieved)

XX SQ Sequence 9 AA;

Query Match 91.7%; Score 44; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.8e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9

DB 1 QQFVEYPFT 9

RESULT 9

AAW39882
 ID AAW39882 standard; protein; 113 AA.

XX AC AAW39882;

XX XX

DT 16-JUN-1998 (first entry)

XX Light chain of the catalytic antibody 2A10.

XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

XX OS Mus sp.

XX PN WO9749800-A1.

XX PD 31-DEC-1997.

XX PF 25-JUN-1997; 97WO-US010965.

XX PR 25-JUN-1996; 96US-00672345.

XX PA (UYCO) UNIV COLUMBIA NEW YORK.

XX PI Landry DW;

XX DR WPI; 1998-077166/07.

XX DR N-PSDB; AAV09789.

XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

PS Disclosure; Fig 21; 147pp; English.

XX The present sequence represents the light chain of a catalytic antibody
 CC which is capable of degrading cocaine. A series of cocaine transition
 CC state analogues (TSAs) were prepared and used to immunise mice for
 CC production of hybridomas. Catalytic antibodies were identified by their
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
 CC antibodies reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used for
 CC treating addiction (by reducing the in vivo concentration that can be
 CC achieved)

XX SQ Sequence 113 AA;

Query Match 91.7%; Score 44; DB 2; Length 113;
 Best Local Similarity 88.9%; Pred. No. 0.72;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9

DB 94 QQFVEYPFT 102

RESULT 10

AAW39804
 ID AAW39804 standard; protein; 113 AA.

XX AC AAW39804;

XX DT 16-JUN-1998 (first entry)

XX Variable domain of the Kappa light chain of catalytic antibody 2A10.

XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

XX OS Mus sp.

XX PN WO9749800-A1.

XX XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US010965.
 XX
 PR 25-JUN-1996; 96US-00672345.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 XX Landry DW;
 XX
 PI WPI; 1998-077166/07.
 XX
 DR New catalytic antibodies able to decompose cocaine, single-chain
 XX analogues - used to treat cocaine overdose and addiction, required in far
 PT smaller doses than antibodies that antagonise cocaine by simply binding.
 PT
 XX Claim 16; Page 73-74; 147pp; English.
 PS
 XX AAW39801-05 represent the amino acid sequences of the variable domain of
 XX the kappa light chain of catalytic antibodies which are able to degrade
 CC cocaine. A series of cocaine transition state analogues (TSAs) were
 CC prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody (AAW39809
 CC represents the heavy chain) was identified using TSA1, which is an
 CC immunogenic conjugate of a phosphate monoester transition state analogue.
 CC Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the
 CC concentration of cocaine in a subject, and are used particularly for the
 CC treatment of an overdose. They are also used for treating addiction (by
 CC reducing the in vivo concentration that can be achieved)
 XX
 XX Sequence 113 AA;
 SQ

Query Match 91.7%; Score 44; DB 2; Length 113;
 Best Local Similarity 88.9%; Pred. No. 0.72;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 |||||
 Db 94 QQFVEYPFT 102
 |||||

RESULT 11
 ADG32323
 ID ADG32323 standard; protein; 248 AA.
 XX
 AC ADG32323;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Mouse scFV VDM1 antibody targeted against V_dahliae SeqID 32.
 XX
 KW mouse; murine; scFV; anti-fungal peptide; AFP; scFV; disease resistant;
 KW transgenic; plant; fungal infection; antibody;
 KW pathogen-specific antibody; fungicidal; agriculture.
 XX
 OS Mus sp.
 XX WO2003089475-A2.
 XX
 XX 30-OCT-2003.
 XX
 XX 14-APR-2003; 2003WO-EP003852.
 XX
 XX 22-APR-2002; 2002EP-00008929.
 XX
 XX 28-MAY-2002; 2002EP-00011807.
 XX
 XX (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
 XX
 XX Peschen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;
 XX WPI; 2003-854088/79.
 XX
 DR N-PSDB; ADG32298.
 XX

PT New fusion protein comprising an anti-fungal protein or peptide and an
 PT antibody fragment, useful in agriculture and horticulture for producing
 PT Ascomyceta-resistant transgenic plants, plant cells or plant tissues.
 XX
 PS Example 13; SEQ ID NO 32; 47pp; English.
 XX
 CC This invention relates to a novel fusion protein comprising an anti-
 CC fungal protein or peptide (AFP) and an antibody fragment (scFV).
 CC Specifically, it refers to AFPs recognizing an epitope of an Ascomyceta
 CC and a cellular targeting sequence, which can be used to generate disease
 CC resistant transgenic plants that are protected against fungal infection.
 CC Accordingly, a method is described for antibody based resistance in
 CC plants such that the undesirable and expensive chemical controls often
 CC used in agriculture are not required. The present invention provides
 CC antibodies, recombinant antibodies and fragments thereof, as well as
 CC fusion proteins that can be used as pathogen-specific antibodies targeted
 CC to different plant cell compartments. As such, these fungicidal agents
 CC confer a broad spectrum of disease resistance in both economically
 CC important crops and ornamental plants. This polypeptide is an antibody
 CC used in an exemplification of the invention.
 XX
 SQ Sequence 248 AA;
 Query Match 87.5%; Score 42; DB 7; Length 248;
 Best Local Similarity 88.9%; Pred. No. 4.2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 |||||
 Db 228 QQLVEYPLT 236
 |||||

RESULT 12
 ADG32360
 ID ADG32360 standard; protein; 317 AA.
 XX
 AC ADG32360;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Precursor fusion protein of AFP AG-scFV VDM1 SeqID 69.
 XX
 KW scFV; anti-fungal peptide; AFP; scFV; disease resistant; transgenic;
 KW plant; fungal infection; antibody; pathogen-specific antibody;
 KW fungicidal; agriculture; mouse; chimeric; murine.
 XX
 OS Chimeric.
 OS Synthetic.
 OS Aspergillus giganteus.
 OS Mus musculus.
 XX
 XX WO2003089475-A2.
 XX
 XX 30-OCT-2003.
 XX
 XX 14-APR-2003; 2003WO-EP003852.
 XX
 XX 22-APR-2002; 2002EP-00008929.
 XX
 XX 28-MAY-2002; 2002EP-00011807.
 XX
 XX (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
 XX
 XX Peschen D, Fischer R, Schillberg S, Liao Y, Dorfmueller S;
 XX WPI; 2003-854088/79.
 XX
 DR N-PSDB; ADG32349.
 XX
 XX New fusion protein comprising an anti-fungal protein or peptide and an
 PT antibody fragment, useful in agriculture and horticulture for producing
 PT Ascomyceta-resistant transgenic plants, plant cells or plant tissues.
 XX
 PS Disclosure; SEQ ID NO 69; 47pp; English.
 XX

CC This invention relates to a novel fusion protein comprising an anti-fungal protein or peptide (AFP) and an antibody fragment (scFv).
 CC Specifically, it refers to AFPs recognizing an epitope of an Ascomyceta and a cellular targeting sequence, which can be used to generate disease resistant transgenic plants that are protected against fungal infection.
 CC Accordingly, a method is described for antibody based resistance in plants such that the undesirable and expensive chemical controls often used in agriculture are not required. The present invention provides antibodies, recombinant antibodies and fragments thereof, as well as fusion proteins that can be used as pathogen-specific antibodies targeted to different plant cell compartments. As such, these fungicidal agents confer a broad spectrum of disease resistance in both economically important crops and ornamental plants. This polypeptide is a precursor fusion protein of the order [AFP - linker - antibody fragment] of the invention.

XX Sequence 317 AA;

Query Match 87.5%; Score 42; DB 7; Length 317;
 Best Local Similarity 88.9%; Pred. No. 5.5;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEXPPT 9
 |||||
 Db 297 QQLVEXPPT 305

RESULT 13

AAE06969
 ID AAE06969 standard; protein; 100 AA.

XX AAE06969;

XX 16-OCT-2001 (first entry)

DE Mouse germline kappa light chain variable (VK) region, 167/24.

XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; neointimal hyperplasia; VK; kappa light chain variable region.

XX Mus sp.

XX WO200157226-A1.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US0005337.

XX 03-FEB-2000; 2000US-00497625.

XX (MILL-) MILLENNIUM PHARM INC.

XX Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T; WPI; 2001-488888/53.

XX Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin.

XX Disclosure; Page 151; 183pp; English.

XX The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies

CC are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherosclerosis and arteriosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR-2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IgE-mediated allergic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is mouse germline kappa light chain variable (VK) region, 167/24

XX Sequence 100 AA;

Query Match 77.1%; Score 37; DB 4; Length 100;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7
 |||||
 Db 94 QQLVEYP 100

RESULT 14

ADQ89254

ID ADQ89254 standard; protein; 100 AA.

XX ADQ89254;

XX 21-OCT-2004 (first entry)

DE Mouse immunoglobulin protein #14.

XX Mouse; immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCR2; inflammatory disease; autoimmune disorder; graft rejection; HIV infection; atherosclerosis; anti-inflammatory; immunosuppressive; anti-HIV; virucide; antiarteriosclerotic.

XX Mus musculus.

XX US2004151721-A1.

XX 05-AUG-2004.

XX 10-DEC-2003; 2003US-00733563.

XX 19-OCT-2001; 2001US-0350166P.

XX 26-JUN-2002; 2002US-0392364P.

XX 17-OCT-2002; 2002US-00272899.

XX (OKEE/) O'KEEFE T.

XX (PONA/) PONA P.

XX O'keefe T, Ponath P;

XX WPI; 2004-580175/56.

XX New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists, useful for diagnosing and/or treating inflammatory or autoimmune diseases, and HIV infection.

XX Example 2; SEQ ID NO 32; 128pp; English.

XX The invention relates to humanised immunoglobulin heavy and light chains which have specificity for the CC-chemokine receptor 2 (CCR2) and an immunoglobulin or its antigen binding fragment comprising the chains. The

CC humanised immunoglobulin or its antigen binding fragment preferably
 CC comprises two heavy chains and two light chains. The humanised
 CC immunoglobulin and its heavy and light chains are useful for the
 CC diagnosis, prevention and/or treatment of diseases or conditions
 CC associated with aberrant expression or activity of the CCR2 polypeptide,
 CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV
 CC infection and atherosclerosis. This sequence represents a mouse
 CC immunoglobulin protein of the invention.

XX Sequence 100 AA;

SQ Query Match 77.1%; Score 37; DB 8; Length 100;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7

Db 94 QQLVEYP 100

RESULT 15

AAW39817

ID AAW39817 standard; peptide; 9 AA.

XX AC

XX AAW39817;

XX AC

DT 16-JUN-1998 (first entry)

XX DE

XX Light chain CDR3 of catalytic antibody 3B9.

XX KW

Variable domain; lambda light chain; catalytic antibody; degradation;

KW cocaine; cocaine transition state analogue; TSA; benzoic acid;

KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;

XX overdose; addiction.

XX OS

Mus sp.

XX PN

WO9749800-A1.

XX PD

31-DEC-1997.

XX PF

25-JUN-1997; 97WO-US010965.

XX PR

25-JUN-1996; 96US-00672345.

XX PA

(UYCO) UNIV COLUMBIA NEW YORK.

XX PI

Landry DW;

XX DR

WPI; 1998-077166/07.

XX PT

New catalytic antibodies able to decompose cocaine, single-chain
 analogues - used to treat cocaine overdose and addiction, required in far
 smaller doses than antibodies that antagonise cocaine by simply binding.

XX PS

Claim 11; Page 81; 147pp; English.

XX CC

AAW39815-17 represent the sequences of the light chain complementarity
 determining regions (CDRs) of the catalytic antibody 3B9, which is able
 to degrade cocaine. A series of cocaine transition state analogues (TSAs)
 were prepared and used to immunise mice for production of hybridomas.

CC Catalytic antibodies were identified by their capacity to release 3H-

benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified

using TSAI, which is an immunogenic conjugate of a phosphate monoester

transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11.

CC The antibodies reduce the concentration of cocaine in a subject, and are

used particularly for the treatment of an overdose. They are also used

for treating addiction (by reducing the in vivo concentration that can be

XX achieved)

XX SQ

Sequence 9 AA;

Query Match

75.0%; Score 36; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9

Db 1 QHFVDYPT 9

Search completed: April 18, 2005, 14:15:16

Job time : 96.8139 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:22:17 ; Search time 68.0233 Seconds
(without alignments)
43.975 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QQLVEVPFT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA*

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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	91.7	9	10	US-09-940-727B-27
2	44	91.7	113	10	US-09-940-727B-8
3	44	91.7	113	10	US-09-940-727B-108
4	37	77.1	100	9	US-09-840-459-32
5	37	77.1	100	16	US-10-766-773-32
6	37	77.1	100	16	US-10-766-610-32
7	37	77.1	100	16	US-10-733-563-32
8	37	77.1	609	16	US-10-437-963-104782
9	36	75.0	9	10	US-09-940-727B-21
10	36	75.0	9	16	US-10-632-706-134
11	36	75.0	113	10	US-09-940-727B-5
12	36	75.0	113	10	US-09-940-727B-7
13	36	75.0	113	10	US-09-940-727B-100

14	36	75.0	113	10	US-09-940-727B-112	Sequence 112, App
15	36	75.0	241	8	US-08-779-457-50	Sequence 50, Appl
16	36	75.0	241	17	US-10-921-710-50	Sequence 50, Appl
17	36	75.0	251	10	US-09-880-748-1310	Sequence 1310, Ap
18	36	75.0	251	15	US-10-293-418-1310	Sequence 1310, Ap
19	36	75.0	253	10	US-09-880-748-936	Sequence 936, App
20	36	75.0	253	15	US-10-293-418-936	Sequence 936, App
21	36	75.0	280	10	US-09-940-727B-119	Sequence 119, App
22	35	72.9	90	16	US-10-767-701-56894	Sequence 56894, A
23	35	72.9	298	15	US-10-425-114-71736	Sequence 71736, A
24	35	72.9	569	15	US-10-425-114-72355	Sequence 72355, A
25	34	70.8	440	15	US-10-282-122A-77411	Sequence 77411, A
26	34	70.8	1074	15	US-10-389-566-2371	Sequence 2371, Ap
27	33	68.8	9	16	US-10-823-253-20	Sequence 20, Appl
28	33	68.8	79	15	US-10-425-114-44597	Sequence 44597, A
29	33	68.8	82	9	US-09-864-761-47635	Sequence 47635, A
30	33	68.8	82	15	US-10-424-599-280477	Sequence 280477, A
31	33	68.8	83	15	US-10-424-599-212368	Sequence 212368, A
32	33	68.8	105	16	US-10-823-253-30	Sequence 30, Appl
33	33	68.8	107	10	US-09-848-798-40	Sequence 40, Appl
34	33	68.8	107	16	US-10-823-253-25	Sequence 25, Appl
35	33	68.8	107	16	US-10-823-253-28	Sequence 28, Appl
36	33	68.8	107	16	US-10-823-253-32	Sequence 32, Appl
37	33	68.8	199	15	US-10-424-599-246437	Sequence 246437, A
38	33	68.8	243	16	US-10-437-963-161157	Sequence 161157, A
39	33	68.8	250	16	US-10-333-235A-55	Sequence 55, Appl
40	33	68.8	337	16	US-10-437-963-130847	Sequence 130847, A
41	33	68.8	368	16	US-10-333-235A-58	Sequence 58, Appl
42	33	68.8	441	15	US-10-282-122A-45037	Sequence 45037, A
43	33	68.8	465	16	US-10-333-235A-59	Sequence 59, Appl
44	33	68.8	561	15	US-10-369-493-870	Sequence 870, Appl
45	33	68.8	726	9	US-09-973-451-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-940-727B-27
; Sequence 27, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-27

Query Match 91.7%; Score 44; DB 10; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.3e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEVPFT 9

Db 1 QQFVEVPFT 9

RESULT 2

US-09-940-727B-8
; Sequence 8, Application US/09940727B

; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-8

Query Match 91.7%; Score 44; DB 10; Length 113;
Best Local Similarity 88.9%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYFPFT 9
Db 94 QQFVEYFPFT 102

RESULT 3
US-09-940-727B-108
; Sequence 108, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-108

Query Match 91.7%; Score 44; DB 10; Length 113;
Best Local Similarity 88.9%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYFPFT 9
Db 94 QQFVEYFPFT 102

RESULT 4
US-09-840-459-32
; Sequence 32, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.

; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-32

Query Match 77.1%; Score 37; DB 9; Length 100;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYYP 7
Db 94 QQLVEYYP 100

RESULT 5
US-10-766-773-32
; Sequence 32, Application US/10766773
; Publication No. US20040128851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-766-773-32

Query Match 77.1%; Score 37; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYYP 7
Db 94 QQLVEYYP 100

RESULT 6
US-10-766-610-32
; Sequence 32, Application US/10766610

Publication No. US20040132980A1
GENERAL INFORMATION:
APPLICANT: Larosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-029
CURRENT APPLICATION NUMBER: US/10/766,610
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: 09/840,459
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 100
TYPE: PRT
ORGANISM: Mus musculus
US-10-766-610-32

Query Match 77.1%; Score 37; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLVEYP 7
| | | | |
Db 94 QQLVEYP 100

RESULT 7
US-10-733-563-32
Sequence 32, Application US/10733563
Publication No. US20040151721A1
GENERAL INFORMATION:
APPLICANT: Ponath, Paul
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
METHODS OF USE THEREOF
FILE REFERENCE: 10448-213001
CURRENT APPLICATION NUMBER: US/10/733,563
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: US 10/272,899
PRIOR FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 60/392,364
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/350,166
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32
LENGTH: 100
TYPE: PRT
ORGANISM: Mus musculus
US-10-733-563-32

Query Match 77.1%; Score 37; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLVEYP 7
| | | | |
Db 94 QQLVEYP 100

RESULT 8

US-10-437-963-104782
Sequence 104782, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 104782
LENGTH: 609
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_102083C.1.pap
US-10-437-963-104782

Query Match 77.1%; Score 37; DB 16; Length 609;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9
| | | | |
Db 569 QQLLEIPPT 577

RESULT 9

US-09-940-727B-21
Sequence 21, Application US/09940727B
Publication No. US2003007793A1
GENERAL INFORMATION:
APPLICANT: Landry, Donald W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 0575/51400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR FILING DATE: 1997-06-25
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 9
TYPE: PRT
ORGANISM: mouse
US-09-940-727B-21

Query Match 75.0%; Score 36; DB 10; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9
| | | | |
Db 1 QHFVDYPT 9

RESULT 10
US-10-632-706-134

; Sequence 134, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROPEPTIDES
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 134
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-134

Query Match 75.0%; Score 36; DB 16; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9
| : |||
DB 1 QQLISYPT 9

RESULT 11
US-09-940-727B-5
; Sequence 5, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-5

Query Match 75.0%; Score 36; DB 10; Length 113;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9
| : |||
DB 94 QHFDYPT 102

RESULT 12
US-09-940-727B-7
; Sequence 7, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-7

Query Match 75.0%; Score 36; DB 10; Length 113;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9
| : |||
DB 94 QHFDYPT 102

RESULT 13
US-09-940-727B-100
; Sequence 100, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-100

Query Match 75.0%; Score 36; DB 10; Length 113;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9
| : |||
DB 94 QHFDYPT 102

RESULT 14
US-09-940-727B-112
; Sequence 112, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25

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; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 112
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-112

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Query Match 75.0%; Score 36; DB 10; Length 113;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels

QY 1 QQLVEYPFT 9
Db 94 QHFVDYPFT 102

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RESULT 15
US-08-779-457-50
; Sequence 50, Application US/08779457
; Publication No. US20020193571A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kyung, Jin Kim
; APPLICANT: Matthews, William
; APPLICANT: Rodrigues, Maria L.
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,457

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Query Match 75.0%; Score 36; DB 8; Length 241;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 2; Indels

Qy 1 QQLVEYPFT 9

Db 223 QQLISYPLT 231
|||: |||

Search completed: April 18, 2005, 14:54:41
Job time : 69.0233 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 14:01:43 ; Search time 24.4884 Seconds
(without alignments)
27.435 Million cell updates/sec

Title: US-09-674-716B-7
Perfect score: 48
Sequence: 1 QQLVEVPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	91.7	9	2	US-08-672-345C-27
2	44	91.7	9	3	US-09-214-095D-27
3	44	91.7	113	2	US-08-672-345C-8
4	44	91.7	113	2	US-08-672-345C-98
5	44	91.7	113	3	US-09-214-095D-8
6	44	91.7	113	3	US-09-214-095D-108
7	37	77.1	100	4	US-08-840-459-32
8	37	77.1	100	4	US-09-497-625A-32
9	36	75.0	9	2	US-08-672-345C-21
10	36	75.0	9	3	US-09-214-095D-21
11	36	75.0	113	2	US-08-672-345C-5
12	36	75.0	113	2	US-08-672-345C-7
13	36	75.0	113	2	US-08-672-345C-95
14	36	75.0	113	2	US-08-672-345C-97
15	36	75.0	113	3	US-09-214-095D-5
16	36	75.0	113	3	US-09-214-095D-7
17	36	75.0	113	3	US-09-214-095D-100
18	36	75.0	113	3	US-09-214-095D-112
19	36	75.0	280	3	US-09-214-095D-119
20	35	72.9	112	3	US-08-483-749A-4
21	34	70.8	9	3	US-09-406-532-20
22	34	70.8	113	3	US-09-406-532-14
23	34	70.8	585	3	US-09-134-001C-4914
24	34	70.8	604	4	US-09-710-279-390
25	33	68.8	9	1	US-08-438-123-3
26	33	68.8	11	1	US-08-438-123-11
27	33	68.8	107	3	US-09-240-274-40

28 33 68.8 108 1 US-08-468-661-3 Sequence 3, Appli
29 33 68.8 108 1 US-08-466-272A-3 Sequence 3, Appli
30 33 68.8 108 1 US-08-478-857-3 Sequence 3, Appli
31 33 68.8 108 2 US-08-471-771-3 Sequence 3, Appli
32 33 68.8 108 3 US-09-130-783-3 Sequence 3, Appli
33 33 68.8 113 3 US-08-483-749A-16 Sequence 16, Appli
34 33 68.8 113 5 PCT-US93-11611-5 Sequence 5, Appli
35 33 68.8 133 1 US-08-253-877C-10 Sequence 10, Appli
36 33 68.8 133 1 US-08-253-877C-28 Sequence 28, Appli
37 33 68.8 133 2 US-08-452-164A-10 Sequence 10, Appli
38 33 68.8 133 2 US-08-452-164A-28 Sequence 28, Appli
39 33 68.8 133 3 US-08-603-024-4 Sequence 4, Appli
40 33 68.8 133 3 US-08-603-024-27 Sequence 27, Appli
41 33 68.8 133 4 US-08-450-809-23 Sequence 23, Appli
42 33 68.8 133 5 PCT-US93-11611-2 Sequence 2, Appli
43 33 68.8 133 5 PCT-US93-11611-9 Sequence 9, Appli
44 33 68.8 141 1 US-08-438-123-7 Sequence 7, Appli
45 33 68.8 437 4 US-09-252-991A-20209 Sequence 20209, A

ALIGNMENTS

RESULT 1
US-08-672-345C-27
; Sequence 27, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-27

Query Match 91.7%; Score 44; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEVPFT 9
Db 1 QQLVEVPFT 9

RESULT 2

US-09-214-095D-27
; Sequence 27, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-27

Query Match 91.7%; Score 44; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
||| |||||
Db 1 QQFVEYPFT 9

RESULT 3
US-08-672-345C-8
; Sequence 8, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-672-345C-8
Query Match 91.7%; Score 44; DB 2; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.34;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QQLVEYPFT 9
||| |||||
Db 94 QQFVEYPFT 102

Query Match 91.7%; Score 44; DB 3; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.34;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QQLVEYPFT 9
||| |||||
Db 94 QQFVEYPFT 102

RESULT 4
US-08-672-345C-98
; Sequence 98, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-672-345C-98
Query Match 91.7%; Score 44; DB 2; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.34;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
||| |||||
Db 94 QQFVEYPFT 102

RESULT 5
US-09-214-095D-8
; Sequence 8, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-8

Query Match 91.7%; Score 44; DB 3; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.34;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYDPT 9
||| |||||
Db 94 QQFVEYDPT 102

RESULT 6
US-09-214-095D-108
; Sequence 108, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
US-09-214-095D-108

Query Match 91.7%; Score 44; DB 3; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.34;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYDPT 9
||| |||||
Db 94 QQFVEYDPT 102

RESULT 7
US-09-840-459-32
; Sequence 32, Application US/09840459
; Patent No. 6698550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-32

Query Match 77.1%; Score 37; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYDPT 7
||| |||||
Db 94 QQLVEYDPT 100

RESULT 8
US-09-497-625A-32
; Sequence 32, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-497-625A-32

Query Match 77.1%; Score 37; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYDPT 7
||| |||||
Db 94 QQLVEYDPT 100

RESULT 9
US-08-672-345C-21
; Sequence 21, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

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;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-21

Query Match 75.0%; Score 36; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
Db 1 QHFVDYPPT 9

RESULT 10
US-09-214-095D-21
; Sequence 21, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen.sp.
US-09-214-095D-21

Query Match 75.0%; Score 36; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
Db 1 QHFVDYPPT 9

RESULT 11
US-08-672-345C-5
; Sequence 5, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-7

Query Match 75.0%; Score 36; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
Db 94 QHFVDYPPT 102

RESULT 12
US-08-672-345C-7
; Sequence 7, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-7

Query Match 75.0%; Score 36; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
Db 94 QHFVDYPPT 102

RESULT 13
US-08-672-345C-95
; Sequence 95, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
```



```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-672-345C-95
;
; Query Match 75.0%; Score 36; DB 2; Length 113;
; Best Local Similarity 66.7%; Pred. No. 12;
; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 QQLVEYPPT 9
; Db 94 QHFVDYPPT 102
;
; RESULT 14
; US-08-672-345C-97
; Sequence 97, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 97:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-672-345C-97
;
; Query Match 75.0%; Score 36; DB 2; Length 113;
; Best Local Similarity 66.7%; Pred. No. 12;
; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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; QY 1 QQLVEYPPT 9
; Db 94 QHFVDYPPT 102
;
; RESULT 15
; US-09-214-095D-5
; Sequence 5, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. Sp.
; US-09-214-095D-5
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; Query Match 75.0%; Score 36; DB 3; Length 113;
; Best Local Similarity 66.7%; Pred. No. 12;
; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 QQLVEYPPT 9
; Db 94 QHFVDYPPT 102
;
; Search completed: April 18, 2005, 14:25:26
; Job time : 24.4884 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:11:18 ; Search time 42 Seconds
(without alignments)
20.618 Million cell updates/sec

Title: US-09-674-716B-7
Perfect score: 48
Sequence: 1 QQLVEYPFT 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	43.8	9	2 S66635	alpha-2-macroglobu
2	19	39.6	5	2 E60274	major protein anti
3	16	33.3	3	3 A43391	TRH-like tripeptid
4	14	29.2	4	2 PT0240	Ig heavy chain CRD
5	14	29.2	4	2 A32039	tyrosine-melanocyt
6	14	29.2	5	2 PQ0009	angiotensin-conver
7	14	29.2	6	2 JN0861	peptidyl-dipectida
8	14	29.2	7	1 A61324	dermorphin - Rohde
9	14	29.2	7	2 S36862	dermorphin (Lys-7)
10	14	29.2	7	2 S21230	dermorphin (Trp-4,
11	14	29.2	7	2 S42620	aggreccan - bovine
12	14	29.2	8	2 S66646	cardioacceleratory
13	14	29.2	9	2 B49712	ATP-binding protei
14	14	29.2	9	2 A61620	locustanyotrocin I
15	13	27.1	5	2 JS0319	subesophageal gang
16	13	27.1	6	2 A61049	halo-toxin - Pseud
17	13	27.1	6	2 I51317	bHLH transcription
18	13	27.1	7	2 E33932	Ig mu chain D regi
19	13	27.1	7	2 PX0008	glucuronosyltransf
20	13	27.1	7	4 I56695	hypothetical L2 pr
21	13	27.1	8	2 S16324	hypothetical prote
22	13	27.1	9	2 S39766	cardioactive pepti
23	13	27.1	9	2 S65433	bradykinin - horn
24	13	27.1	9	2 PT0285	Ig heavy chain CRD
25	13	27.1	9	2 S39767	cardioactive pepti
26	13	27.1	9	2 A26363	cardioactive pepti
27	13	27.1	9	2 S27233	cardioactive pepti
28	13	27.1	9	2 PT0080	60K Ca binding pro
29	13	27.1	9	2 S10784	enamelin i - bovin

30 13 27.1 9 2 I46023 growth hormone rec
31 13 27.1 9 2 A43065 hydroxyproline-3-b
32 13 27.1 9 2 S15850 vitamin D3 26-mono
33 13 27.1 9 2 A26744 bradykinin-like pe
34 13 27.1 9 2 A61057 Thr-6 bradykinin -
35 13 27.1 9 2 A60579 bradykinin-like pe
36 13 27.1 9 2 A61363 bradykinin - commo
37 13 27.1 9 2 A61358 pap fibrinial regul
38 12 25.0 5 2 B37325 phytoosulfokine alp
39 12 25.0 5 3 JT0870 pIL6 protein - Esc
40 12 25.0 7 2 S25266 amine oxidase (cop
41 12 25.0 7 2 A38081 capsid protein VP-
42 12 25.0 8 2 PL0184 serum albumin - do
43 12 25.0 8 2 B45800 neuropeptide calla
44 12 25.0 8 2 D47393 neuropeptide calla
45 12 25.0 8 2 E47393

ALIGNMENTS

RESULT 1

S66635
alpha-2-macroglobulin isoform 1 - bovine (fragment)
C:Species: Bos primigenius indicus (zebu cattle)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S66635

R:Dotmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottr
PERS Lett. 372, 93-95, 1995
A:Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain
A:Reference number: S66634; MUID:96032553; PMID:7556651
A:Accession: S66635

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <DOL>
A:Cross-references: UNIPROT:Q7M2N8

Query Match 43.8%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 EYPF 8
DB 3 EPPF 6

RESULT 2

E60274
major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)

C:Species: Mycobacterium tuberculosis
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C:Accession: E60274

R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A:Title: Isolation and partial characterization of major protein antigens in the cultur

A:Reference number: A60274; MUID:91099989; PMID:1898899
A:Accession: E60274
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <NAG>

Query Match 39.6%; Score 19; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 YPFT 9
DB 2 YPIT 5

RESULT 3

A43391
TRH-like tripeptide - alfalfa

C:Species: Medicago sativa (alfalfa)
 C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C:Accession: A43391
 R:Lackey, D.B.

J. Biol. Chem. 267, 17508-17511, 1992
 A:Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroglutamate, from Medicago sativa (alfalfa)
 A:Reference number: A43391; PMID:92388092; PMID:1517203
 A:Accession: A43391
 A:Molecule type: protein
 A:Residues: 1-3 <LAC>
 C:Keywords: amidated carboxyl end; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 33.3%; Score 16; DB 3; Length 3;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 EYP 7
 ||
 Db 1 QVP 3

RESULT 4

PT0240

Ig heavy chain CDR3 region (clone 2-100B) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0240

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A:Reference number: PT0222; PMID:91108337; PMID:1899102

A:Accession: PT0240

A:Molecule type: DNA

A:Residues: 1-4 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 29.2%; Score 14; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7
 ||
 Db 1 YP 2

RESULT 5

A32039

tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000

C:Accession: A32039

R:Horvath, A.; Kastin, A.J.

J. Biol. Chem. 264, 2175-2179, 1989

A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor

A:Reference number: A32039; PMID:89123285; PMID:2563371

A:Accession: A32039

A:Molecule type: protein

A:Residues: 1-4 <HOR>

A:Experimental source: brain

C:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end

F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 29.2%; Score 14; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7
 ||
 Db 1 YP 2

RESULT 6

PQ0009

angiotensin-converting enzyme inhibitor (FLP-2) - common fig

N:Alternate names: ficus latex peptide 2

C:Species: Ficus carica (common fig)

C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995

C:Accession: PQ0009

R:Maruyama, S.; Miyoshi, S.; Tanaka, H.

Agric. Biol. Chem. 53, 2763-2767, 1989

A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.

A:Reference number: PQ0008

A:Accession: PQ0009

A:Molecule type: protein

A:Residues: 1-5 <MAR>

A:Experimental source: latex

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 29.2%; Score 14; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7
 ||
 Db 2 YP 3

RESULT 7

JN0861

peptidyl-diesterase A inhibitory peptide C111 - striped bonito

C:Species: Sarda orientalis (striped bonito)

C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999

C:Accession: JN0861

R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.

Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993

A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe

A:Reference number: JN0859; PMID:94080036; PMID:7764272

A:Accession: JN0861

A:Molecule type: protein

A:Residues: 1-6 <MAT>

A:Experimental source: liver

C:Comment: The carboxyl end is essential for the protein's expression of angiotensin I-c

C:Superfamily: bradykinin-potentiating peptide

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 29.2%; Score 14; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7
 ||
 Db 3 YP 4

RESULT 8

A61324

dermorphin - Rohde's leaf frog

C:Species: Phyllomedusa rohdei (Rohde's leaf frog)

C:Date: 17-Jul-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999

C:Accession: A61324

R:Montecucchi, P.C.; De Castiglione, R.; Erspamer, V.

Int. J. Pept. Protein Res. 17, 316-321, 1981

A:Title: Identification of dermorphin and Hyp(6)-dermorphin in skin extracts of the Bra

A:Reference number: A61324; PMID:82029915; PMID:7287302

A:Accession: A61324

A:Molecule type: protein

A:Residues: 1-7 <MON>

C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

C:Keywords: amidated carboxyl end; D-amino acid; hydroxyproline; neuropeptide; skin

F:2/Modified site: D-alanine (Ala) #status experimental

F:6/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental

F:7/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 29.2%; Score 14; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 YP 7
DB 5 YP 6

RESULT 9
S36662
dermorphin (Lys-7) [validated] - two-colored leaf frog
C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 18-Aug-2000
C;Accession: S36662
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
FEBS Lett. 302, 151-154, 1992
A;Title: Identification and characterization of two dermorphins from skin extracts of the
A;Reference number: S21152; MUID:92339502; PMID:1633846
A;Accession: S36662
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIG>
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 29.2%; Score 14; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 YP 7
DB 5 YP 6

RESULT 10
S21230
dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)
C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000
C;Accession: S21230
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
FEBS Lett. 302, 151-154, 1992
A;Title: Identification and characterization of two dermorphins from skin extracts of the
A;Reference number: S21152; MUID:92339502; PMID:1633846
A;Accession: S21230
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIG>
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 29.2%; Score 14; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 YP 7
DB 5 YP 6

RESULT 11
S42620
aggreCAN - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C;Accession: S42620
R;Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.
Matrix Biol. 14, 171-179, 1994
A;Title: AggreCAN in bovine tendon.
A;Reference number: S42620; MUID:94340214; PMID:7520336
A;Accession: S42620
A;Molecule type: protein
A;Residues: 1-7 <VOG>

A;Experimental source: flexor tendon
C;Keywords: cartilage

Query Match 29.2%; Score 14; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 YP 7
DB 1 YP 2

RESULT 12
S66646
cardioacceleratory protein 2b - tobacco hornworm
C;Species: Manduca sexta (tobacco hornworm)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66646
R;Huesmann, G.R.; Cheung, C.C.; Loi, P.K.; Lee, T.D.; Swiderek, K.M.; Tublitz, N.J.
FEBS Lett. 371, 311-314, 1995
A;Title: Amino acid sequence of CAP(2b), an insect cardioacceleratory peptide from the
A;Reference number: S66646; MUID:96013159; PMID:7556618
A;Accession: S66646
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <HUE>
A;Cross-references: UNIPROT:Q7M3N2

Query Match 29.2%; Score 14; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 QLVFYP 7
DB 1 ELYAFP 6

RESULT 13
B49712
ATP-binding protein p46 - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C;Accession: B49712
R;Nigam, S.K.; Goldberg, A.L.; Ho, S.; Rohde, M.F.; Bush, K.T.; Sherman, M.Y.
J. Biol. Chem. 269, 1744-1749, 1994
A;Title: A set of endoplasmic reticulum proteins possessing properties of molecular cha
A;Reference number: A49712; MUID:94124514; PMID:8294423
A;Accession: B49712
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <NIG>
C;Keywords: ATP; endoplasmic reticulum; molecular chaperone

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Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 YP 7
DB 5 YP 6

RESULT 14
A61620
locustamytropin III - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
C;Accession: A61620
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.
Insect Biochem. Mol. Biol. 22, 447-452, 1992
A;Title: Isolation, identification and synthesis of locustamytropin III and IV, two ad
A;Reference number: A61620
A;Accession: A61620

Tue Apr 19 06:15:07 2005

A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <SCH>
A:Cross-references: UNIPROT:P41489
C:Keywords: amidated carboxyl end; neuropeptide
F:9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 29.2%; Score 14; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 EYPF 8
: ||
Db 2 QOPF 5

RESULT 15

JS0319
subesophageal ganglion pentapeptide - house cricket
C:Species: Acheta domesticus (house cricket)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: JS0319
R:Wicker, C.; Wicker, C.
Comp. Biochem. Physiol. C 88, 185-187, 1987
A:Title: Isolation and structure of a peptide isolated from the subesophageal ganglion
A:Reference number: JS0319
A:Accession: JS0319
A:Molecule type: protein
A:Residues: 1-5 <WIC>
A:Cross-references: UNIPROT:P19991

Query Match 27.1%; Score 13; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PF 8
: ||
Db 4 PF 5

Search completed: April 18, 2005, 15:21:13
Job time : 52 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:02:28 ; Search time 180 Seconds
(without alignments)
25.604 Million cell updates/sec

Title: US-09-674-716B-7
Perfect score: 48
Sequence: 1 QQLVEYPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1455

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	17	35.4	8	2 Q49534	Q49534 mycoplasma
3	17	35.4	9	2 Q8WFT4	Q8wft4 diadema ant
4	16	33.3	8	2 Q9MSX1	Q9msx1 jurinea hum
5	16	33.3	8	2 Q8J3J5	Q8jj35 ficedula hy
6	16	33.3	9	2 Q9TRU7	Q9tru7 bos taurus
7	15	31.2	8	1 ANG2 BOTJA	Q10582 bothrops ja
8	15	31.2	8	1 UPAA HUMAN	F30096 homo sapien
9	15	31.2	8	2 Q15898	Q15898 homo sapien
10	15	31.2	8	2 Q70KG9	Q70kg9 sus scrofa
11	15	31.2	8	2 Q70Y88	Q70y88 platostoma
12	15	31.2	8	2 Q6LQD5	Q6ldq5 rhodobacter
13	15	31.2	8	2 Q7T282	Q7t282 geochelone
14	15	31.2	9	1 FLA2 TREHY	P80159 treponema h
15	15	31.2	9	2 Q14277	Q14277 homo sapien
16	15	31.2	9	2 Q96T78	Q96t78 homo sapien
17	15	31.2	9	2 Q65711	Q65711 berne virus
18	15	31.2	9	2 Q7SX77	Q7sx77 geochelone
19	14	29.2	8	1 AL17 CARMA	P81820 carcinus ma
20	14	29.2	8	2 P82858	P82858 puccinia re
21	14	29.2	8	2 Q6BCZ9	Q6bcz9 homo sapien
22	14	29.2	8	2 Q7M3N2	Q7m3n2 manduca sex
23	14	29.2	8	2 Q95213	Q95213 cryptotagus
24	14	29.2	8	2 Q6EX61	Q6ex61 isodon hisp
25	14	29.2	8	2 Q8GTG5	Q8gtg5 lycopersico
26	14	29.2	8	2 Q934S4	Q934s4 thiobacillu
27	14	29.2	8	2 Q98YK9	Q98yk9 human immun
28	14	29.2	9	1 AL11 CARMA	P81814 carcinus ma
29	14	29.2	9	1 LMT3 LOCM1	P41489 locusta mig
30	14	29.2	9	1 UP43 HUMAN	F30089 homo sapien
31	14	29.2	9	1 UP47 HUMAN	F30093 homo sapien

32 14 29.2 9 2 Q9UC36 Q9uc36 homo sapien
33 14 29.2 9 2 Q7RSP2 Q7rsp2 plasmodium
34 14 29.2 9 2 Q78337 Q78337 caloglossa
35 14 29.2 9 2 Q81964 Q81964 caloglossa
36 14 29.2 9 2 Q81966 Q81966 caloglossa
37 14 29.2 9 2 Q81968 Q81968 caloglossa
38 14 29.2 9 2 Q8HSL0 Q8hsl0 murrayella
39 14 29.2 9 2 Q8HSL5 Q8hsl5 spyridia fi
40 14 29.2 9 2 Q8MDU2 Q8mdu2 hypnea sp.
41 14 29.2 9 2 Q8ME56 Q8me56 porphyra mi
42 14 29.2 9 2 Q8ME58 Q8me58 porphyra li
43 14 29.2 9 2 Q8W7T9 Q8wt9 bostrychia
44 14 29.2 9 2 Q76FS7 Q76fs7 hypnea japo
45 14 29.2 9 2 Q76FU1 Q76fu1 plocamium t

ALIGNMENTS

RESULT 1

Q7M2N8 PRELIMINARY; PRT; 9 AA.
AC Q7M2N8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Alpha-2-macroglobulin isoform 1 (Fragment).
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9915;
RN [1]
RP SEQUENCE
RX MEDLINE=96032553; PubMed=7556651; DOI=10.1016/0014-5793(95)00960-H;
RA Doimer K., Jenner L.B., Jacobsen L., Andersen G.R., Koch T.J.,
RA Thirup S., Sottrup-Jensen L., Nyborg J.;
RT "Crystallisation and preliminary X-ray analysis of the receptor-
binding domain of human and bovine alpha(2)-macroglobulin.";
RL FEBS Lett. 372:93-95(1995).
DR PIR; S66635; S66635.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 1095 MW; 87B02DD9D769CB1A CRC64;

Query Match 43.8%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred.No. 1.6e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 1;

QY 5 EYPF 8
DB 3 EYPF 6

RESULT 2

Q49534 PRELIMINARY; PRT; 8 AA.
AC Q49534;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE P120 (Fragment).
GN Name=p120;
OS Mycoplasma hominis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2098;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V2785;
RA Nyvold C., Birkelund S., Christiansen G.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U22025; AAA67455.1; -.
FT NON_TER 1 1

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SQ SEQUENCE 8 AA; 869 MW; 914457605B02C05D CRC64;
Query Match 35.4%; Score 17; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Gaps 0;

QY 3 LVEYYP 7
Db 2 IVEIIP 6

RESULT 3
ID Q8WFT4 PRELIMINARY; PRT; 9 AA.
AC Q8WFT4;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN Name=COII;
OS Diadema antillarum.
OS Diadema antillarum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Echinoidea; Diademataceae; Diadematoidea; Diadematiidae;
OC Diadema.
OC NCBI_TaxID=105358;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RT phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21561594; PubMed=11703875; DOI=10.1098/rspb.2001.1806;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
RT Caribbean reefs.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
DR EMBL; AY012858; AAL33832.2;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1115 MW; EDF8DB1B173B46CA CRC64;

Query Match 35.4%; Score 17; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QOLVEYP 7
Db 3 QYLEEQP 9

RESULT 4
Q9MSX1 PRELIMINARY; PRT; 8 AA.
AC Q9MSX1;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE pBa (Fragment).
GN Name=pBa;
OS Jurinea humilis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Asterales; Asteraceae; Carduoideae; Cardueae; Jurinea.
OX NCBI_TaxID=41594;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Hanlon P.C., Briese D.T.;

Submitted (FEB-1999) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF129846; AAF78138.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 788 MW; 457451B5A76DDB10 CRC64;

Query Match 33.3%; Score 16; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VEYPT 9
Db 1 IEAPT 6

RESULT 5
ID Q8JJ35 PRELIMINARY; PRT; 8 AA.
AC Q8JJ35;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE ATP-citrate lyase (Fragment).
GN Name=ACL;
OS Ficedula hypoleuca.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=46689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21918460; PubMed=11918793;
RA Primmer C.R., Borge T., Lindell J., Saetre G.P.;
RT "Single-nucleotide polymorphism characterization in species with
RT limited available sequence information: high nucleotide diversity
RT revealed in the avian genome.";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454211; AAM22897.1; -.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Lyase.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 981 MW; 98C77B544681AB02 CRC64;

Query Match 33.3%; Score 16; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QIVEYP 7
Db 2 ETMYYP 7

RESULT 6
Q9TRU7 PRELIMINARY; PRT; 9 AA.
AC Q9TRU7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE GAP-3, GTPase-activating protein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92112868; PubMed=1309786;
RA Nice E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,
RA Burgess A.W.;
RT "The purification of a Rap1 GTPase-activating protein from bovine
RT brain cytosol.";

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RL J. Biol. Chem. 267:1546-1553 (1992).
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1063 MW; 89EDA77B47604B5A CRC64;

Query Match 33.3%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VEYP 7
:
Db 4 IYYP 7

RESULT 7
ANG2_BOTJA STANDARD; PRT; 8 AA.
AC Q10532;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
NCBI_TaxID=8724;
RN [1]
RP SEQUENCE
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801; DOI=10.1016/0305-0491(95)02072-1;
RA Borgehesi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca."
RL Comp Biochem. Physiol. 113B:467-473 (1996).
CC -!- SIMILARITY: Belongs to the serpin family.
DR InterPro; IPR00215; Prot inh serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Direct protein sequencing; Plasma; Serpin; Vasoconstrictor.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 31.2%; Score 15; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 YPF 8
:
Db 6 HPF 8

RESULT 8
UPAA_HUMAN STANDARD; PRT; 8 AA.
ID UPAA_HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=9302937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714 (1992).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown

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CC protein is: 7, its MW is: 12 kDa.
DR SWISS-2DPAGE; P30096; HUMAN.
KW Direct protein sequencing.
FT NON_TER 1 1
FT NON_TER 5 5
FT VARIANT 5 5
FT NON_TER 8 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVEYP 7
:
Db 3 LTFYP 7

RESULT 9
Q15898 PRELIMINARY; PRT; 8 AA.
AC Q15898;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Homo sapiens (clone XP6A11B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coobauhn M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries."
RL Hum. Mol. Genet. 0:0-0 (1995).
DR EMBL; L32078; AAA73888.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 938 MW; 34A415B0477B45BB CRC64;

Query Match 31.2%; Score 15; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 YPFT 9
:
Db 3 YPIS 6

RESULT 10
Q70KG9 PRELIMINARY; PRT; 8 AA.
AC Q70KG9;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Putative lysosomal glucocerebrosidase (EC 3.2.1.45) (Fragment).
GN Name=GBA;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Stratil A., Wagenknecht D., Van Poucke M., Kubickova S.,
RA Bartschlag H., Musilova P., Rubes J., Geldermann H., Feelman L.J.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ575652; CAE06500.1; -.
DR EMBL; AJ575653; CAE06501.1; -.

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DR EMBL; AJ575654; CAE06502.1; --
 DR EMBL; AJ575651; CAE06499.1; --
 DR GO; GO:0004348; F:glucosylceramidase activity; IEA.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 KW Glycosidase; Hydrolase.
 FT NON_TER 1 1
 FT CHAIN <1 8
 FT NON_TER 8 8
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 1019 MW; 5FD40050545B5B10 CRC64;
 Query Match 31.2%; Score 15; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VEY 6
 Db :|||
 1 IEY 3
 RESULT 11
 Q70Y88 PRELIMINARY; PRT; 8 AA.
 AC Q70Y88;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Ribosomal protein (Fragment).
 GN Name=rp16;
 OS Placostoma fimbriatum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Placostoma.
 OX NCBI_TaxID=204168;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
 RA Paton A., Springate D.A., Sudde S., Ormeno D., Grayer R., Harley M.M.,
 RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
 RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
 based on three plastid DNA regions."
 RL Mol. Phylogenet. Evol. 31:277-299(2004).
 DR EMBL; AJ505368; CAD45489.1; --
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON_TER 1 1
 FT NON_TER 8 8
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 789 MW; 86786772D1BB4772 CRC64;
 Query Match 31.2%; Score 15; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 7 PFT 9
 Db :|||
 2 PYT 4
 RESULT 12
 Q6LDO5 PRELIMINARY; PRT; 8 AA.
 AC Q6LDO5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Nitrogen fixation protein (nifH) (Fragment).
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
 OC Rhodobacteraceae; Rhodobacter.
 OX NCBI_TaxID=1061;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=89213944; PubMed=2708314;
 RA Moreno-Vivian C., Hennecke S., Puehler A., Klipp W.;
 RT "Open reading frame 5 (ORF5), encoding a ferredoxinlike protein, and
 RT nifH are cotranscribed with nifE, nifN, nifX, and ORF4 in Rhodobacter
 RT capsulatus."
 RL J. Bacteriol. 171:2591-2598(1989).
 DR EMBL; M26323; AAA26145.1; --
 DR NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 890 MW; 2CC40DDDD80769CB CRC64;
 Query Match 31.2%; Score 15; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 5 EYP 7
 Db :|||
 1 EFP 3
 RESULT 13
 Q7T282 PRELIMINARY; PRT; 8 AA.
 AC Q7T282;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Calmodulin (Fragment).
 OS Geochelone nigra (Galapagos giant tortoise).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Testudinidae; Testudinidae; Geochelone.
 OX NCBI_TaxID=66189;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15062813; DOI=10.1016/j.ympev.2004.02.004;
 RA Caccione A., Gentile G., Burns C., Sezzi E., Bergman W., Ruelle M.,
 RA Saltonstall K., Powell J.R.;
 RT "Extreme difference in rate of mitochondrial and nuclear evolution in
 RT a large ectotherm, Galapagos tortoises."
 RL Mol. Phylogenet. Evol. 31:794-798(2004).
 DR EMBL; AY101722; AAM47127.1; --
 FT NON_TER 1 1
 FT NON_TER 8 8
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 892 MW; 5D0769CAA041A874 CRC64;
 Query Match 31.2%; Score 15; DB 2; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VEYP 7
 Db :|||
 4 IDFP 7
 RESULT 14
 FLA2 TREHY STANDARD; PRT; 9 AA.
 ID FLA2 TREHY
 AC P80159;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Flagellar filament outer layer protein flaA2 (35 kDa sheath protein)
 DE (Fragment).
 GN Name=flaA2;
 OS Treponema hyodysenteriae (Serpulina hyodysenteriae).
 OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspirae.
 OX NCBI_TaxID=159;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=C5;
 RX MEDLINE=93139764; PubMed=1487733;
 RA Koopman M.B.H., Baats E., van Vorstenbosch C.J.A.H.V.,
 RA van der Zeijst B.A.M., Kusters J.G.;
 RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are

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RT composed of two sheath proteins and three core proteins.";
RL J. Gen. Microbiol. 138:2697-2706(1992).
CC -|- FUNCTION: Component of the outer layer of the flagella.
CC -|- SUBUNIT: The flagellum consists of an outer layer composed of two
CC sheath proteins, flaA1 (44 kDa) and flaA2 (35 kDa) around a core
CC that contains three proteins flaB1 (37 kDa), flaB2 (34 kDa) and
CC flaB3 (32 kDa).
CC -|- SUBCELLULAR LOCATION: Periplasmic flagellum.
KW Direct protein sequencing; Flagellum; Periplasmic.
FT UNSURE 2 2
FT UNSURE 8 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QLVVEYPF 8
Db 1 ETVPYMF 7

RESULT 15
Q14277 PRELIMINARY; PRT; 9 AA.
AC Q14277;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RET protein short form (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94071887; PubMed=7902707;
RA Ceccherini I., Bocciardi R., Luo Y., Pasini B., Hofstra R.,
RA Takahashi M., Romeo G.;
RT "Exon structure and flanking intronic sequences of the human RET
RT proto-oncogene.";
RL Biochem. Biophys. Res. Commun. 196:1288-1295(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94366753; PubMed=8084609;
RA Ceccherini I., Hofstra R., Yin L., Stulp R., Barone V., Stelwagen T.,
RA Bocciardi R., Nijveen H., Bolino A., Seri M., Ronchetto P., Pasini B.,
RA Bozzano M., Buys C., Romeo G.;
RT "DNA polymorphisms and conditions for SSCP analysis of the 20 exons of
RT the ret proto-oncogene.";
RL Oncogene 9:3025-3029(1994).
DR EMBL; U11532; AAC50102.1; -.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 1134 MW; 034E11A9CDD1F5B0 CRC64;

Query Match 31.2%; Score 15; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 VEYPT 9
Db 2 ISHAFT 7

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Search completed: April 18, 2005, 15:19:26
 Job time : 182 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:01:43 ; Search time 172 Seconds
(without alignments)
20.237 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QQLVEYFPFT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 330156

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	3 AAY32256	Aay32256 Light cha
2	44	91.7	9	2 AAW39823	Aaw39823 Light cha
3	36	75.0	9	2 AAW39817	Aaw39817 Light cha
4	35	75.0	9	8 ADR38732	Adr38732 Mouse lig
5	34	70.8	9	3 AAY92171	Aay92171 Murine l3
6	33	68.8	9	2 AAR30450	Aar30450 C242:11 M
7	33	68.8	9	8 ADO43568	Ado43568 Complemen
8	33	68.8	9	8 ADO43562	Ado43562 Complemen
9	31	64.6	9	3 AAY97234	Aay97234 Complemen
10	31	64.6	9	4 AAB82708	Aab82708 VEGF anta
11	31	64.6	9	4 AAE13142	Aae13142 Humanised
12	31	64.6	9	4 AAB82896	Aab82896 Anti-huma
13	31	64.6	9	4 AAG63993	Aag63993 Complemen
14	31	64.6	9	5 AAE25954	Aae25954 Mouse ant
15	31	64.6	9	5 AAU74411	Aau74411 Light cha
16	31	64.6	9	6 ABJ26723	Abj26723 VEGF bind
17	31	64.6	9	8 ADR18200	Adr18200 Mouse VEG
18	31	64.6	9	8 ADR03426	Adr03426 Humanised
19	30	62.5	9	2 AAW39820	Aaw39820 Light cha
20	30	62.5	9	2 AAW39826	Aaw39826 Light cha
21	30	62.5	9	2 AAW59175	Aaw59175 Mouse PAP
22	30	62.5	9	7 ABO33877	Abo33877 Anti-GPI-
23	30	62.5	9	8 ADR03425	Adr03425 Humanised
24	30	62.5	9	8 ADR38731	Adr38731 Mouse lig
25	28	58.3	9	2 AAW24776	Aaw24776 Human imm

26	28	58.3	9	2 AAW73171	Aaw73171 CDR3 of 1
27	28	58.3	9	2 AAW62016	Aaw62016 Light cha
28	28	58.3	9	2 AAW80146	Aaw80146 Light cha
29	28	58.3	9	2 AAY28392	Aay28392 Peptide f
30	28	58.3	9	2 AAY40428	Aay40428 Amino aci
31	28	58.3	9	3 AAY82342	Aay82342 Humanised
32	28	58.3	9	4 AAB83165	Aab83165 Mouse gan
33	28	58.3	9	8 ADG39003	Adg39003 Humanised
34	28	58.3	9	8 ADO36522	Ado36522 Human ant
35	28	58.3	9	8 ADO36516	Ado36516 Human ant
36	28	58.3	9	8 ADO36534	Ado36534 Human ant
37	28	58.3	9	8 ADR03423	Adr03423 Humanised
38	27	56.2	8	2 AAR35879	Aar35879 Hepatitis
39	27	56.2	8	2 AAR35878	Aar35878 Hepatitis
40	27	56.2	8	2 AAR35880	Aar35880 Hepatitis
41	27	56.2	8	6 ADA90363	Ada90363 MS-Roche
42	27	56.2	8	6 ADA89991	Ada89991 Anti-Abet
43	27	56.2	9	2 AAW23435	Aaw23435 CDR-3 of
44	27	56.2	9	2 AAW39877	Aaw39877 Light cha
45	27	56.2	9	2 AAW89158	Aaw89158 Anti-p53

ALIGNMENTS

RESULT 1

AAV32256

ID AAY32256 standard; peptide; 9 AA.

XX AAY32256;

XX

DT 15-FEB-2000 (first entry)

XX

DE Light chain CDR L3 of mouse anti-CD23 MAb C11.

XX

KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
therapy.

XX Mus musculus.

OS

XX WO9558679-A1.

PD 18-NOV-1999.

XX

PF 07-MAY-1999; 99WO-GB001434.

XX

PR 09-MAY-1998; 98GB-00009839.

XX (GLAX) GLAXO GROUP LTD.

PA

PI Bonney JUMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WPI; 2000-053101/04.

DR N-PSDB; AA234741.

XX

DR Cell receptor specific antibodies useful for treating e.g. arthritis,

XX diabetes, multiple sclerosis and psoriasis.

PT

XX Claim 1; Page 40; 81pp; English.

XX

CC This sequence represents complementarity determining region 3 (CDR L3)

XX of the light chain of murine anti-CD23 (FCERII) monoclonal antibody C11

CC (see also AAY32262). The invention provides altered antibodies, such as

XX chimeric or humanised antibodies, which comprise sufficient of the amino

CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on
CC haematopoietic cells. The antibodies are used to block soluble CD23
CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's
CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,
CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,
CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute
CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,
CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes
CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They
CC are also useful for studying interactions between CD23 and various
CC ligands and determining the binding agents

XX SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9
| | | | |
Db 1 QQLVEYPPT 9

RESULT 2
AAW39823
ID AAW39823 standard; peptide; 9 AA.

XX AC AAW39823;

XX DT 16-JUN-1998 (first entry)

XX DE Light chain CDR3 of catalytic antibody 2A10.

XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
XX KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX KW overdose; addiction.

XX OS Mus sp.

XX PN WO9749800-A1.

XX PD 31-DEC-1997.

XX PF 25-JUN-1997; 97WO-US010965.

XX PR 25-JUN-1996; 96US-00672345.

XX PA (UYCO) UNIV COLUMBIA NEW YORK.

XX PI Landry DW;

XX PS WPI; 1998-077166/07.

XX PT New catalytic antibodies able to decompose cocaine, single-chain
XX PT analogues - used to treat cocaine overdose and addiction, required in far
XX PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX PS Claim 15; Page 82; 147pp; English.

XX CC AAW39821-23 represent the sequences of the light chain complementarity
XX CC determining regions (CDRs) of the catalytic antibody 2A10, which is able
XX CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
XX CC were prepared and used to immunise mice for production of hybridomas.
XX CC Catalytic antibodies were identified by their capacity to release 3H-
XX CC benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was identified
XX CC using TSA1, which is an immunogenic conjugate of a phosphate monoester
XX CC transition state analogue. Antibody 2A10 has a per minute Kcat of 0.011.
XX CC The antibodies reduce the concentration of cocaine in a subject, and are
XX CC used particularly for the treatment of an overdose. They are also used
XX CC for treating addiction (by reducing the in vivo concentration that can be
XX CC achieved)

XX SQ Sequence 9 AA;

Query Match 91.7%; Score 44; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9
| | | | |
Db 1 QQFVEYPPT 9

RESULT 3

AAW39817
ID AAW39817 standard; peptide; 9 AA.

XX AC AAW39817;

XX DT 16-JUN-1998 (first entry)

XX DE Light chain CDR3 of catalytic antibody 3B9.

XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
XX KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX KW overdose; addiction.

XX OS Mus sp.

XX PN WO9749800-A1.

XX PD 31-DEC-1997.

XX PF 25-JUN-1997; 97WO-US010965.

XX PR 25-JUN-1996; 96US-00672345.

XX PA (UYCO) UNIV COLUMBIA NEW YORK.

XX PI Landry DW;

XX PS WPI; 1998-077166/07.

XX PT New catalytic antibodies able to decompose cocaine, single-chain
XX PT analogues - used to treat cocaine overdose and addiction, required in far
XX PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX PS Claim 11; Page 81; 147pp; English.

XX CC AAW39815-17 represent the sequences of the light chain complementarity
XX CC determining regions (CDRs) of the catalytic antibody 3B9, which is able
XX CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
XX CC were prepared and used to immunise mice for production of hybridomas.
XX CC Catalytic antibodies were identified by their capacity to release 3H-
XX CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was identified
XX CC using TSA1, which is an immunogenic conjugate of a phosphate monoester
XX CC transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11.
XX CC The antibodies reduce the concentration of cocaine in a subject, and are
XX CC used particularly for the treatment of an overdose. They are also used
XX CC for treating addiction (by reducing the in vivo concentration that can be
XX CC achieved)

XX SQ Sequence 9 AA;

Query Match 75.0%; Score 36; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9
| | | | |
Db 1 QQFVEYPPT 9

CC molecules of the invention useful in preparing a composition for
 CC diagnosing or treating cancer, especially oesophageal, ovarian and
 CC stomach cancers.

XX Sequence 9 AA;

Query Match 58.8%; Score 33; DB 8; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPPT 9

DB 2 QHLEYPTT 9

RESULT 9

AAAY97234

ID AAY97234 standard; protein; 9 AA.

XX

AC AAY97234;

XX

DT 19-DEC-2000 (first entry)

DE Complementary determining region (CDRL3) of anti-SI (KDR) antibody.

XX Immunoglobulin; antibody; complementary determining region; CDR; VEGF;
 KW vascular endothelial growth factor; KDR;
 KW kinase insert domain containing receptor; multivalent; monovalent;
 KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
 KW glioblastoma multiforme; hemangioblastoma; AIDS;
 KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;
 KW acquired immune deficiency syndrome; AIDS; human.

XX Homo sapiens.

OS Synthetic.

OS

XX WO200044777-A1.

XX

PD 03-AUG-2000.

XX

PF 28-JAN-2000; 2000WO-US002180.

XX

XX 29-JAN-1999; 99US-00240736.

PR

PR 29-JAN-1999; 99US-0117726P.

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XX (IMCL-) IMCLONE SYSTEMS INC.

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Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

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Query Match 64.6%; Score 31; DB 3; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.8e+06;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9

DB 1 QQRSSYPPT 9

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CC The present sequence is that of complementarity determining region 3 of
 CC the light chain variable region (see also AAB82702) of IMC-1C11, a mouse-
 CC human chimeric antibody that has vascular endothelial growth factor
 CC (VEGF) antagonist activity. The antibody, or a fragment of it, can be
 CC used as an anti-angiogenic molecule, together with a chemotherapeutic
 CC acid, for the treatment of an angiogenic dependent condition in a mammal,
 CC especially a human. The invention relates generally to a method of
 CC treating or controlling an angiogenic dependent condition by
 CC administering an anti-angiogenic molecule and a chemotherapeutic agent,
 CC to produce a regression or arrest of the condition while minimising or
 CC preventing significant toxicity of the chemotherapeutic agent. The anti-
 CC angiogenic molecule inhibits or blocks the action of a vascular
 CC endothelium survival factor such as VEGF or its receptor, and is
 CC especially IMC-1C11. Conditions that can be treated include a neoplasm, a
 CC collagen-vascular disease or an autoimmune disease, especially a solid
 CC tumour, including breast carcinoma, lung carcinoma, prostate carcinoma,
 CC colon carcinoma, prostate carcinoma, ovarian carcinoma, neuroblastoma,

CC central nervous system tumour, neuroblastoma, glioblastoma multiforme or
 CC melanoma (all claimed). (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 9 AA;

Query Match 64.6%; Score 31; DB 4; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 |||||
 DB 1 QQRSSYPFT 9

RESULT 11
 AAEL13142
 ID AAEL13142 standard; peptide; 9 AA.

XX
 AC AAEL13142;

XX 28-JAN-2002 (first entry)

XX Humanised antibody murine light chain hypervariable region (VL) CDR3.

XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
 KW cytosolic; light chain hypervariable region; VL; myelocytic leukaemia;
 KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;
 KW Hodgkin's disease; complementarity determining region-3; CDR-3; mouse.

XX Mus sp.

XX WO200174296-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US010504.

XX 31-MAR-2000; 2000US-00540770.

XX (IMCL-) IMCLONE SYSTEMS INC.
 PA (CORR) CORNELL RES FOUND INC.

XX Witte L, Rafil S;

XX WPI; 2001-662942/76.

XX N-PSDB; AAD21668.

PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
 PT tumors such as leukemias or multiple myeloma comprises treatment with an
 PT antagonist of a vascular endothelial growth factor receptor.

XX Claim 8; Page 15; 68pp; English.

CC The invention relates to a method for inhibiting the growth of non-solid
 CC tumour cells that are stimulated by a ligand of vascular endothelial
 CC growth factor receptor (VEGFR) in mammals particularly humans. The method
 CC involves treating the mammals with humanised VEGFR monoclonal antibodies
 CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
 CC variable region joined to human constant region, where the humanised
 CC mouse variable region contains mouse complementarity determining region
 CC (CDR) grafted into human variable region. The method is useful for
 CC treating leukaemias such as acute or chronic myelocytic leukaemia, acute
 CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
 CC multiple myelomas and lymphoid cells, particularly those related to non-
 CC Hodgkin's and Hodgkin's disease. The present sequence is humanised
 CC antibody murine light chain hypervariable region (VL) CDR-3 used in the
 CC exemplification of the invention

XX Sequence 9 AA;

Query Match 64.6%; Score 31; DB 4; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 |||||
 DB 1 QQRSSYPFT 9

RESULT 12

AAE82896

ID AAE82896 standard; peptide; 9 AA.

XX AAE82896;

XX 26-NOV-2001 (first entry)

XX Anti-human CD154 antibody ABI793 light chain variable region CDR3.

XX CD154; gp39; CD40-L; antibody; ABI793; transplant rejection;
 KW autoimmune disease; inflammation; atherosclerosis; Alzheimer's disease;
 KW antiinflammatory; antiarteriosclerotic; immunosuppressive; therapy;
 KW complementarity determining region; CDR3.

XX Mus musculus.

XX WO200168860-A1.

XX 20-SEP-2001.

XX 14-MAR-2001; 2001WO-EP002875.

XX 16-MAR-2000; 2000GB-00006398.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERINDUNGEN VERW GES MBH.

XX Di Padova FE, Schuler W;

XX WPI; 2001-590062/66.

XX CD154 binding molecule, in particular antibody to human CD154 for use in
 XX treatment, prevention of autoimmune, inflammatory diseases,
 XX atherosclerosis, Alzheimer's disease and prevention of transplant
 XX rejection.

XX Claim 2; Page 23; 37pp; English.

XX The present sequence is that of complementarity determining region 3
 XX (CDR3) of the light chain variable region (VL; see also AAE82896) of
 XX mouse anti-human CD154 monoclonal antibody ABI793. The invention provides
 XX a CD154 binding molecule, in particular an antibody to human CD154, in
 XX which the VH region has the CDR1, CDR2 and CDR3 of ABI793 VH and the VL
 XX region has the CDR1, CDR2 and CDR3 of ABI793 VL. The CD154 binding
 XX molecule is especially a human antibody in which the VH and VL domains
 XX are essentially those of ABI793, with constant regions from human heavy
 XX and light chains. The antibodies are used to inhibit an immune response
 XX mediated by CD154-positive cell interactions with CD40-positive cells, in
 XX the treatment and/or prevention of diseases, disorders or conditions
 XX where CD154 modulation and/or interference with or inhibition of the
 XX CD154:CD40 interactions is therapeutically beneficial, prevention of
 XX macrophage-associated inflammatory processes and in the treatment of
 XX diseases where suppression of antibody responses to antigens is desirable
 XX (claimed). The CD154 binding molecules are useful for prevention of cell,
 XX tissue or organ graft rejection, in the prevention and treatment of
 XX autoimmune or inflammatory diseases, atherosclerosis or Alzheimer's
 XX disease, and also for inhibiting B cell proliferation and
 XX differentiation, T cell responses, induction or modulation of T or B cell
 XX tolerance or inhibition of the growth of tumour cells expressing CD154
 XX antigen. Such conditions include autoimmune and non-autoimmune disorders,
 XX in particular, Addison's disease, Celiac sprue, glomerulonephritis,
 XX Grave's disease, Hashimoto's thyroiditis, haemolytic disease of the
 XX newborn, keratitis, multiple sclerosis, polymyositis, psoriasis,
 XX rheumatic fever, rheumatoid arthritis, sarcoidosis, syphilis,
 XX tuberculosis, ulcerative colitis, HIV infection, leukaemia or lymphoma

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SQ Sequence 9 AA;
Query Match 64.6%; Score 31; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
DB 1 QQYNSVPPT 9

RESULT 13
AAG63993
ID AAG63993 standard; peptide; 9 AA.
XX
AC AAG63993;
XX
DT 26-NOV-2001 (first entry)
XX
DE Complementarity determining region of light chain of antibody 2C4.
XX
KW Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;
KW allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;
KW leukemia; eosinophil.
XX
OS Mus sp.
XX
PN WO200166126-A1.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-US007193.
XX
PR 07-MAR-2000; 2000US-0187595P.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Abrahamson JA, Bochner B, Erickson-Miller CL, Kikly KK;
PI Schleimer R;
XX
XX WPI; 2001-570749/64.
XX
XX Novel monoclonal antibody specific for human sialoadhesin factor-2 for
PT diagnosis, prevention, treatment of allergy, asthma, eczema or diseases
PT such as lymphoma, leukemia or systemic mastocytosis, in a mammal.
XX
PS Claim 10; Page 34; 35pp; English.
XX
XX AAG63991-93 represent the complementarity determining regions (CDRs) of
CC the light chain variable region of murine monoclonal antibody 2C4. This
CC antibody binds to human sialoadhesin factor-2 (SAF-2). The antibody is
CC useful for treating or preventing allergic rhinitis, allergies, asthma,
CC anemia, eczema or diseases such as lymphoma, leukemia or systemic
CC mastocytosis in a mammal. It is also useful for detecting the presence of
CC a cell, especially eosinophil in a sample, by detecting binding of the
CC antibody to SAF-2. The antibody can be coupled to toxins,
CC antiproliferative drugs or radionuclides to kill cells in areas of
CC excessive SAF-2 expression
XX
XX Sequence 9 AA;
Query Match 64.6%; Score 31; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
DB 1 QQRSSVPPT 9

RESULT 14
AAG63993
ID AAG63993 standard; peptide; 9 AA.
XX
AC AAG63993;
XX
DT 26-NOV-2001 (first entry)
XX
DE Complementarity determining region of light chain of antibody 2C4.
XX
KW Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;
KW allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;
KW leukemia; eosinophil.
XX
OS Mus sp.
XX
PN WO200166126-A1.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-US007193.
XX
PR 07-MAR-2000; 2000US-0187595P.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Abrahamson JA, Bochner B, Erickson-Miller CL, Kikly KK;
PI Schleimer R;
XX
XX WPI; 2001-570749/64.
XX
XX Novel monoclonal antibody specific for human sialoadhesin factor-2 for
PT diagnosis, prevention, treatment of allergy, asthma, eczema or diseases
PT such as lymphoma, leukemia or systemic mastocytosis, in a mammal.
XX
PS Claim 10; Page 34; 35pp; English.
XX
XX AAG63991-93 represent the complementarity determining regions (CDRs) of
CC the light chain variable region of murine monoclonal antibody 2C4. This
CC antibody binds to human sialoadhesin factor-2 (SAF-2). The antibody is
CC useful for treating or preventing allergic rhinitis, allergies, asthma,
CC anemia, eczema or diseases such as lymphoma, leukemia or systemic
CC mastocytosis in a mammal. It is also useful for detecting the presence of
CC a cell, especially eosinophil in a sample, by detecting binding of the
CC antibody to SAF-2. The antibody can be coupled to toxins,
CC antiproliferative drugs or radionuclides to kill cells in areas of
CC excessive SAF-2 expression
XX
XX Sequence 9 AA;
Query Match 64.6%; Score 31; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
DB 1 QQRSSVPPT 9

RESULT 15
AAU74411
ID AAU74411 standard; peptide; 9 AA.
XX
AC AAU74411;
XX
DT 26-MAR-2002 (first entry)
XX
DE Light chain complementarity determining region L3 (CDRL3).
XX
KW Complementarity determining region; CDR; CDRL3; antigen; cytostatic;
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
KW antibody light chain variable domain.
XX

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AAE25954
ID AAE25954 standard; peptide; 9 AA.
XX
AC AAE25954;
XX
DT 15-NOV-2002 (first entry)
XX
DE Mouse anti-KDR p1C11 scFv antibody CDRL3 peptide.
XX
KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;
KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;
KW VEGF; tumour growth; light chain complementarity determining region 3;
KW CDRL3; angiogenesis; p1C11; scFv antibody.
XX
OS Mus musculus.
XX
PN US2002064528-A1.
XX
PD 30-MAY-2002.
XX
PF 12-OCT-2001; 2001US-00976787.
XX
PR 28-JAN-2000; 2000US-00493539.
XX
PA (ZHUZ/) ZHU Z.
PA (WITT/) WITTE L.
XX
XX Zhu Z, Witte L;
XX
XX WPI; 2002-589175/63.
XX
XX N-PSDB; AAD42819.
XX
XX Novel immunoglobulin molecule for reducing tumor growth, binds to kinase
PT insert domain-containing receptor with an affinity comparable to human
PT vascular endothelial growth factor, and neutralizes activation of KDR.
XX
XX Claim 3; Page 11; 34pp; English.
XX
XX The present invention relates to novel immunoglobulin molecules that bind
CC to kinase insert domain-containing receptor (KDR) (a human homologue of
CC mouse foetal liver kinase (Flk)-1 receptor) with an affinity comparable
CC to human vascular endothelial growth factor (VEGF) and that neutralises
CC activation of KDR. Sequences of the invention are useful for neutralising
CC the activation of KDR, for reducing tumour growth and for inhibiting
CC angiogenesis. The present sequence is mouse anti-KDR p1C11 scFv antibody
CC light chain complementarity determining region 3 (CDRL3) protein
XX
XX Sequence 9 AA;
Query Match 64.6%; Score 31; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
DB 1 QQRSSVPPT 9

RESULT 15
AAU74411
ID AAU74411 standard; peptide; 9 AA.
XX
AC AAU74411;
XX
DT 26-MAR-2002 (first entry)
XX
DE Light chain complementarity determining region L3 (CDRL3).
XX
KW Complementarity determining region; CDR; CDRL3; antigen; cytostatic;
KW angiogenesis inhibitor; vascular endothelial growth factor receptor;
KW VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
KW antibody light chain variable domain.
XX

```

Mus sp.
 XX WO200190192-A2.
 XX
 XX PD 29-NOV-2001.
 XX PF 24-MAY-2001; 2001WO-US016924.
 XX PR 24-MAY-2000; 2000US-0206749P.
 XX PA (IMCL-) IMCLONE SYSTEMS INC.
 XX
 XX PI Zhu Z;
 XX WPI; 2002-106189/14.
 XX N-PSDB; AAS20282.
 XX
 PT New bispecific immunoglobulin-like antigen-binding protein for reducing
 PT tumor growth and for inhibiting angiogenesis, comprises a complex of two
 PT polypeptides and two second polypeptides.
 XX
 PS Claim 55; Page 57; 64pp; English.
 XX
 CC The invention describes an antigen-binding protein (I) comprising a
 CC complex of two polypeptides (P1) and two second polypeptides (P2) which
 CC are stably associated in an immunoglobulin like complex. P1 has an
 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
 CC light chain constant domain (CL domain), and P2 has an antigen-binding
 CC site located to the N terminus of the CH1 domain. (I) is useful for:
 CC neutralising the activation of a vascular endothelial growth factor
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
 CC reducing endothelial cell proliferation; blocking interaction of a protein and
 CC migration of human leukaemia cells; blocking interaction of a protein and
 CC its ligand; promoting interactions between immune cells and target cells;
 CC and in vivo and in vitro for investigative, diagnostic or treatment
 CC methods. The design of (I) provides for efficient production so that
 CC substantially all of the antigen-binding proteins produced are assembled
 CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
 CC and in tetrameric form. The heavy chain constant domains which constitute
 CC the Fc region (e.g., CH2 and CH3 for an IgG molecule) of a natural
 CC antibody and which provide other antibody functions can be present. There
 CC is no requirement for processing in vitro to obtain the complete product.
 CC This peptide sequence represents the light chain variable domain
 CC complementarity determining region L3 (CDRL3) incorporated into an
 CC antigen-binding protein described in the method of the invention
 XX
 SQ Sequence 9 AA;

Query Match 64.6%; Score 31; DB 5; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEVPFT 9
 |||||
 Db 1 QQRSSVPFT 9

Search completed: April 18, 2005, 15:16:19
 Job time : 175 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:16:30 ; Search time 129 Seconds
(without alignments)
23.189 Million cell updates/sec

Title: US-09-674-716B-7
Perfect score: 48
Sequence: 1 QQLVEVPFT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370583 residues

Total number of hits satisfying chosen parameters: 138632

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	91.7	9	10	US-09-940-727B-27
2	36	75.0	9	10	US-09-940-727B-21
3	36	75.0	9	16	US-10-632-706-134
4	33	68.8	9	16	US-10-823-253-20
5	31	64.6	9	9	US-09-976-787-6
6	31	64.6	9	9	US-09-865-198-6
7	31	64.6	9	10	US-09-798-689-6
8	31	64.6	9	14	US-10-232-187-10
9	31	64.6	9	15	US-10-221-529-10
10	30	62.5	9	9	US-09-828-708-51
11	30	62.5	9	10	US-09-940-727B-24
12	30	62.5	9	10	US-09-940-727B-30
13	30	62.5	9	16	US-10-632-706-133

14	29	60.4	9	17	US-10-842-011-20	Sequence 20, Appl
15	29	60.4	9	17	US-10-842-011-37	Sequence 37, Appl
16	28	58.3	9	10	US-09-795-798-15	Sequence 15, Appl
17	28	58.3	9	14	US-10-195-752-110	Sequence 110, Appl
18	28	58.3	9	16	US-10-703-714-30	Sequence 30, Appl
19	28	58.3	9	16	US-10-703-714-36	Sequence 36, Appl
20	28	58.3	9	16	US-10-703-711-48	Sequence 48, Appl
21	28	58.3	9	17	US-10-783-311-138	Sequence 138, Appl
22	27	56.2	9	10	US-09-155-106-6	Sequence 6, Appl
23	27	56.2	9	10	US-09-940-727B-81	Sequence 81, Appl
24	27	56.2	9	13	US-10-091-236-16	Sequence 16, Appl
25	27	56.2	9	13	US-10-032-482-14	Sequence 14, Appl
26	27	56.2	9	14	US-10-091-313-6	Sequence 6, Appl
27	27	56.2	9	14	US-10-091-268-6	Sequence 6, Appl
28	27	56.2	9	14	US-10-268-501-12	Sequence 12, Appl
29	27	56.2	9	15	US-10-372-715-13	Sequence 13, Appl
30	27	56.2	9	15	US-10-608-626-12	Sequence 12, Appl
31	27	56.2	9	17	US-10-808-538-6	Sequence 6, Appl
32	26	54.2	7	14	US-10-128-581-7	Sequence 7, Appl
33	26	54.2	7	15	US-10-463-699-7	Sequence 7, Appl
34	26	54.2	7	16	US-10-776-172-34	Sequence 7, Appl
35	26	54.2	7	17	US-10-897-005-7	Sequence 7, Appl
36	26	54.2	8	14	US-10-128-581-6	Sequence 6, Appl
37	26	54.2	8	15	US-10-463-699-6	Sequence 6, Appl
38	26	54.2	8	16	US-10-776-172-6	Sequence 6, Appl
39	26	54.2	8	17	US-10-897-005-6	Sequence 6, Appl
40	26	54.2	9	9	US-09-808-037-17	Sequence 17, Appl
41	26	54.2	9	9	US-09-808-037-19	Sequence 19, Appl
42	26	54.2	9	9	US-09-293-854-7	Sequence 7, Appl
43	26	54.2	9	9	US-09-996-288-16	Sequence 16, Appl
44	26	54.2	9	10	US-09-977-797A-62	Sequence 62, Appl
45	26	54.2	9	10	US-09-977-797A-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-09-940-727B-27
; Sequence 27, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940, 727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-27

Query Match 91.7%; Score 44; DB 10; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.3e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEVPFT 9
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Db 1 QQFVEVPFT 9

RESULT 2
US-09-940-727B-21
; Sequence 21, Application US/09940727B

; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-21

Query Match 75.0%; Score 36; DB 10; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
| | | | |
DB 1 QHFDVYPPT 9

RESULT 3
US-10-632-706-134
; Sequence 134, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-8951200S
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 134
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-134

Query Match 75.0%; Score 36; DB 16; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
| | | | |
DB 1 QQLISYPLT 9

RESULT 4
US-10-823-253-20
; Sequence 20, Application US/10823253
; Publication No. US2005002934A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Jennifer
; TITLE OF INVENTION: RECOMBINANT IL-9 ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10271-112-999

; CURRENT APPLICATION NUMBER: US/10/823,253
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: 60/462,259
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/477,797
; PRIOR FILING DATE: 2003-06-10
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-823-253-20

Query Match 68.8%; Score 33; DB 16; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
| | | | |
DB 1 QQFVEYPLT 9

RESULT 5
US-09-976-787-6
; Sequence 6, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-6

Query Match 64.6%; Score 31; DB 9; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
| | | | |
DB 1 QQRSSYPPT 9

RESULT 6
US-09-865-198-6
; Sequence 6, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methods
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,749
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT

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; ORGANISM: Mouse
US-09-865-198-6

Query Match          64.6%; Score 31; DB 9; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
DB 1 QQRSSYPFT 9

RESULT 7
US-09-798-689-6
; Sequence 6, Application US/09798689
; Publication No. US20030103973A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; TITLE OF INVENTION: Combined with Radiation and Chemotherapy
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
; CURRENT APPLICATION NUMBER: US/09/798,689
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/401,163
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/967,113
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/706,804
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/476,533
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/326,552
; PRIOR FILING DATE: 1994-10-20
; PRIOR APPLICATION NUMBER: 08/196,041
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mouse
US-09-798-689-6

Query Match          64.6%; Score 31; DB 10; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
DB 1 QQRSSYPFT 9

RESULT 8
US-10-232-187-10
; Sequence 10, Application US/10232187
; Publication No. US20030092091A1
; GENERAL INFORMATION:
; APPLICANT: Abrahamson, Julie A.
; APPLICANT: Bochner, Bruce
; APPLICANT: Erickson-Miller, Connie L.
; APPLICANT: Kikly, Kristine K.
; APPLICANT: Schleimer, Robert
; APPLICANT: Nulku, Turkan E.
; TITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies
; FILE REFERENCE: GH50042-1
; CURRENT APPLICATION NUMBER: US/10/232,187
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/187,595
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: PCT/US01/07193
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/315,943
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; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/349,830
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/394,741
; PRIOR FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-187-10

Query Match          64.6%; Score 31; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
DB 1 QQRSSYPFT 9

RESULT 9
US-10-221-529-10
; Sequence 10, Application US/10221529
; Publication No. US20040038293A1
; GENERAL INFORMATION:
; APPLICANT: NOVARTIS AG
; TITLE OF INVENTION: ANTIBODIES TO HUMAN CD154
; FILE REFERENCE: 4-31266A
; CURRENT APPLICATION NUMBER: US/10/221,529
; CURRENT FILING DATE: 2003-05-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-221-529-10

Query Match          64.6%; Score 31; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
DB 1 QQVNSYPFT 9

RESULT 10
US-09-828-708-51
; Sequence 51, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Burton, D.
; APPLICANT: Ditzel, H.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-51

Query Match          62.5%; Score 30; DB 9; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 QQLVEYPFT 9
||| |||
Db 1 QQLNSYPLT 9

RESULT 11

US-09-940-727B-24
; Sequence 24, Application US/09940727B
; Publication No. US2003007793A1

GENERAL INFORMATION:

; APPLICANT: Landry, Donald W

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 0575/51400-B

; CURRENT APPLICATION NUMBER: US/09/940, 727B

; CURRENT FILING DATE: 2002-09-04

; PRIOR APPLICATION NUMBER: 09/214,095

; PRIOR FILING DATE: 1998-12-28

; PRIOR APPLICATION NUMBER: PCT/US97/10965

; PRIOR FILING DATE: 1997-06-25

; PRIOR APPLICATION NUMBER: 08/672,345

; PRIOR FILING DATE: 1996-06-25

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 24

; LENGTH: 9

; TYPE: PRT

; ORGANISM: mouse

US-09-940-727B-24

Query Match 62.5%; Score 30; DB 10; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
||| |||
Db 1 QHFEDYPT 9

RESULT 12

US-09-940-727B-30

; Sequence 30, Application US/09940727B

; Publication No. US2003007793A1

GENERAL INFORMATION:

; APPLICANT: Landry, Donald W

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 0575/51400-B

; CURRENT APPLICATION NUMBER: US/09/940, 727B

; CURRENT FILING DATE: 2002-09-04

; PRIOR APPLICATION NUMBER: 09/214,095

; PRIOR FILING DATE: 1998-12-28

; PRIOR APPLICATION NUMBER: PCT/US97/10965

; PRIOR FILING DATE: 1997-06-25

; PRIOR APPLICATION NUMBER: 08/672,345

; PRIOR FILING DATE: 1996-06-25

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 30

; LENGTH: 9

; TYPE: PRT

; ORGANISM: mouse

US-09-940-727B-30

Query Match 62.5%; Score 30; DB 10; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
||| |||
Db 1 QHFEDYPT 9

RESULT 13

US-10-632-706-133

; Sequence 133, Application US/10632706

; Publication No. US20040175385A1

GENERAL INFORMATION:

; APPLICANT: MARKS, JAMES D.

; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM

; FILE REFERENCE: 407T-895120US

; CURRENT APPLICATION NUMBER: US/10/632,706

; CURRENT FILING DATE: 2003-08-01

; PRIOR APPLICATION NUMBER: US 60/400,721

; PRIOR FILING DATE: 2002-08-01

; PRIOR APPLICATION NUMBER: US 09/144,806

; PRIOR FILING DATE: 1998-08-31

; NUMBER OF SEQ ID NOS: 278

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 133

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: single chain antibody fragment

US-10-632-706-133

Query Match 62.5%; Score 30; DB 16; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
||| |||
Db 1 QQLNSYPLT 9

RESULT 14

US-10-842-011-20

; Sequence 20, Application US/10842011

; Publication No. US20050025763A1

GENERAL INFORMATION:

; APPLICANT: Protein Design Labs

; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES

; FILE REFERENCE: 05882.0110.NPUS04

; CURRENT APPLICATION NUMBER: US/10/842,011

; CURRENT FILING DATE: 2004-05-07

; NUMBER OF SEQ ID NOS: 93

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 20

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-842-011-20

Query Match 60.4%; Score 29; DB 17; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
||| |||
Db 1 QQYSSYPPT 9

RESULT 15

US-10-842-011-37

; Sequence 37, Application US/10842011

; Publication No. US20050025763A1

GENERAL INFORMATION:

; APPLICANT: Protein Design Labs

; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES

; FILE REFERENCE: 05882.0110.NPUS04

; CURRENT APPLICATION NUMBER: US/10/842,011

; CURRENT FILING DATE: 2004-05-07

; NUMBER OF SEQ ID NOS: 93

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 37
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-842-011-37

Query Match 60.4%; Score 29; DB 17; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYDPT 9
|||
Db 1 QQYSSVEPT 9

Search completed: April 18, 2005, 15:31:28
Job time : 130 secs

This Page Blank (uspio)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:10:42 ; Search time 44 Seconds
(without alignments)
15.269 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QQLVEYPFT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 99282

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	91.7	9	2	US-08-672-345C-27
2	44	91.7	9	3	US-09-214-095D-27
3	36	75.0	9	2	US-08-672-345C-21
4	36	75.0	9	3	US-09-214-095D-21
5	34	70.8	9	3	US-09-406-532-20
6	33	68.8	9	1	US-08-438-123-3
7	32	66.7	9	1	US-08-264-093-26
8	31	64.6	9	4	US-09-798-689-6
9	30	62.5	9	2	US-08-672-345C-24
10	30	62.5	9	2	US-08-672-345C-30
11	30	62.5	9	3	US-09-214-095D-24
12	30	62.5	9	3	US-09-214-095D-30
13	28	58.3	9	2	US-08-116-778E-11
14	28	58.3	9	2	US-08-438-562-11
15	28	58.3	9	2	US-08-483-528B-99
16	28	58.3	9	3	US-08-974-899-15
17	28	58.3	9	3	US-09-042-353-368
18	28	58.3	9	3	US-08-758-417A-216
19	28	58.3	9	4	US-09-393-385B-110
20	28	58.3	9	4	US-09-795-798-15
21	27	56.2	8	3	US-08-444-818-362
22	27	56.2	8	3	US-08-444-818-363
23	27	56.2	8	3	US-08-444-818-364
24	27	56.2	9	2	US-08-672-345C-81
25	27	56.2	9	3	US-09-214-095D-81
26	27	56.2	9	4	US-09-170-769A-24
27	27	56.2	9	4	US-09-155-106-6

28	27	56.2	9	4	US-09-830-748B-3	Sequence 3, Appli
29	26	54.2	7	2	US-08-627-173-7	Sequence 7, Appli
30	26	54.2	7	2	US-08-535-882A-7	Sequence 7, Appli
31	26	54.2	7	3	US-08-981-384-1	Sequence 1, Appli
32	26	54.2	7	3	US-09-005-546-7	Sequence 7, Appli
33	26	54.2	7	4	US-10-128-581-7	Sequence 7, Appli
34	26	54.2	7	4	US-08-832-443C-7	Sequence 6, Appli
35	26	54.2	8	2	US-08-627-173-6	Sequence 6, Appli
36	26	54.2	8	2	US-08-535-882A-6	Sequence 6, Appli
37	26	54.2	8	3	US-09-005-546-6	Sequence 6, Appli
38	26	54.2	8	4	US-10-128-581-6	Sequence 6, Appli
39	26	54.2	8	4	US-08-832-443C-6	Sequence 6, Appli
40	26	54.2	9	2	US-08-627-173-5	Sequence 5, Appli
41	26	54.2	9	2	US-08-535-882A-5	Sequence 5, Appli
42	26	54.2	9	2	US-08-814-806-7	Sequence 7, Appli
43	26	54.2	9	3	US-09-005-546-5	Sequence 5, Appli
44	26	54.2	9	3	US-08-918-148-24	Sequence 24, Appli
45	26	54.2	9	4	US-09-293-854-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-672-345C-27
; Sequence 27, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-27

Query Match 91.7%; Score 44; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
|||
Db 1 QQFVEYPFT 9

RESULT 2

```

US-09-214-095D-27
; Sequence 27, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-27

Query Match          91.7%; Score 44; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
Db 1 QQFVEYPFT 9

RESULT 3
US-08-672-345C-21
; Sequence 21, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-21

Query Match          75.0%; Score 36; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
Db 1 QHFDVYPFT 9

US-09-214-095D-21
; Sequence 21, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen.sp.
US-09-214-095D-21

Query Match          75.0%; Score 36; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
Db 1 QHFDVYPFT 9

RESULT 4
US-09-214-095D-21
; Sequence 21, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen.sp.
US-09-214-095D-21

Query Match          75.0%; Score 36; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
Db 1 QHFDVYPFT 9

RESULT 5
US-09-406-532-20
; Sequence 20, Application US/09406532A
; Patent No. 6365154
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: TIE2 Agonist Antibodies
; FILE REFERENCE: P50843
; CURRENT APPLICATION NUMBER: US/09/406,532A
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,098
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(9)
; OTHER INFORMATION: light chain CDR 3
US-09-406-532-20

Query Match          70.8%; Score 34; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPFT 9
Db 2 QRLVEYPFT 9

RESULT 6
US-08-438-123-3
; Sequence 3, Application US/08438123
; Patent No. 5552293
; GENERAL INFORMATION:
; APPLICANT: Lindholm et al
; TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Lowe, Price, LeBlanc & Becker
STREET: Suite 300, 99 Canal Center Plaza
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,123
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/906,350
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: J.G. Mullins
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 149-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Polypeptide
US-08-438-123-3

Query Match 68.8%; Score 33; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVYEPFT 9
|:|||||
Db 2 QHLEYPFT 9

RESULT 7
US-08-264-093-26
; Sequence 26, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081

REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
US-08-264-093-26

Query Match 66.7%; Score 32; DB 1; Length 9;
Best Local Similarity 62.5%; Pred. No. 4.1e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVYEPFT 9
|:|||||
Db 2 QRIEFPFT 9

RESULT 8
US-09-798-689-6
; Sequence 6, Application US/09798689
; Patent No. 6811779
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; TITLE OF INVENTION: Combined With Radiation and Chemotherapy
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
; Patent No. 6811779
; CURRENT APPLICATION NUMBER: US/09/798,689
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/401,163
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/967,113
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/706,804
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/476,533
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/326,552
; PRIOR FILING DATE: 1994-10-20
; PRIOR APPLICATION NUMBER: 08/196,041
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; TYPE: PRT
; LENGTH: 9
; ORGANISM: Mouse
US-09-798-689-6

Query Match 64.6%; Score 31; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYFPFT 9
|:|||||
Db 1 QQRSSYPFT 9

RESULT 9
US-08-672-345C-24
; Sequence 24, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP

STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-24

Query Match 62.5%; Score 30; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
| :||||
Db 1 QHFEDYPPT 9

RESULT 10
US-08-672-345C-30
; Sequence 30, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-30

Query Match 62.5%; Score 30; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
| :||||
Db 1 QHFEDYPPT 9

RESULT 11
US-09-214-095D-24
; Sequence 24, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-24

Query Match 62.5%; Score 30; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
| :||||
Db 1 QHFEDYPPT 9

RESULT 12
US-09-214-095D-30
; Sequence 30, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-30

Query Match 62.5%; Score 30; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
| :||||
Db 1 QHFEDYPPT 9

RESULT 13
US-08-116-778E-11
; Sequence 11, Application US/08116778E
; Patent No. 5830470

GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KAWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-116-778E-11

Query Match 58.3%; Score 28; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9
|||
Db 1 QQRSSYPPT 9

RESULT 14
US-08-438-562-11
Sequence 11, Application US/08438562
Patent No. 5874255
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KAWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-438-562-11

Query Match 58.3%; Score 28; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QQLVEYPPT 9
|||
Db 1 QQRSSYPPT 9

RESULT 15
US-08-483-528B-99
Sequence 99, Application US/08483528B
Patent No. 5939532
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KAWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-483-528B-99

Tue Apr 19 06:15:06 2005

Query Match 58.3%; Score 28; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
|||
Db 1 QQRSSYPYT 9

Search completed: April 18, 2005, 15:20:15
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:59:59 ; Search time 9.88372 Seconds
(without alignments)
48.674 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	67	2 A84376	hypothetical prote
2	33	100.0	117	1 G2MSU1	Ig heavy chain V r
3	33	100.0	444	2 S09681	citrate transport
4	33	100.0	1043	2 E97302	hypothetical prote
5	30	90.9	86	2 T42185	conserved hypothet
6	30	90.9	298	2 AB1752	hypothetical prote
7	30	90.9	298	2 AH1728	AbiD phage protein
8	30	90.9	315	2 H86836	carbamate kinase (
9	30	90.9	348	2 G69142	GDP-D-mannose dehy
10	30	90.9	358	2 H83554	hypothetical prote
11	30	90.9	375	2 E83163	hypothetical prote
12	30	90.9	417	2 T08724	hypothetical prote
13	30	90.9	448	2 B95249	PTS system, IIC co
14	30	90.9	448	2 G98113	conserved hypothet
15	30	90.9	452	2 T00113	undecaprenyl-phosp
16	30	90.9	464	2 T28818	hypothetical prote
17	30	90.9	475	2 T46745	arginine/ornithine
18	30	90.9	476	2 D84505	probable membrane
19	30	90.9	480	2 D90038	PTS system, sucros
20	30	90.9	480	2 S39878	scRA protein - Sta
21	30	90.9	490	2 C86879	arginine/ornithine
22	30	90.9	518	1 G69804	multidrug-efflux t
23	30	90.9	535	2 S78598	D-ribulokinase (EC
24	30	90.9	583	2 C72544	probable glycyl-tr
25	30	90.9	592	1 IKBBCA	colicin A - Citrob
26	30	90.9	592	2 T15600	hypothetical prote
27	30	90.9	608	2 JQ1462	phosphoenolpyruvat
28	30	90.9	667	1 VCLJGL	env polyprotein pr
29	30	90.9	847	2 JC4836	alpha-glucuronidas

30	30	90.9	851	2 T47495	hypothetical prote
31	30	90.9	1063	2 A33830	cation efflux syst
32	30	90.9	1063	2 JC4700	cadmium, zinc, cob
33	30	90.9	1215	2 A86595	SWI/SNF family hel
34	30	90.9	1215	2 B72029	helicase, Snf2/Rad
35	30	90.9	1502	2 T42216	multidrug resistanc
36	29	87.9	71	2 AF0683	hypothetical prote
37	29	87.9	101	2 S13692	Ig heavy chain V r
38	29	87.9	102	2 B72742	hypothetical prote
39	29	87.9	111	2 S13693	Ig heavy chain V r
40	29	87.9	112	2 S13690	Ig heavy chain V r
41	29	87.9	115	2 S13694	Ig heavy chain V r
42	29	87.9	116	2 S13691	Ig heavy chain V r
43	29	87.9	122	2 A83756	hypothetical prote
44	29	87.9	137	2 S03326	Ig heavy chain pre
45	29	87.9	152	2 D84436	hypothetical prote

ALIGNMENTS

RESULT 1

A84376

hypothetical protein Vng2253h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: A84376

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,

; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: A84376

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-67 <STO>

C;Cross-references: UNIPROT:Q9HN48; GB:AE004437; NID:g10581666; PIDN:AAG20373.1; GSPDB:

C;Genetics:

A;Gene: VNG2253H

Query Match 100.0%; Score 33; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5

Db 59 GYWMS 63

RESULT 2

G2MSU1

Ig heavy chain V region (UPC10) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004

C;Accession: A02081

R;Auffray, C.; Sikorav, J.L.; Ollio, R.; Rougeon, F.

Ann. Immunol. (Paris) 132D, 77-88, 1981

A;Title: Correlation between D region structure and antigen-binding specificity: evidence

A;Reference number: A02081; MUID:83021113; PMID:6181731

A;Accession: A02081

A;Molecule type: mRNA

A;Residues: 1-117 <AUF>

A;Cross-references: UNIPROT:P01811

C;Comment: This chain was isolated from an Ig gamma-2a myeloma protein binding 2,6-leva

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

F;22-96/Disulfide bonds: #status predicted

Query Match 100.0%; Score 33; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 27;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||||

Db 31 GYWMS 35

RESULT 3

S09681
citrate transport protein - klebsiella pneumoniae plasmid pES1
N;Alternate names: citrate carrier
C;Species: Klebsiella pneumoniae
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: S09681
R;van der Rest, M.E.; Schwarz, E.; Oosterhelt, D.; Konings, W.N.
Eur. J. Biochem. 189, 401-407, 1990
A;Title: DNA sequence of a citrate carrier of Klebsiella pneumoniae.
A;Reference number: S09681; MUID:90249385; PMID:2186908
A;Accession: S09681
A;Molecule type: DNA
A;Residues: 1-444 <RES>
A;Cross-references: UNIPROT:P16482; EMBL:X51479; NID:G43800; PIDN:CAA35844.1; PID:G43801
C;Genetics:
A;Genome: plasmid pES1
C;Superfamily: citrate utilization determinant
C;Keywords: membrane protein

Query Match 100.0%; Score 33; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||||

Db 415 GYWMS 419

RESULT 4

F97302
hypothetical protein CAC3275 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97302
R;Nolling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: F97302
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1043 <KUR>
A;Cross-references: UNIPROT:Q97E41; GB:AB001437; PIDN:AAK81209.1; PID:G15026351; GSPDB:G15026351
C;Genetics:
A;Gene: CAC3275

Query Match 100.0%; Score 33; DB 2; Length 1043;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||||

Db 580 GYWMS 584

RESULT 5

T42185
conserved hypothetical protein L7085 - Escherichia coli plasmid pO157
C;Species: Escherichia coli
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42185
R;Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
Nucleic Acids Res. 26, 4196-4204, 1998

A;Title: The complete DNA sequence and analysis of the large virulence plasmid of Escherichia coli strain 9580
A;Reference number: 222068; MUID:98391744; PMID:9722640
A;Accession: T42185
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-86 <BUR>
A;Cross-references: UNIPROT:Q9ZGR9; EMBL:AF074613; PIDN:AAC70153.1
A;Experimental source: strain EDL933; serotype O157:H7
C;Genetics:
A;Genome: plasmid pO157
A;Note: L7085

Query Match 90.9%; Score 30; DB 2; Length 86;
Best Local Similarity 80.0%; Pred. No. 71;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||||

Db 72 GYWMS 76

RESULT 6

AB1752
hypothetical protein homolog lin2562 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB1752
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative Genomics of Listeria species
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1752
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-298 <GLA>
A;Cross-references: UNIPROT:Q925X5; GB:AL592022; PIDN:CAC97789.1; PID:G16415084; GSPDB:G16415084
C;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2562

Query Match 90.9%; Score 30; DB 2; Length 298;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||||

Db 45 GYWMS 49

RESULT 7

AB1728
ABid phage protein homolog lin2373 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB1728
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative Genomics of Listeria species
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1728
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-298 <GLA>
A;Cross-references: UNIPROT:Q925X5; GB:AL592022; PIDN:CAC97600.1; PID:G16414896; GSPDB:G16414896
C;Experimental source: strain Clip11262

C;Genetics:
A;Gene: lin2373

Query Match 90.9%; Score 30; DB 2; Length 298;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||:
Db 45 GYWLS 49

RESULT 8

H86836
carbamate kinase (EC 2.7.2.2) [imported] - Lactococcus lactis subsp. lactis (strain IL14)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86836
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86836
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-315 <STO>
A;Cross-references: UNIPROT:Q9CEY7; GB:AE005176; PID:g12724712; PIDN:AAK05794.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: arcC3
C;Superfamily: carbamate kinase
C;Keywords: phosphotransferase

Query Match 90.9%; Score 30; DB 2; Length 315;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||:
Db 88 GYWNA 92

RESULT 9

G69142
GDP-D-mannose dehydratase - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 12-Jul-2004
C;Accession: G69142
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiawani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: G69142
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-348 <MTH>
A;Cross-references: UNIPROT:O26433; GB:AE000818; GB:AE000666; NID:g2621384; PIDN:AAE8483
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH333
C;Superfamily: GDP-D-mannose 4,6 dehydratase

Query Match 90.9%; Score 30; DB 2; Length 348;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||:
Db 156 GYWT 160

RESULT 10

H83554
hypothetical protein PA0736 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H83554
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83554
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-358 <STO>
A;Cross-references: UNIPROT:Q9I5J3; GB:AE004508; GB:AE004091; NID:g9946611; PIDN:AAG041
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0736

Query Match 90.9%; Score 30; DB 2; Length 358;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||:
Db 203 GYWLS 207

RESULT 11

E83163
hypothetical protein PA3863 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 16-Aug-2004
C;Accession: E83163
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83163
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-375 <STO>
A;Cross-references: UNIPROT:Q9HXE3; GB:AE004803; GB:AE004091; NID:g9950035; PIDN:AAG072
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3863
C;Superfamily: Sarcosine oxidase

Query Match 90.9%; Score 30; DB 2; Length 375;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||:
Db 19 GYWLS 23

RESULT 12

T08724
hypothetical protein DKFZp566D213.1 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08724
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16468
A;Accession: T08724
A;Molecule type: mRNA
A;Residues: 1-417 <KOE>

Tue Apr 19 06:15:13 2005

us-09-674-716b-9.open.rpr

A;Cross-references: UNIPROT:Q9Y409; EMBL:AL050275
A;Experimental source: fetal kidney; clone DKFZp566D213
C;Genetics:
A;Note: DKFZp566D213.1

Query Match 90.9%; Score 30; DB 2; Length 417;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
|||:
Db 402 GYWS 406

RESULT 13

B95249
FTS system, IIC component, probable [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: B95249
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: B95249
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448 <KUR>
A;Cross-references: UNIPROT:Q97NC2; GB:AE005672; PIDN:AAK76187.1; PID:G14973641; GSPDB:G
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP2129

Query Match 90.9%; Score 30; DB 2; Length 448;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
|||:
Db 186 GYWS 190

RESULT 14

G98113
conserved hypothetical protein spr1938 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: G98113
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
y, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
e, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: G98113
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448 <KUR>
A;Cross-references: UNIPROT:Q8DN40; GB:AE007317; PIDN:AAL00740.1; PID:G15459636; GSPDB:G
C;Genetics:
A;Gene: spr1938

Query Match 90.9%; Score 30; DB 2; Length 448;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
|||:
Db 186 GYWS 190

RESULT 15

T00113
undecaprenyl-phosphate galactosephosphotransferase homolog - Actinobacillus actinomycet-
C;Species: Actinobacillus actinomycetemcomitans
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Accession: T00113
R;Nakano, Y.; Yoshida, Y.; Yamashita, Y.; Koga, T.
Biochim. Biophys. Acta 1442, 409-414, 1998
A;Title: A gene cluster for 6-deoxy-L-talan synthesis in Actinobacillus actinomycetemcom
A;Reference number: Z14111; MUID:99023768; PMID:9805002
A;Accession: T00113
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-452 <NAK>
A;Cross-references: UNIPROT:O6G260; EMBL:AB010415; NID:G3132248; PIDN:BA28142.1; PID:G
A;Experimental source: strain NCTC 9710
C;Superfamily: xps2A protein

Query Match 90.9%; Score 30; DB 2; Length 452;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
|||:
Db 11 GYWS 15

Search completed: April 18, 2005, 14:23:30
Job time : 14.8837 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:57:43 ; Search time 45.4651 Seconds
(without alignments)
56.316 Million cell updates/sec

Title: US-09-674-716B-9
Perfect score: 33
Sequence: 1 GYVMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	67	Q9HN48	Q9HN48 halobacteri
2	33	100.0	73	Q8PR71	Q8PR71 xanthomonas
3	33	100.0	85	Q8PBB4	Q8PBB4 xanthomonas
4	33	100.0	117	HV41 MOUSE	P01811 mus musculu
5	33	100.0	285	Q8W52	Q8W52 lactobacill
6	33	100.0	377	Q8AWR8	Q8AWR8 pollimyrus
7	33	100.0	377	Q91B67	Q91B67 campyloform
8	33	100.0	377	Q91AD5	Q91AD5 stomatorhin
9	33	100.0	377	Q91AD6	Q91AD6 stomatorhin
10	33	100.0	377	Q91AD7	Q91AD7 stomatorhin
11	33	100.0	377	Q91AD8	Q91AD8 stomatorhin
12	33	100.0	377	Q91AD9	Q91AD9 pollimyrus
13	33	100.0	377	Q91AE0	Q91AE0 pollimyrus
14	33	100.0	377	Q91AE1	Q91AE1 pollimyrus
15	33	100.0	377	Q91AE6	Q91AE6 paramormyro
16	33	100.0	377	Q91AE9	Q91AE9 mormyrus ru
17	33	100.0	377	Q91AF0	Q91AF0 mormyrus ov
18	33	100.0	377	Q91AF4	Q91AF4 marcusenius
19	33	100.0	377	Q91AF5	Q91AF5 marcusenius
20	33	100.0	377	Q91AF6	Q91AF6 marcusenius
21	33	100.0	377	Q91AF7	Q91AF7 marcusenius
22	33	100.0	377	Q91AF8	Q91AF8 marcusenius
23	33	100.0	377	Q91AF9	Q91AF9 ivindomyrus
24	33	100.0	377	Q91AG1	Q91AG1 hyperopsisus
25	33	100.0	377	Q91AG2	Q91AG2 hippopotamy
26	33	100.0	377	Q91AG3	Q91AG3 hippopotamy
27	33	100.0	377	Q91AG4	Q91AG4 hippopotamy
28	33	100.0	377	Q91AG6	Q91AG6 gnathomus
29	33	100.0	377	Q91AG7	Q91AG7 genomyrus
30	33	100.0	377	Q91AG9	Q91AG9 campyloform
31	33	100.0	377	Q91AH0	Q91AH0 campyloform

32	33	100.0	377	2	Q9IAH1	Q9IAH1 brienyomys
33	33	100.0	377	2	Q9IAH2	Q9IAH2 brienyomys
34	33	100.0	377	2	Q9IAH3	Q9IAH3 brienyomys
35	33	100.0	377	2	Q9IAH4	Q9IAH4 brienyomys
36	33	100.0	377	2	Q9IAH6	Q9IAH6 boulengerom
37	33	100.0	396	2	Q7SY78	Q7SY78 xenopus lae
38	33	100.0	399	2	Q6BRL7	Q6BRL7 debaryomyce
39	33	100.0	444	1	CITI_KLEPN	P16482 klebsiella
40	33	100.0	721	2	Q7XBS0	Q7XBS0 oryza sativ
41	33	100.0	721	2	Q9FRN4	Q9FRN4 oryza sativ
42	33	100.0	1028	2	Q8XA6	Q8XA6 drosophila
43	33	100.0	1043	2	Q97EA1	Q97EA1 clostridium
44	33	100.0	1254	2	Q86NS1	Q86NS1 drosophila
45	33	100.0	1254	2	Q9VF51	Q9VF51 drosophila

ALIGNMENTS

RESULT 1

Q9HN48	PRELIMINARY;	PRT;	67 AA.
AC Q9HN48;			
DT 01-MAR-2001	(TrEMBLrel. 16, Created)		
DT 01-MAR-2001	(TrEMBLrel. 16, Last sequence update)		
DT 01-JUN-2003	(TrEMBLrel. 24, Last annotation update)		
DE Vng2253h.			
GN OrderedLocusNames=VNG2253H;			
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).			
OC Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;			
OC Halobacteriaceae; Halobacterium.			
OX NCBI_TaxID=64091;			
RP [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE-20504483; PubMed-11016950; DOI=10.1073/pnas.190337797;			
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Fan M.,			
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,			
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,			
RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,			
RA Maddocks D.G., Jabloncki P.E., Krebs M.P., Angevine C.M., Dale H.,			
RA Tsenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,			
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,			
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.,			
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).			
DR EMBL; A3005110; AAG20373.1; -			
DR PIR; A84376; A84376.			
KW Complete proteome.			
SQ SEQUENCE 67 AA; 6601 MW; A6BAF23FCBE8B648 CRC64;			

Query Match 100.0%; Score 33; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GYVMS 5
Db	59	GYVMS 63

RESULT 2

Q8PR71	PRELIMINARY;	PRT;	73 AA.
AC Q8PR71;			
DT 01-OCT-2002	(TrEMBLrel. 22, Created)		
DT 01-OCT-2002	(TrEMBLrel. 22, Last sequence update)		
DT 01-OCT-2002	(TrEMBLrel. 22, Last annotation update)		
DE Hypothetical protein XAC0095.			
GN OrderedLocusNames=XAC0095;			
OS Xanthomonas axonopodis (pv. citri).			
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;			
OC Xanthomonadaceae; Xanthomonas.			
OX NCBI_TaxID=92829;			
RP [1]			

SEQUENCE FROM N.A.
 STRAIN=306 / ATCC 13902 / XV 101;
 MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
 da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.P.,
 Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
 Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 Setubal J.C., Kitaajima J.P.;
 "Comparison of the genomes of two Xanthomonas pathogens with differing
 host specificities."
 Nature 417:459-463(2002).
 EMBL: AE011632; AAM34987.1; --
 Complete proteome, Hypothetical protein.
 SEQUENCE 73 AA; 8296 MW; 89C3771680F46C3D CRC64;
 Query Match 100.0%; Score 33; DB 2; Length 73;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 DB 6 GYWS 10
 RESULT 3
 Q8PEB4 PRELIMINARY; PRT; 85 AA.
 ID Q8PEB4
 AC Q8PEB4; 22, Created
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein XCC0067.
 GN OrderedLocusNames=XCC0067.
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 ON NCBI_TaxID=340;
 RX SEQUENCE FROM N.A.
 RP STRAIN=ATCC 33913 / NCPPB 528;
 RC MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
 RX da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.P.,
 Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
 Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 Setubal J.C., Kitaajima J.P.;
 "Comparison of the genomes of two Xanthomonas pathogens with differing
 host specificities."
 Nature 417:459-463(2002).
 EMBL: AE012100; AAM39386.1; --
 Complete proteome.
 SEQUENCE 85 AA; 9609 MW; C6FDC29D07155274 CRC64;
 Query Match 100.0%; Score 33; DB 2; Length 85;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 DB 18 GYWS 22
 RESULT 4
 HV41 MOUSE
 ID HV41 MOUSE STANDARD; PRT; 117 AA.
 AC P01811;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE IG heavy chain V region UPC10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83021113; PubMed=6181731;
 RA Auffray C., Sikorav J.L., Ollo R., Rougeon F.;
 RT "Correlation between D region structure and antigen-binding
 specificity: evidences from the comparison of closely related
 immunoglobulin VH sequences."
 RT Ann. Immunol. (Paris) 132D:77-88(1981).
 CC -!- MISCELLANEOUS: This chain was isolated from an Ig gamma-2a myeloma
 protein binding 2,6-levan.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
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 entities requires a license agreement (See <http://www.isb-sib.ch/annouce/>)
 or send an email to license@isb-sib.ch.
 CC EMBL: M36631; AAA38078.1; --
 DR PIR: A02081; GZMSUL.
 DR HSSP: P01810; 2FSJ.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; ig; 1.
 DR SMART: SM00406; Igv; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 116
 FT NON TER 117 117
 FT Ig-like.
 SQ SEQUENCE 117 AA; 13001 MW; B20A1074F8E99E7F CRC64;
 Query Match 100.0%; Score 33; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 DB 31 GYWS 35
 RESULT 5
 Q88W52 PRELIMINARY; PRT; 285 AA.
 ID Q88W52
 AC Q88W52;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Integral membrane protein.
 GN OrderedLocusNames=lp.1809;
 OS Lactobacillus plantarum.

OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1590;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIMB 8826 / WCFS1;
 RA MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;
 RX Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
 RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
 RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
 RA De Vos W.M., Siezen R.J.;
 RT "Complete genome sequence of *Lactobacillus plantarum* WCFS1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
 DR EMBL; AL935257; CAD64219.1; -;
 DR InterPro; IPR007163; DUF368.
 DR Pfam; PF04018; DUF368; 1.
 KW Complete proteome.
 SQ SEQUENCE 285 AA; 30888 MW; D93DB9353EA9D881 CRC64;
 Query Match 100.0%; Score 33; DB 2; Length 285;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 Db 274 GYWS 278
 RESULT 6
 Q8AWR8 PRELIMINARY; PRT; 377 AA.
 ID Q8AWR8
 AC Q8AWR8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS *Pollimyrus adspersus*.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Pollimyrus.
 OX NCBI_TaxID=203438;
 [1]
 RP SEQUENCE FROM N.A.
 RC Lavoue S., Sullivan J.P., Hopkins C.D.;
 RA "Phylogenetic utility of the first two introns of the S7 ribosomal
 RT protein gene in African electric fishes (Mormyroidea: Teleostei) and
 RT congruence with other molecular markers.";
 RL Biol. J. Linn. Soc. Lond. 78:273-292(2003).
 DR EMBL; AY124315; AAM92557.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA recombination; IEA.
 DR GO; GO:006310; P:DNA recombination; IEA.
 DR InterPro; IPR011043; Gal_oxid_central.
 DR Pfam; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 FT NON_TER 1
 FT NON_TER 377
 SQ SEQUENCE 377 AA; 41472 MW; 1D90B1F4CCTADAFE CRC64;
 Query Match 100.0%; Score 33; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 Db 368 GYWS 372
 RESULT 7
 Q9I867 PRELIMINARY; PRT; 377 AA.
 ID Q9I867
 AC Q9I867;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS *Campylomormyrus tamandua*.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Campylomormyrus.
 OX NCBI_TaxID=91719;
 [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20115608; PubMed=10648209;
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;
 RT "Molecular systematics of the african electric fishes (Mormyroidea:
 RT teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683(2000).
 DR EMBL; AF201625; AAF43336.1; -;
 DR EMBL; AF201624; AAF43335.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:006310; P:DNA recombination; IEA.
 DR InterPro; IPR011043; Gal_oxid_central.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 FT NON_TER 1
 FT NON_TER 377
 SQ SEQUENCE 377 AA; 41387 MW; D52A9E361A56AB43 CRC64;
 Query Match 100.0%; Score 33; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 Db 368 GYWS 372
 RESULT 8
 Q9IAD5 PRELIMINARY; PRT; 377 AA.
 ID Q9IAD5
 AC Q9IAD5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS *Stomatichnus* sp. AMNH228158.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Stomatichnus.
 OX NCBI_TaxID=112282;
 [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20115608; PubMed=10648209;
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;
 RT "Molecular systematics of the african electric fishes (Mormyroidea:
 RT teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683(2000).
 DR EMBL; AF201659; AAF43370.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:006310; P:DNA recombination; IEA.
 DR InterPro; IPR011043; Gal_oxid_central.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 FT NON_TER 1
 FT NON_TER 377
 SQ SEQUENCE 377 AA; 41485 MW; 4AA141FC3B092825 CRC64;
 Query Match 100.0%; Score 33; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5

DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR InterPro; IPR011043; Gal_oxid_central.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 FT NON_TER 1 377
 FT NON_TER 377 377
 SQ SEQUENCE 377 AA; 41424 MW; 1B84D6E64659A1C7 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 DB 368 GYWS 372

RESULT 13

Q9IAE0 PRELIMINARY; PRT; 377 AA.
 ID Q9IAE0
 AC Q9IAE0
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS Pollimyrus isidori.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Pollimyrus.
 OX NCBI_TaxID=91713;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20115608; PubMed=10648209;
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;
 RT "Molecular systematics of the african electric fishes (Mormyroidae;
 RT teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683(2000).
 DR EMBL; AF201654; AAF43365.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR InterPro; IPR011043; Gal_oxid_central.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 FT NON_TER 1 377
 FT NON_TER 377 377
 SQ SEQUENCE 377 AA; 41457 MW; 393E1B1FA838E9C8 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 DB 368 GYWS 372

RESULT 14

Q9IAE1 PRELIMINARY; PRT; 377 AA.
 ID Q9IAE1
 AC Q9IAE1
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS Pollimyrus petricolus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Pollimyrus.
 OX NCBI_TaxID=91715;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20115608; PubMed=10648209;
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;
 RT "Molecular systematics of the african electric fishes (Mormyroidae;
 RT teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683(2000).
 DR EMBL; AF201653; AAF43364.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR InterPro; IPR011043; Gal_oxid_central.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 FT NON_TER 1 377
 FT NON_TER 377 377
 SQ SEQUENCE 377 AA; 41473 MW; E7970A9EC67D6193 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 DB 368 GYWS 372

RESULT 15

Q9IAE6 PRELIMINARY; PRT; 377 AA.
 ID Q9IAE6
 AC Q9IAE6
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS Paramormyrops gabonensis.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Paramormyrops.
 OX NCBI_TaxID=91733;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20115608; PubMed=10648209;
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;
 RT "Molecular systematics of the african electric fishes (Mormyroidae;
 RT teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683(2000).
 DR EMBL; AF201648; AAF43359.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR InterPro; IPR011043; Gal_oxid_central.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 FT NON_TER 1 377
 FT NON_TER 377 377
 SQ SEQUENCE 377 AA; 41403 MW; 0A4599C604C8123 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 DB 368 GYWS 372

Search completed: April 18, 2005, 14:21:55
 Job time : 46.4651 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:32:07 ; Search time 52.6744 Seconds
(without alignments)
36.712 Million cell updates/sec

Title: US-09-674-716B-9
Perfect score: 33
Sequence: 1 GYMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	5	3 AAY32257	Aay32257 Light cha
2	33	100.0	10	7 ADM07744	Adm07744 Canine im
3	33	100.0	73	7 ADG30700	Adg30700 Xanthomon
4	33	100.0	137	3 AAY32260	Aay32260 Mouse ant
5	33	100.0	163	7 ABM73967	Abm73967 DNA clone
6	33	100.0	345	7 ABM73656	Abm73656 DNA clone
7	33	100.0	444	3 AAY32263	Aay32263 Humanised
8	33	100.0	466	7 ABO67808	Aboc67808 Klebsiell
9	33	100.0	1096	8 ADP99004	Adp99004 C. albica
10	33	100.0	1254	4 ABB62006	Abb62006 Drosophil
11	30	90.9	40	4 ABG07533	Abg07533 Novel hum
12	30	90.9	43	2 AAR95472	Aar95472 V39, mono
13	30	90.9	63	6 ABR48102	Abr48102 Human sec
14	30	90.9	63	6 ABR00271	Abr00271 Human gen
15	30	90.9	63	7 ADB91793	Adb91793 Human sec
16	30	90.9	63	7 ADC74531	Adc74531 Human sec
17	30	90.9	64	2 AAY07813	Aay07813 Human sec
18	30	90.9	175	8 ADN74285	Adn74285 Thale cre
19	30	90.9	181	2 AAY35482	Aay35482 Chlamydia
20	30	90.9	210	4 AAU17327	Aau17327 Novel sig
21	30	90.9	210	7 ADB94035	Adb94035 Human nov
22	30	90.9	242	3 AAY76114	Aay76114 Rat HT gl
23	30	90.9	242	4 AAB56053	Aab56053 Skin cell
24	30	90.9	242	5 ABB72253	Abb72253 Rat prote
25	30	90.9	242	5 ABB72301	Abb72301 Rat prote

ALIGNMENTS

RESULT 1

AAY32257
ID AAY32257 standard; peptide; 5 AA.

XX AAY32257;

XX 15-FEB-2000 (first entry)

XX Light chain CDR H1 of mouse anti-CD23 Mab C11.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
therapy.

XX Mus musculus.

XX WO9558679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAX) GLAXO GROUP LTD.

XX Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WPI; 2000-053101/04.

XX N-PSDB; AA234742.

XX Cell receptor specific antibodies useful for treating e.g. arthritis,
diabetes, multiple sclerosis and psoriasis.

XX Claim 1; Page 40; 81pp; English.

XX This sequence represents complementarity determining region 1 (CDR H1)
of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11
(see also AAY32263). The invention provides altered antibodies, such as
chimeric or humanised antibodies, which comprise sufficient of the amino
acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

Abb72290 Rat prote
Abp39269 Staphyloc
Abm72990 Staphyloc
Ade05885 Staphyloc
Aau35317 Enterococ
Aab39867 GALV retr
Abu29423 Protein e
Abb55045 Lactococc
Adh88144 Bacterial
Adh88144 Enterococ
Adn18477 Bacterial
Aag1982 Arabidops
Aab19870 Activatin
Aag1981 Arabidops
Abo80711 Pseudomon
Aab38394 Human sec
Ada41195 Human sec
Abr48101 Human sec
Abr00270 Human gen
Adb91792 Human sec

CC render them capable of binding to the CD23 type II molecule expressed on
 CC haematopoietic cells. The antibodies are used to block soluble CD23
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They
 CC are also useful for studying interactions between CD23 and various
 CC ligands and determining the binding agents
 XX
 XX Sequence 5 AA;
 SQ

Query Match 100.0%; Score 33; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
 |||||
 Db 1 GYWMS 5

RESULT 2
 ADM07744
 ID ADM07744 standard; peptide; 10 AA.
 XX
 AC ADM07744;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Canine immunoglobulin heavy chain variable domain CDR1 peptide 12.
 XX
 KW canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
 KW antiallergic; allergy; IGE; gene therapy;
 KW complementarity determining region; CDR1.
 XX
 OS Canis familiaris.
 XX
 PN WO2003060080-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 20-DEC-2002; 2002WO-US041362.
 XX
 PR 21-DEC-2001; 2001US-0344874P.
 XX
 PA (IDEX-) IDEXX LAB INC.
 XX
 PI Krah ER, Guo H, Aiyappa A, Lawton R;
 XX
 DR WPI; 2003-598521/56.
 XX
 PT New canine heavy and light chain variable domain polypeptides, useful for
 PT treating canine allergy.
 XX
 PS Claim 15; Page 95; 130pp; English.
 XX
 CC The invention relates to a novel canine heavy or light chain variable
 CC domain polypeptide. The protein of the invention demonstrates
 CC antiallergic activity and may be useful for treating canine allergy,
 CC possibly via gene therapy. The current sequence is that of a canine
 CC immunoglobulin heavy chain variable domain complementarity determining
 CC region (CDR) peptide of the invention.
 XX
 XX Sequence 10 AA;
 SQ

Query Match 100.0%; Score 33; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 11;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5

Db |||||
 6 GYWMS 10

RESULT 3
 ADG30700
 ID ADG30700 standard; protein; 73 AA.
 XX
 AC ADG30700;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Xanthomonas axonopodis pv citri plant pathology-related XAC0095 protein.
 XX
 KW Xanthomonas microorganism; plant; pathology; bacterial pest; Xac; Xcc;
 XX
 OS Xanthomonas axonopodis pv. citri.
 XX
 PN WO2003089647-A1.
 XX
 PD 30-OCT-2003.
 XX
 PF 22-APR-2003; 2003WO-BR000060.
 XX
 PR 22-APR-2002; 2002US-0374620P.
 XX
 PA (AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.
 XX
 PI Da Silva ACR, Farah SC, Quaggio RB, Reinach FDC, Ferro JA;
 PI De Oliveira JCF, De Laia ML, Setubal JC, Furlan LR;
 XX
 DR WPI; 2003-865444/80.
 DR N-PSDB; ADG30699.
 XX
 PT New nucleic acid molecule from a Xanthomonas microorganism, useful in
 PT determining the presence of Xanthomonas bacteria in a sample.
 XX
 PS Claim 8; SEQ ID NO 57; 145pp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid molecule from a
 CC Xanthomonas microorganism where the nucleic acid molecule is associated
 CC with pathogenicity caused by the Xanthomonas microorganism, or its
 CC variant, that causes reduced or enhanced pathogenicity. The nucleic acid
 CC of the invention may be useful in detecting the presence of Xanthomonas
 CC bacteria in a sample, as well as in plant pathology, for example, for
 CC identifying nucleic acid molecules and proteins involved in pathology
 CC caused by bacterial pests. The current sequence is that of the
 CC Xanthomonas axonopodis pv. citri (Xac) plant pathology-related XAC
 CC protein of the invention.
 XX
 SQ Sequence 73 AA;

Query Match 100.0%; Score 33; DB 7; Length 73;
 Best Local Similarity 100.0%; Pred. NO. 85;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
 |||||
 Db 6 GYWMS 10

RESULT 4
 AAY32260
 ID AAY32260 standard; protein; 137 AA.
 XX
 AC AAY32260;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Mouse anti-CD23 MAb C11 heavy chain variable region.
 XX
 KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;

KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 KW therapy.
 XX
 XX
 OS Mus musculus.
 XX
 XX

PH Key Location/Qualifiers
 FT Region 59. .63
 FT Region /note= "CDR H1"
 FT Region 78. .96
 FT Region /note= "CDR H2"
 FT Region 129. .131
 FT Region /note= "CDR H3"

XX WO9958679-A1.
 XX
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-GB001434.
 XX
 XX 09-MAY-1998; 98GB-00009839.
 XX
 XX (GLAX) GLAXO GROUP LTD.
 PA
 XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 PI
 DR WPI; 2000-053101/04.
 DR N-PSDB; AA234745.
 XX

PT Call receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis.

XX Claim 8; Fig 1; 8lpp; English.

XX This sequence represents the heavy chain variable region (VH) of murine
 CC anti-CD23 (PCERII) monoclonal antibody C11. The invention provides
 CC altered antibodies, such as chimeric or humanised antibodies (see
 CC AA32262 and AA32263), which comprise sufficient of the amino acid
 CC sequences of the C11 light and heavy chain complementarity determining
 CC regions (see AA32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies are
 CC used to block soluble CD23 formation in human therapy, for the treatment
 CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
 CC malignancies (claimed). They are also useful for studying interactions
 CC between CD23 and various ligands and determining the binding agents
 XX

SQ Sequence 137 AA;

Query Match 100.0%; Score 33; DB 3; Length 137;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
 DB 59 GYWMS 63

RESULT 5
 ABM73967
 ID ABM73967 standard; protein; 163 AA.
 XX

AC ABM73967;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE DNA clone originating in barley containing SNP sequence #377.
 XX
 KW Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
 XX
 OS Hordeum vulgare.
 XX
 PN WO2003057877-A1.
 XX
 PD 17-JUL-2003.
 XX
 XX 16-DEC-2002; 2002WO-IB005403.
 XX
 PR 20-DEC-2001; 2001JP-00387059.
 PR 20-DEC-2001; 2001JP-00387131.
 PR 20-DEC-2001; 2001JP-00403299.
 PR 20-DEC-2001; 2001JP-00403300.
 PR 27-SEP-2002; 2002JP-00327515.
 XX
 XX (UYN1-) UNIV JAPAN OKAYAMA.
 PA
 XX Sato K, Takeda K, Kohara Y;
 PI
 DR WPI; 2003-587127/55.
 XX
 XX Single nucleotide polymorphism sites in barley varieties and DNA
 PT sequences containing them for analysis and identification of barley
 PT varieties and production of barley transformants with desired
 PT characteristics.
 XX
 PS Disclosure; SEQ ID XX; 284bp; Japanese.
 XX

CC The present invention relates to oligonucleotide clones originating in
 CC barley (Hordeum vulgare) which contain single nucleotide polymorphisms
 CC (SNP). The oligonucleotides may be used for analysis of SNPs among barley
 CC varieties, identification of particular varieties and genotype-phenotype
 CC analysis, isolation of specific genes and creation of new varieties by
 CC transformation of barley varieties with them and production of new barley
 CC varieties with desired properties. The present sequence represents an
 CC oligonucleotide clone sequence featured in the specification. The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published-pct-sequences

XX SQ Sequence 163 AA;

Query Match 100.0%; Score 33; DB 7; Length 163;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
 DB 84 GYWMS 88

RESULT 6
 ABM73656
 ID ABM73656 standard; protein; 345 AA.
 XX

AC ABM73656;

XX 17-OCT-2003 (first entry)

XX DNA clone originating in barley containing SNP sequence #66.

XX Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.

XX Hordeum vulgare.

XX WO2003057877-A1.

XX PD 17-JUL-2003.
XX XX
XX PF 16-DEC-2002; 2002WO-IB005403.
XX XX
XX PR 20-DEC-2001; 2001JP-00387059.
XX PR 20-DEC-2001; 2001JP-00387131.
XX PR 20-DEC-2001; 2001JP-00403299.
XX PR 20-DEC-2001; 2001JP-00403300.
XX PR 27-SEP-2002; 2002JP-00327515.
XX PA (UYN1-) UNIV JAPAN OKAYAMA.
XX XX
XX PI Sato K, Takeda K, Kohara Y;
XX DR WPI; 2003-587127/55.
XX XX
XX PT Single nucleotide polymorphism sites in barley varieties and DNA
XX PT sequences containing them for analysis and identification of barley
XX PT varieties and production of barley transformants with desired
XX PT characteristics.
XX PS Disclosure; SEQ ID XX; 284bp; Japanese.
XX CC
XX CC The present invention relates to oligonucleotide clones originating in
XX CC barley (Hordeum vulgare) which contain single nucleotide polymorphisms
XX CC (SNP). The oligonucleotides may be used for analysis of SNPs among barley
XX CC varieties, identification of particular varieties and genotype-phenotype
XX CC analysis, isolation of specific genes and creation of new varieties by
XX CC transformation of barley varieties with them and production of new barley
XX CC varieties with desired properties. The present sequence represents an
XX CC oligonucleotide clone sequence featured in the specification. The
XX CC sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published-pct-sequences
XX XX
XX SQ Sequence 345 AA;

Query Match 100.0%; Score 33; DB 7; Length 345;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 266 GYWS 270
|||||

RESULT 7
AAY32263
ID AAY32263 standard; protein; 444 AA.
XX AC
XX AC AAY32263;
XX DT 15-FEB-2000 (first entry)
XX XX
XX DE Humanised anti-CD23 MAB C11 heavy chain.
XX XX
XX KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human;
XX KW monoclonal antibody; chimeric antibody; humanised antibody;
XX KW complementarity determining region; CDR; autoimmune disease;
XX KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
XX KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
XX KW urticaria; nephrotic syndrome; glomerulonephritis;
XX KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
XX KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
XX KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
XX KW therapy.
XX XX
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT Region 1. .30

/note= "framework region 1"
31. .35
/note= "CDR 1"
36. .49
/note= "framework region 2"
50. .68
/note= "CDR 2"
69. .100
/note= "framework region 3"
101. .103
/note= "CDR 3"
104. .111
/note= "framework region 4"
112. .444
/note= "constant region"

WO9958679-A1.
18-NOV-1999.
07-MAY-1999; 99WO-GB001434.
09-MAY-1998; 98GB-00009839.
(GLAX) GLAXO GROUP LTD.
Bonneyfey JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
WPI; 2000-053101/04.
N-PSDB; AA234748.
Cell receptor specific antibodies useful for treating e.g. arthritis,
diabetes, multiple sclerosis and psoriasis.
Claim 9; Fig 4; 81pp; English.

This amino acid sequence represents the heavy chain of humanised anti-
CD23 (FCERII) monoclonal antibody C11, composed of a human framework
(HSIGKVII) and the heavy chain complementarity determining regions (see
AAY32257-59) of murine antibody C11. The DNA was constructed by splice
overlap PCR. The invention provides altered antibodies, such as chimeric
or humanised antibodies, which comprise sufficient of the amino acid
sequences of the C11 light and heavy chain complementarity determining
regions to render them capable of binding to the CD23 type II molecule
expressed on haematopoietic cells. The antibodies are used to block
soluble CD23 formation in human therapy, for the treatment of arthritis,
lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,
glomerulonephritis, inflammatory bowel disease, ulcerative colitis,
Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
malignancies (claimed). They are also useful for studying interactions
between CD23 and various ligands and determining the binding agents
Sequence 444 AA;

Query Match 100.0%; Score 33; DB 3; Length 444;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 31 GYWS 35
|||||

RESULT 8
ABO67808
ID ABO67808 standard; protein; 466 AA.
XX XX
XX AC ABO67808;
XX XX

DT 29-JUL-2004 (first entry)
 DE Klebsiella pneumoniae polypeptide seqid 14325.
 XX
 KW Recombinant expression vector; transcription regulatory element;
 KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
 XX
 OS Klebsiella pneumoniae.
 XX
 XX US6610836-B1.
 FN
 XX 26-AUG-2003.
 PD
 XX
 XX 27-JAN-2000; 2000US-00489039.
 PF
 XX
 XX 29-JAN-1999; 99US-0117747P.
 PR
 XX
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA
 XX
 PI Breton GL, Osborne M;
 FI
 XX WPI; 2003-895346/82.
 DR
 XX N-PSDB; ABD01379.
 DR
 XX
 PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 PT preparing a vaccine composition against Klebsiella pneumoniae.
 XX
 XX Disclosure; SEQ ID NO 14325; 932pp; English.
 XX
 CC The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention
 XX
 SQ Sequence 466 AA;
 Query Match 100.0%; Score 33; DB 7; Length 466;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GYWS 5
 Db |||||
 437 GYWS 441
 RESULT 9
 ADP99004
 ID ADP99004 standard; protein; 1096 AA.
 XX
 AC ADP99004;
 AC
 XX 23-SEP-2004 (first entry)
 DT
 XX
 DE C. albicans specific gene, CayMR047C, protein sequence.
 XX
 KW Diploid fungal cell; allele; gene disruption cassette;
 KW promoter replacement fragment; antifungal; fungicide; gene therapy;
 KW infection; Candida albicans.
 XX
 XX Candida albicans.
 OS
 XX
 XX WO2004056965-A2.
 PN
 XX
 PD 08-JUL-2004.
 XX
 XX 19-DEC-2003; 2003WO-US040618.
 PF
 XX
 XX 19-DEC-2002; 2002US-0434832P.
 PR
 XX
 XX (ELIT-) ELITRA PHARM INC.
 PA

PA (ELIT-) ELITRA CANADA LTD.
 XX
 XX Roemer T, Jiang B, Boone C, Bussey H;
 PI
 XX WPI; 2004-500296/47.
 DR
 XX N-PSDB; ADP98694.
 DR
 XX
 PT Constructing a strain of diploid fungal cells in which both alleles of a
 PT gene are modified comprises modifying the alleles of a gene in the fungal
 PT cells by recombination using a gene disruption cassette and a promoter
 PT replacement fragment.
 XX
 XX Claim 44; SEQ ID NO 7179; 163pp; English.
 PS
 XX
 CC The invention relates to a novel method for constructing a strain of
 CC diploid fungal cells in which both alleles of a gene are modified. The
 CC method comprises modifying the alleles of a gene in diploid fungal cells
 CC by recombination using a gene disruption cassette and a promoter
 CC replacement fragment. The invention further comprises: assembling a
 CC collection of diploid fungal cells each of which comprises modified
 CC alleles of a different gene; a strain of diploid fungal cells comprising
 CC modified alleles of a gene, where the first allele of the gene is
 CC inactivated by a gene disruption cassette comprising a nucleotide
 CC sequence encoding an expressible selectable marker; and the expression of
 CC the second allele of the gene is regulated by a heterologous promoter
 CC that is operably linked to the coding region of the second allele of the
 CC gene, and where the gene encodes the polypeptide mentioned above; a
 CC collection of diploid fungal strains comprising the diploid strains cited
 CC above, where substantially all the different genes that encode the above
 CC amino acid sequences are modified and are present in different diploid
 CC strains in the collection; a nucleic acid molecule microarray comprising
 CC nucleic acid molecules, where each nucleic acid molecule comprises a
 CC nucleotide sequence that is hybridizable to a target nucleotide sequence
 CC comprising any of the 310 nucleotide sequences listed in the
 CC specification (ADP98516-ADP98825); identifying a gene that is essential
 CC to the survival or growth of a fungus, that contributes to the virulence
 CC and/or pathogenicity of a fungus, or that contributes to the virulence
 CC of a diploid fungus to an antifungal agent; identifying an antifungal
 CC agent that inhibits the growth of a diploid fungus, or a therapeutic
 CC agent for treatment of a mammalian disease; correlating changes in the
 CC levels of proteins or gene transcripts with the inhibition of growth or
 CC proliferation of a diploid fungal cell; a purified or isolated nucleic
 CC acid molecule comprising a nucleotide sequence encoding a gene product
 CC required for proliferation of Candida albicans, where the gene product
 CC consists of any of the above-mentioned amino acid sequences; a vector
 CC comprising a promoter operably linked to the nucleic acid molecule cited
 CC above; a host cell containing the vector; a purified or isolated
 CC polypeptide comprising any of the 61 amino acid sequences given in the
 CC specification (ADP96718-ADP96778); a fusion protein comprising a fragment
 CC of a first polypeptide fused to a second polypeptide, the fragment
 CC consisting of at least 6 consecutive residues of any of ADP98826-ADP99135
 CC; producing a polypeptide; identifying a compound which modulates the
 CC activity of a gene product encoded by a nucleic acid comprising any of
 CC ADP98516-ADP98825; eliciting an immune response in an animal; a strain of
 CC Candida albicans, where a first allele of a gene comprising any of
 CC ADP98516-ADP98825 is inactive and a second allele of the gene is under
 CC the control of a heterologous promoter; identifying a compound or binding
 CC partner that binds to the polypeptide comprising any of ADP98826-
 CC ADP99135, or its fragment; identifying a compound having the ability to
 CC inhibit growth or proliferation of Candida albicans; inhibiting growth or
 CC proliferation of Candida albicans cells; manufacturing an antimycotic
 CC compound; treating an infection of a subject by Candida albicans;
 CC preventing or containing contamination of an object by Candida albicans,
 CC or for preventing or inhibiting formation on a surface of a biofilm
 CC comprising Candida albicans; a pharmaceutical composition comprising a
 CC therapeutic amount of an agent which reduces the activity or level of a
 CC gene product encoded by a nucleic acid comprising any of ADP98516-
 CC ADP98825 in a pharmaceutical carrier; an antibody preparation which binds
 CC the polypeptide; methods for evaluating a compound against a target gene
 CC product encoded by any of ADP98516-ADP98825; identifying an antimycotic
 CC compound; a computer or a computer readable medium that comprises at
 CC least one of the nucleotide sequences mentioned in the specification or
 CC at least one amino acid sequence selected from ADP98826-ADP99135; a

CC method assisted by a computer for identifying a putatively essential gene
CC of a fungus; and a protein array comprising proteins, where at least one
CC protein comprises an amino acid sequence or a portion of an amino acid
CC sequence selected from ADF98516-ADF98825. The novel methods and
CC compositions have fungicide activity. The compositions may be used in
CC gene therapy. The composition and methods are useful for drug screening
CC purposes or for diagnosing, preventing or treating infections associated
CC with Candida albicans. These may also be used for constructing strains
CC useful for identification and validation of gene products as effective
CC targets for therapeutic intervention, for identifying and validating gene
CC products as effective targets for therapeutic intervention, and for
CC collecting identified essential genes. This sequence represents the
CC protein of a Candida albicans fungal specific gene of the invention.
CC NOTE: This sequence was downloaded from an electronic sequence listing
CC provided on the WIPO website.

XX SQ Sequence 1096 AA;
Query Match 100.0%; Score 33; DB 8; Length 1096;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYVMS 5
Db 955 GYVMS 959
|||||

RESULT 10
ABB62006
ID ABB62006 standard; protein; 1254 AA.

AC ABB62006;

DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 12810.

XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI: 2001-656860/75.

XX N-PSDB; ABL06109.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.

XX Disclosure; SEQ ID NO 12810; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1254 AA;

Query Match 100.0%; Score 33; DB 4; Length 1254;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYVMS 5
Db 1139 GYVMS 1143
|||||

RESULT 11

ABG07533

ID ABG07533 standard; protein; 40 AA.

XX AC ABG07533;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #7524.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.

XX N-PSDB; AAS71720.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20; SEQ ID NO 37892; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 40 AA;

Query Match 90.9%; Score 30; DB 4; Length 40;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 Db 33 GYWS 37
 |||:|

RESULT 12
 AAR95472
 ID AAR95472 standard; peptide; 43 AA.
 XX AC
 XX AAR95472;
 XX DT
 XX 05-NOV-1996 (first entry)
 XX DE
 XX V39, monoclonal antibody SM-3 derived antigen binding peptide.
 XX KW
 XX Abtide; prostate specific mucin antigen; human prostate cancer; LNCap;
 XX KW diagnostic; detection; imaging; tumour; phage; peptide library; breast;
 XX KW polymorphic; epithelial.
 XX OS Synthetic.
 XX PN WO9609411-A1.
 XX PD 28-MAR-1996.
 XX PF 20-SEP-1995; 95WO-US011934.
 XX PR 21-SEP-1994; 94US-00310192.
 XX PR 07-JUN-1995; 95US-00488161.
 XX PA (CYTO-) CYTOGEN CORP.
 XX PI Alvarez VL;
 XX DR WPI; 1996-188471/19.
 XX PT New isolated peptide(s) with specific binding activities - obtd. by
 PT screening random peptide libraries, for use in diagnostic and therapeutic
 PT compans.
 XX PS Claim 38; Page 75; 106pp; English.
 XX CC AAR95459-R95509 are antigen binding peptides ("abtides") derived from the
 CC monoclonal antibody SM-3 which recognises a specific polymorphic
 CC epithelial mucin tumour antigen found on human breast cancer cells. The
 CC abtides are identified from random peptide libraries using specific
 CC ligand binding. Abtides mimic the binding specificity of large molecules
 CC such as antibodies and receptors but have a much smaller size allowing
 CC their production at a lower cost and reducing the extent of their
 CC immunogenicity aiding in vivo delivery. The abtides are useful for the
 CC diagnosis, detection, imaging and treatment of disease, e.g. tumours,
 CC prostate cancer and breast cancer
 XX SQ Sequence 43 AA;

Query Match 90.9%; Score 30; DB 2; Length 43;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 Db 6 GYWS 10
 |||:|

RESULT 13
 ABR48102
 ID ABR48102 standard; protein; 63 AA.

XX AC ABR48102;
 XX DT 12-JUN-2003 (first entry)
 XX DE Human secreted protein, SEQ ID 993.
 XX KW Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
 XX KW vulnery; antiinflammatory; nootropic; neuroprotective;
 XX KW antiparkinsonian; gene therapy; human; cardiovascular disorder.
 XX OS Homo sapiens.
 XX PN WO200295010-A2.
 XX PD 28-NOV-2002.
 XX PF 19-MAR-2002; 2002WO-US009785.
 XX PR 21-MAR-2001; 2001US-0277340P.
 XX PR 19-JUL-2001; 2001US-0306171P.
 XX PR 13-NOV-2001; 2001US-0331287P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM;
 XX DR WPI; 2003-129429/12.
 XX PT Novel human secreted proteins, useful for detecting, preventing,
 PT diagnosing, prognosticating, treating and/or ameliorating cardiovascular
 PT disorders such as arrhythmia.
 XX PS Claim 13; SEQ ID NO 993; 1881pp; English.
 XX CC The present invention relates to novel human secreted proteins (ABR47633-
 CC ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
 CC and their coding sequences are useful for the preparation of a diagnostic
 CC or pharmaceutical composition for diagnosing or treating a cardiovascular
 CC disorder (e.g. arrhythmia, tachycardia, cardiac arrest, coronary
 CC arteriosclerosis and myocardial ischaemia), neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, renal disorders,
 CC proliferative disorders and/or cancerous diseases and conditions, for
 CC wound healing and epithelial cell proliferation, to treat inflammation or
 CC infection, for treating thrombosis and arteriosclerosis, for treating or
 CC preventing neural damage which occurs in neuronal disorders or
 CC neurodegenerative conditions such as Alzheimer's disease and Parkinson's
 CC disease, to enhance bone and periodontal regeneration and aid in tissue
 CC transplants or bone grafts, to prevent skin aging or hair loss, to
 CC stimulate growth and differentiation of haematopoietic cells and bone
 CC marrow cells when used in combination with other cytokines, to maintain
 CC organs before transplantation or for supporting cell culture of primary
 CC tissues, to increase or decrease differentiation or proliferation of
 CC embryonic stem cells, or to modulate mammalian characteristics or
 CC metabolism. Note: The sequence data for this patent was published in
 CC electronic format and is available from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 63 AA;

Query Match 90.9%; Score 30; DB 6; Length 63;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 Db 45 GYWS 49
 |||:|

RESULT 14
 ABR00271
 ID ABR00271 standard; protein; 63 AA.

```
XX ABR00271;
AC
XX
XX
DT 03-APR-2003 (first entry)
XX
XX DE
XX DE Human gene 139 encoded secreted protein HPRAL78, SEQ ID NO:560.
XX
XX Human; secreted protein; digestive disorder; gastrointestinal disorder;
KW mouth; oesophagus; stomach; small intestine; large intestine; liver;
KW biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;
KW immune disorder; inflammation; infection; wound healing; drug screening;
KW chromosome identification; chromosome mapping; cytostatic; gene therapy;
KW antiinflammatory; immunosuppressive; vulnery; chromosome 3p25.2.
XX
XX OS Homo sapiens.
XX
XX WO200276488-A1.
XX
XX PD 03-OCT-2002.
XX
XX PF 19-MAR-2002; 2002WO-US008276.
XX
XX 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2003-029900/02.
XX
XX N-PSDB; ABZ71450.
XX
XX New human secreted proteins and nucleic acids, useful for detecting,
PT preventing, diagnosing, prognosticating, treating and/or ameliorating
PT e.g. gastrointestinal diseases and disorders, or cancers.
XX
XX Claim 13; Page 1107; 1216pp; English.
XX
XX ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted
CC protein genes, and ABP00011-ABP00299 represent the proteins they encode.
CC ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The
CC invention also encompasses antibodies specific for the secreted proteins,
CC the use of the secreted proteins in drug screening, and recombinant
CC vectors and host cells comprising a nucleic acid of the invention. The
CC secreted proteins, nucleic acids encoding them, antibodies or antibody
CC fragments specific for the secreted proteins, and modulators of protein
CC activity are useful for diagnosing, treating, ameliorating or preventing
CC digestive disorders. Such conditions include disorders of the mouth,
CC oesophagus, stomach, small intestine, large intestine, liver, biliary
CC tract and pancreas, and include cancers of these organs and tissues. The
CC secreted proteins and their nucleic acids may also be used in the
CC treatment of immune disorders, inflammation, infection,
CC hyperproliferative disorders, and to promote wound healing. Nucleic acids
CC of the invention may be used for chromosome identification, chromosome
CC mapping, in gene therapy, for identifying individuals from minute
CC biological samples, as hybridisation probes, and as molecular weight
CC markers. The present sequence represents a human secreted protein of the
XX invention
XX
XX Sequence 63 AA;
Query Match 90.9%; Score 30; DB 6; Length 63;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYWMS 5
Db 45 GYWLS 49
RESULT 15
ADB91793
```

```
ADB91793 standard; protein; 63 AA.
XX
XX ADB91793;
AC
XX
XX DT 04-DEC-2003 (first entry)
XX
XX DE Human secreted protein #SEQ ID 739.
XX
XX Secreted protein; gene therapy; antidiabetic; diabetes; human.
KW
XX OS Homo sapiens.
XX
XX WO2003004622-A2.
XX
XX PD 16-JAN-2003.
XX
XX PF 19-MAR-2002; 2002WO-US008124.
XX
XX 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2003-229407/22.
XX
XX Nucleic acid encoding a human secreted protein is useful in diagnosing or
PT treating diabetes or conditions related to diabetes.
PT
XX
XX Claim 3; SEQ ID NO 739; 1537pp; English.
XX
XX The invention relates to isolated nucleic acid molecules ADB91065-
CC ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-
CC ADB91834. Also disclosed is a recombinant vector comprising a
CC polynucleotide of the invention, and a recombinant host cell comprising
CC the recombinant vector. The polypeptide of the invention is useful in
CC identifying a binding partner by contacting the polypeptide with a
CC binding partner, and determining whether the binding partner increases or
CC decreases activity of the polypeptide. The polypeptide, polynucleotide,
CC antibody or its fragment, agonist or antagonist are useful for preparing
CC a pharmaceutical composition for diagnosing or treating diabetes or
CC conditions related to diabetes. The present sequence is that of the human
CC immunoglobulin Fc portion used to generate fusion proteins, increasing
CC the stability of the fused protein as compared to the secreted protein
CC only. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 63 AA;
Query Match 90.9%; Score 30; DB 7; Length 63;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYWMS 5
Db 45 GYWLS 49
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OM protein - protein search, using sw model

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Title: US-09-674-716B-9

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Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 12: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	33	100.0	5	17 US-10-783-311-315	Sequence 315, App
3	33	100.0	10	16 US-10-327-598-450	Sequence 450, App
4	33	100.0	73	15 US-10-418-861B-57	Sequence 57, Appl
5	33	100.0	103	16 US-10-437-963-178878	Sequence 178878, App
6	33	100.0	132	17 US-10-783-311-279	Sequence 279, App
7	33	100.0	132	17 US-10-783-311-311	Sequence 311, App
8	33	100.0	504	16 US-10-437-963-128079	Sequence 128079, App
9	33	100.0	721	16 US-10-437-963-144813	Sequence 144813, App
10	33	100.0	1096	17 US-10-741-849-7179	Sequence 7179, App
11	30	90.9	64	14 US-10-144-929-162	Sequence 162, App
12	30	90.9	64	15 US-10-144-929-162	Sequence 162, App
13	30	90.9	77	15 US-10-424-599-231107	Sequence 231107, App

14	30	90.9	88	16	US-10-767-701-41902	Sequence 41902, A
15	30	90.9	95	16	US-10-767-701-53836	Sequence 53836, A
16	30	90.9	167	15	US-10-424-599-178190	Sequence 178190, App
17	30	90.9	181	15	US-10-289-762-900	Sequence 900, App
18	30	90.9	210	9	US-09-764-868-892	Sequence 892, App
19	30	90.9	229	15	US-10-424-599-210785	Sequence 210785, App
20	30	90.9	242	10	US-09-866-050A-393	Sequence 393, App
21	30	90.9	242	10	US-09-866-050A-502	Sequence 502, App
22	30	90.9	242	10	US-09-866-050A-625	Sequence 625, App
23	30	90.9	310	9	US-09-815-242-10910	Sequence 10910, A
24	30	90.9	310	15	US-10-282-122A-57347	Sequence 57347, A
25	30	90.9	315	15	US-10-369-493-18477	Sequence 18477, A
26	30	90.9	348	15	US-10-369-493-1130	Sequence 1130, App
27	30	90.9	381	16	US-10-437-963-149574	Sequence 149574, App
28	30	90.9	392	14	US-10-050-704-180	Sequence 180, App
29	30	90.9	392	14	US-10-144-929-156	Sequence 156, App
30	30	90.9	392	15	US-10-144-929-156	Sequence 156, App
31	30	90.9	392	16	US-10-798-512-180	Sequence 180, App
32	30	90.9	414	13	US-10-087-192-828	Sequence 828, App
33	30	90.9	419	16	US-10-437-963-141970	Sequence 141970, App
34	30	90.9	420	9	US-09-909-320-109	Sequence 109, App
35	30	90.9	420	9	US-09-909-088B-109	Sequence 109, App
36	30	90.9	420	9	US-09-905-291A-109	Sequence 109, App
37	30	90.9	420	9	US-09-902-853-109	Sequence 109, App
38	30	90.9	420	9	US-09-907-824-109	Sequence 109, App
39	30	90.9	420	9	US-09-907-841-109	Sequence 109, App
40	30	90.9	420	10	US-09-904-011-109	Sequence 109, App
41	30	90.9	420	10	US-09-903-640-109	Sequence 109, App
42	30	90.9	420	10	US-09-908-093-109	Sequence 109, App
43	30	90.9	420	10	US-09-906-742-109	Sequence 109, App
44	30	90.9	420	10	US-09-906-838-109	Sequence 109, App
45	30	90.9	420	10	US-09-907-613-109	Sequence 109, App

ALIGNMENTS

RESULT 1
US-10-783-311-283
; Sequence 283, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10783,311
; PRIOR FILING DATE: 2004-02-19
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-283

Query Match 100.0%; Score 33; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
|||
Db 1 GYWS 5

RESULT 2
US-10-783-311-315
; Sequence 315, Application US/10783311
; Publication No. US20050009136A1

; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 315
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-315

Query Match 100.0%; Score 33; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

*QY 1 GYWS 5
Db 1 GYWS 5

RESULT 3
US-10-327-598-450
; Sequence 450, Application US/10327598
; Publication No. US2004010139A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Hongliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 450
; LENGTH: 10
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-450

Query Match 100.0%; Score 33; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 33; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 GYWS 5
Db 6 GYWS 10

RESULT 4
US-10-418-861B-57
; Sequence 57, Application US/1041861B
; Publication No. US20040010131A1
; GENERAL INFORMATION:
; APPLICANT: da Silva, Ana Claudia Rasera
; APPLICANT: Farah, Shaker Chuck
; APPLICANT: Quaggio, Ronaldo Bento
; APPLICANT: Reinach, Fernando de Castro
; APPLICANT: Ferro, Jesus Aparecido
; APPLICANT: De Oliveira, Julio Cesar Franco
; APPLICANT: De Laia, Marcelo Luiz

; APPLICANT: Setubal Joao C.
; APPLICANT: Furlan, Luiz Roberto
; TITLE OF INVENTION: Isolated Xanthomonas nucleic acid molecules, proteins encoded th
; FILE REFERENCE: FAPESP 205.1 US
; CURRENT APPLICATION NUMBER: US/10/418,861B
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/374,620
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 85
; SEQ ID NO 57
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Xanthomonas
; FEATURE:
US-10-418-861B-57

Query Match 100.0%; Score 33; DB 15; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 GYWS 5
Db 6 GYWS 10

RESULT 5
US-10-437-963-178878
; Sequence 178878, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 178878
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Oryza sativa
; NAME/KEY: unsure
; LOCATION: (1)..(103)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_76394C.1.pgp
US-10-437-963-178878

Query Match 100.0%; Score 33; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 GYWS 5
Db 15 GYWS 19

RESULT 6
US-10-783-311-279
; Sequence 279, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon

; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 279
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-279

Query Match 100.0%; Score 33; DB 17; Length 132;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
| | | | |
Db 31 GYWS 35

RESULT 7
US-10-783-311-311
; Sequence 311, Application US/10783311
; Publication No. US2005009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 311
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-311

Query Match 100.0%; Score 33; DB 17; Length 132;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
| | | | |
Db 31 GYWS 35

RESULT 8
US-10-437-963-128079
; Sequence 128079, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128079
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(504)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_30468C.1.pap
US-10-437-963-128079

Query Match 100.0%; Score 33; DB 16; Length 504;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
| | | | |
Db 4 GYWS 8

RESULT 9
US-10-437-963-144813
; Sequence 144813, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 144813
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_45593C.1.pap
US-10-437-963-144813

Query Match 100.0%; Score 33; DB 16; Length 721;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
| | | | |
Db 319 GYWS 323

RESULT 10
US-10-741-849-7179
; Sequence 7179, Application US/10741849
; Publication No. US20050019931A1
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; APPLICANT: Use
; TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 10182-023-999
; CURRENT APPLICATION NUMBER: US/10/741,849

; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/434,832
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7179
; LENGTH: 1096
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-741-849-7179

Query Match 100.0%; Score 33; DB 17; Length 1096;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
Db 955 GYWMS 959

RESULT 11
US-10-144-929-162
; Sequence 162, Application US/10144929
; Publication No. US20030069405A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2014P1
; CURRENT APPLICATION NUMBER: US/10/144,929
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/09/251,329
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: PCT/US98/17044
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (64)
; OTHER INFORMATION: Xaa equals stop translation
US-10-144-929-162

Query Match 90.9%; Score 30; DB 14; Length 64;
Best Local Similarity 80.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
Db 45 GYWLS 49

RESULT 12
US-10-144-929-162
; Sequence 162, Application US/10144929
; Publication No. US20040014954A9
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2014P1
; CURRENT APPLICATION NUMBER: US/10/144,929
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/09/251,329
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: PCT/US98/17044
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 64

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (64)
; OTHER INFORMATION: Xaa equals stop translation
US-10-144-929-162

Query Match 90.9%; Score 30; DB 15; Length 64;
Best Local Similarity 80.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
Db 45 GYWLS 49

RESULT 13
US-10-424-599-231107
; Sequence 231107, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 231107
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_50710C.1.pap
US-10-424-599-231107

Query Match 90.9%; Score 30; DB 15; Length 77;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
Db 36 GYWLS 40

RESULT 14
US-10-767-701-41902
; Sequence 41902, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 41902
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(88)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3478-024-P1-K1-F2.pap

US-10-767-701-41902

Query Match 90.9%; Score 30; DB 16; Length 88;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
| | | | |
Db 70 GYWLS 74

RESULT 15

US-10-767-701-53836
; Sequence 53836, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 53836
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 13586731.pap
US-10-767-701-53836

Query Match 90.9%; Score 30; DB 16; Length 95;
Best Local Similarity 80.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
| | | | |
Db 16 GYWLS 20

Search completed: April 18, 2005, 14:54:42
Job time : 38.7907 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:01:43 ; Search time 13.6047 Seconds
(without alignments)
27.435 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA.*
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4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	466	4	US-09-489-039A-14325
2	33	100.0	637	4	US-09-248-796A-19134
3	30	90.9	43	2	US-08-488-161-39
4	30	90.9	43	3	US-09-273-685-39
5	30	90.9	43	5	PCT-US95-11934-39
6	30	90.9	181	4	US-09-198-452A-900
7	30	90.9	181	4	US-09-902-540-9914
8	30	90.9	238	4	US-09-902-540-13083
9	30	90.9	242	4	US-09-312-283C-393
10	30	90.9	243	3	US-09-134-001C-4114
11	30	90.9	334	4	US-09-134-000C-6029
12	30	90.9	383	4	US-09-252-991A-29457
13	30	90.9	396	4	US-09-252-991A-20263
14	30	90.9	408	4	US-09-107-532A-6992
15	30	90.9	414	4	US-09-949-016-6862
16	30	90.9	420	4	US-09-907-794A-109
17	30	90.9	420	4	US-09-905-125A-109
18	30	90.9	420	4	US-09-902-775A-109
19	30	90.9	420	4	US-09-906-700-109
20	30	90.9	420	4	US-09-903-603A-109
21	30	90.9	420	4	US-09-904-920A-109
22	30	90.9	420	4	US-09-909-064-109
23	30	90.9	420	4	US-09-905-381A-109
24	30	90.9	420	4	US-09-906-618-109
25	30	90.9	448	4	US-09-583-110-4257
26	30	90.9	452	4	US-09-107-433-4995
27	30	90.9	478	4	US-09-107-532A-6868

28	30	90.9	484	4	US-09-634-238-216	Sequence 216, Appl
29	30	90.9	534	4	US-09-107-532A-6549	Sequence 5549, Ap
30	30	90.9	538	4	US-09-489-039A-8363	Sequence 8363, Ap
31	30	90.9	667	4	US-09-315-127-5	Sequence 5, Appli
32	30	90.9	667	4	US-09-315-127-6	Sequence 6, Appli
33	30	90.9	667	4	US-09-070-630-13	Sequence 13, Appl
34	30	90.9	685	4	US-09-489-039A-12981	Sequence 12981, A
35	30	90.9	911	4	US-09-902-540-14901	Sequence 14901, A
36	30	90.9	1218	4	US-09-438-185A-837	Sequence 837, Appl
37	30	90.9	1498	4	US-09-792-616-9	Sequence 9, Appli
38	30	90.9	1503	4	US-09-792-616-3	Sequence 3, Appli
39	30	90.9	1503	4	US-09-647-140B-8	Sequence 8, Appli
40	29	87.9	5	2	US-08-480-434-22	Sequence 22, Appl
41	29	87.9	5	2	US-08-480-434-31	Sequence 31, Appl
42	29	87.9	5	2	US-08-053-451B-22	Sequence 22, Appl
43	29	87.9	5	2	US-08-053-451B-31	Sequence 31, Appl
44	29	87.9	14	1	US-08-204-656B-11	Sequence 11, Appl
45	29	87.9	14	1	US-08-470-702-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-489-039A-14325
; Sequence 14325, Application US/09489039A
; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489, 039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 14325

; LENGTH: 466

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-14325

Query Match 100.0%; Score 33; DB 4; Length 466;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
|||
Db 437 GYWS 441

RESULT 2

US-09-248-796A-19134
; Sequence 19134, Application US/09248796A
; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 19134

; LENGTH: 637

; TYPE: PRT

; ORGANISM: Candida albicans

; FEATURE:

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; NAME/KEY: UNSURE
; LOCATION: (338)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-19134

Query Match          100.0%; Score 33; DB 4; Length 637;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      496 GYWS 500

RESULT 3
US-08-488-161-39
; Sequence 39, Application US/08488161
; Patent No. 5885577
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Vernon L.
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
; TITLE OF INVENTION: Peptide Libraries
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,161
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-161-39

Query Match          90.9%; Score 30; DB 2; Length 43;
Best Local Similarity 80.0%; Pred. No. 95;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      6 GYWS 10

RESULT 4
US-09-273-685-39
; Sequence 39, Application US/09273685
; Patent No. 6015561
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Vernon L.
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
; TITLE OF INVENTION: Peptide Libraries
```

```
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/273,685
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,161
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-273-685-39

Query Match          90.9%; Score 30; DB 3; Length 43;
Best Local Similarity 80.0%; Pred. No. 95;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      6 GYWS 10

RESULT 5
PCT-US95-11934-39
; Sequence 39, Application PC/TUS9511934
; GENERAL INFORMATION:
; APPLICANT: Cytogen Corporation
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
; TITLE OF INVENTION: Peptide Libraries
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11934
; FILING DATE: 20-SEP-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
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	REFERENCE/DOCKET NUMBER: 1101-196-228	
:	TELECOMMUNICATION INFORMATION:	
:	TELEPHONE: (212) 790-9090	
:	TELEFAX: (212) 869-9741/8864	
:	TELEX: 66141 PENNIE	
:	INFORMATION FOR SEQ ID NO: 39:	
:	SEQUENCE CHARACTERISTICS:	
:	LENGTH: 43 amino acids	
:	TYPE: amino acid	
:	STRANDEDNESS: single	
:	TOPOLOGY: linear	
:	MOLECULE TYPE: peptide	
:	PCT-US95-11934-39	
	Query Match	90.9%; Score 30; DB 5; Length 43;
:	Best Local Similarity	80.0%; Pred. No. 95;
:	Matches	4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 GYWMS 5	
DB	6 GWLS 10	
	RESULT 6	
:	US-09-198-452A-900	
:	; Sequence 900, Application US/09198452A	
:	; Patent No. 6559294	
:	; GENERAL INFORMATION:	
:	; APPLICANT: Grifais, R.	
:	; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection	
:	; FILE REFERENCE: 9710-003-999	
:	; CURRENT APPLICATION NUMBER: US/09/198,452A	
:	; CURRENT FILING DATE: 1998-11-24	
:	; NUMBER OF SEQ ID NOS: 6849	
:	; SEQ ID NO 900	
:	; LENGTH: 181	
:	; TYPE: PRT	
:	; ORGANISM: Chlamydia pneumoniae	
:	; FEATURE:	
:	; NAME/KEY: SITE	
:	; LOCATION: 1...181	
:	; OTHER INFORMATION: Xaa=unknown or other	
:	US-09-198-452A-900	
	Query Match	90.9%; Score 30; DB 4; Length 181;
:	Best Local Similarity	80.0%; Pred. No. 3.6e+02;
:	Matches	4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 GYWMS 5	
DB	48 GWLS 52	
	RESULT 7	
:	US-09-902-540-9914	
:	; Sequence 9914, Application US/09902540	
:	; Patent No. 6833447	
:	; GENERAL INFORMATION:	
:	; APPLICANT: Goldman, Barry S.	
:	; APPLICANT: Hinkle, Gregory J.	
:	; APPLICANT: Slater, Steven C.	
:	; APPLICANT: Wiegand, Roger C.	
:	; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof	
:	; FILE REFERENCE: 38-10(15849)B	
:	; CURRENT APPLICATION NUMBER: US/09/902,540	
:	; CURRENT FILING DATE: 2001-07-10	
:	; PRIOR APPLICATION NUMBER: 60/217,883	
:	; PRIOR FILING DATE: 2000-07-10	
:	; NUMBER OF SEQ ID NOS: 16825	
:	; SEQ ID NO 9914	
:	; LENGTH: 181	
:	US-09-902-540-9914	
:	; ORGANISM: Myxococcus xanthus	
:	; GENERAL INFORMATION:	
:	; APPLICANT: Watson, James D.	
:	; APPLICANT: Strachan, Lorna	
:	; APPLICANT: Sleeman, Matthew	
:	; APPLICANT: Onrust, Rene	
:	; APPLICANT: Murison, James G.	
:	; APPLICANT: Kumble, Krishanand D.	
:	; TITLE OF INVENTION: Compositions Isolated from Skin Cells	
:	; FILE REFERENCE: 11000.1011C2	
:	; CURRENT APPLICATION NUMBER: US/09/312,283C	
:	; CURRENT FILING DATE: 1999-05-14	
:	; NUMBER OF SEQ ID NOS: 425	
:	; SOFTWARE: FastSeq for Windows Version 4.0	
:	; SEQ ID NO 393	
:	; LENGTH: 242	
:	; TYPE: PRT	
:	; ORGANISM: Mouse	
:	US-09-312-283C-393	
	Query Match	90.9%; Score 30; DB 4; Length 242;
:	Best Local Similarity	80.0%; Pred. No. 4.8e+02;
:	Matches	4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 GYWMS 5	

	REFERENCE/DOCKET NUMBER: 1101-196-228	
:	TELECOMMUNICATION INFORMATION:	
:	TELEPHONE: (212) 790-9090	
:	TELEFAX: (212) 869-9741/8864	
:	TELEX: 66141 PENNIE	
:	INFORMATION FOR SEQ ID NO: 39:	
:	SEQUENCE CHARACTERISTICS:	
:	LENGTH: 43 amino acids	
:	TYPE: amino acid	
:	STRANDEDNESS: single	
:	TOPOLOGY: linear	
:	MOLECULE TYPE: peptide	
:	PCT-US95-11934-39	
	Query Match	90.9%; Score 30; DB 5; Length 43;
:	Best Local Similarity	80.0%; Pred. No. 95;
:	Matches	4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 GYWMS 5	
DB	6 GWLS 10	
	RESULT 6	
:	US-09-198-452A-900	
:	; Sequence 900, Application US/09198452A	
:	; Patent No. 6559294	
:	; GENERAL INFORMATION:	
:	; APPLICANT: Grifais, R.	
:	; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection	
:	; FILE REFERENCE: 9710-003-999	
:	; CURRENT APPLICATION NUMBER: US/09/198,452A	
:	; CURRENT FILING DATE: 1998-11-24	
:	; NUMBER OF SEQ ID NOS: 6849	
:	; SEQ ID NO 900	
:	; LENGTH: 181	
:	; TYPE: PRT	
:	; ORGANISM: Chlamydia pneumoniae	
:	; FEATURE:	
:	; NAME/KEY: SITE	
:	; LOCATION: 1...181	
:	; OTHER INFORMATION: Xaa=unknown or other	
:	US-09-198-452A-900	
	Query Match	90.9%; Score 30; DB 4; Length 181;
:	Best Local Similarity	80.0%; Pred. No. 3.6e+02;
:	Matches	4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 GYWMS 5	
DB	48 GWLS 52	
	RESULT 7	
:	US-09-902-540-9914	
:	; Sequence 9914, Application US/09902540	
:	; Patent No. 6833447	
:	; GENERAL INFORMATION:	
:	; APPLICANT: Goldman, Barry S.	
:	; APPLICANT: Hinkle, Gregory J.	
:	; APPLICANT: Slater, Steven C.	
:	; APPLICANT: Wiegand, Roger C.	
:	; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof	
:	; FILE REFERENCE: 38-10(15849)B	
:	; CURRENT APPLICATION NUMBER: US/09/902,540	
:	; CURRENT FILING DATE: 2001-07-10	
:	; PRIOR APPLICATION NUMBER: 60/217,883	
:	; PRIOR FILING DATE: 2000-07-10	
:	; NUMBER OF SEQ ID NOS: 16825	
:	; SEQ ID NO 9914	
:	; LENGTH: 181	
:	US-09-902-540-9914	
:	; ORGANISM: Myxococcus xanthus	
:	; GENERAL INFORMATION:	
:	; APPLICANT: Watson, James D.	
:	; APPLICANT: Strachan, Lorna	
:	; APPLICANT: Sleeman, Matthew	
:	; APPLICANT: Onrust, Rene	
:	; APPLICANT: Murison, James G.	
:	; APPLICANT: Kumble, Krishanand D.	
:	; TITLE OF INVENTION: Compositions Isolated from Skin Cells	
:	; FILE REFERENCE: 11000.1011C2	
:	; CURRENT APPLICATION NUMBER: US/09/312,283C	
:	; CURRENT FILING DATE: 1999-05-14	
:	; NUMBER OF SEQ ID NOS: 425	
:	; SOFTWARE: FastSeq for Windows Version 4.0	
:	; SEQ ID NO 393	
:	; LENGTH: 242	
:	; TYPE: PRT	
:	; ORGANISM: Mouse	
:	US-09-312-283C-393	
	Query Match	90.9%; Score 30; DB 4; Length 242;
:	Best Local Similarity	80.0%; Pred. No. 4.8e+02;
:	Matches	4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 GYWMS 5	

	REFERENCE/DOCKET NUMBER: 1101-196-228	
:	TELECOMMUNICATION INFORMATION:	
:	TELEPHONE: (212) 790-9090	
:	TELEFAX: (212) 869-9741/8864	
:	TELEX: 66141 PENNIE	
:	INFORMATION FOR SEQ ID NO: 39:	
:	SEQUENCE CHARACTERISTICS:	
:	LENGTH: 43 amino acids	
:	TYPE: amino acid	
:	STRANDEDNESS: single	
:	TOPOLOGY: linear	
:	MOLECULE TYPE: peptide	
:	PCT-US95-11934-39	
	Query Match	90.9%; Score 30; DB 5; Length 43;
:	Best Local Similarity	80.0%; Pred. No. 95;
:	Matches	4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 GYWMS 5	
DB	6 GWLS 10	
	RESULT 6	
:	US-09-198-452A-900	
:	; Sequence 900, Application US/09198452A	
:	; Patent No. 6559294	
:	; GENERAL INFORMATION:	
:	; APPLICANT: Grifais, R.	
:	; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection	
:	; FILE REFERENCE: 9710-003-999	
:	; CURRENT APPLICATION NUMBER: US/09/198,452A	
:	; CURRENT FILING DATE: 1998-11-24	
:	; NUMBER OF SEQ ID NOS: 6849	
:	; SEQ ID NO 900	
:	; LENGTH: 181	
:	; TYPE: PRT	
:	; ORGANISM: Chlamydia pneumoniae	
:	; FEATURE:	
:	; NAME/KEY: SITE	
:	; LOCATION: 1...181	
:	; OTHER INFORMATION: Xaa=unknown or other	
:	US-09-198-452A-900	
	Query Match	90.9%; Score 30; DB 4; Length 181;
:	Best Local Similarity	80.0%; Pred. No. 3.6e+02;
:	Matches	4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 GYWMS 5	
DB	48 GWLS 52	
	RESULT 7	
:	US-09-902-540-9914	
:	; Sequence 9914, Application US/09902540	
:	; Patent No. 6833447	
:	; GENERAL INFORMATION:	
:	; APPLICANT: Goldman, Barry S.	
:	; APPLICANT: Hinkle, Gregory J.	
:	; APPLICANT: Slater, Steven C.	
:	; APPLICANT: Wiegand, Roger C.	
:	; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof	
:	; FILE REFERENCE: 38-10(15849)B	
:	; CURRENT APPLICATION NUMBER: US/09/902,540	
:	; CURRENT FILING DATE: 2001-07-10	
:	; PRIOR APPLICATION NUMBER: 60/217,883	
:	; PRIOR FILING DATE: 2000-07-10	
:	; NUMBER OF SEQ ID NOS: 16825	
:	; SEQ ID NO 9914	
:	; LENGTH: 181	
:	US-09-902-540-9914	
:	; ORGANISM: Myxococcus xanthus	
:	; GENERAL INFORMATION:	
:	; APPLICANT: Watson, James D.	
:	; APPLICANT: Strachan, Lorna	
:	; APPLICANT: Sleeman, Matthew	
:	; APPLICANT: Onrust, Rene	
:	; APPLICANT: Murison, James G.	
:	; APPLICANT: Kumble, Krishanand D.	
:	; TITLE OF INVENTION: Compositions Isolated from Skin Cells	
:	; FILE REFERENCE: 11000.1011C2	
:	; CURRENT APPLICATION NUMBER: US/09/312,283C	
:	; CURRENT FILING DATE: 1999-05-14	
:	; NUMBER OF SEQ ID NOS: 425	
:	; SOFTWARE: FastSeq for Windows Version 4.0	
:	; SEQ ID NO 393	
:	; LENGTH: 242	
:	; TYPE: PRT	
:	; ORGANISM: Mouse	
:	US-09-312-283C-393	
	Query Match	90.9%; Score 30; DB 4; Length 242;
:	Best Local Similarity	80.0%; Pred. No. 4.8e+02;
:	Matches	4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 GYWMS 5	

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Db      224 GYWS 228
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; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29457
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-29457

Query Match      90.9%; Score 30; DB 4; Length 383;
Best Local Similarity 80.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
||||:|
Db      228 GYWS 232

RESULT 13
US-09-252-991A-20263
; Sequence 20263, Application US/09252991A
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20263
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-20263

Query Match      90.9%; Score 30; DB 4; Length 396;
Best Local Similarity 80.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
||||:|
Db      40 GYWS 44

RESULT 14
US-09-107-532A-6992
; Sequence 6992, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC

Db      111 GYWS 115

RESULT 12
US-09-252-991A-29457
; Sequence 29457, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Db      224 GYWS 228
||||:|
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29457
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-29457

Query Match      90.9%; Score 30; DB 4; Length 383;
Best Local Similarity 80.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
||||:|
Db      228 GYWS 232

RESULT 13
US-09-252-991A-20263
; Sequence 20263, Application US/09252991A
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20263
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-20263

Query Match      90.9%; Score 30; DB 4; Length 396;
Best Local Similarity 80.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
||||:|
Db      40 GYWS 44

RESULT 14
US-09-107-532A-6992
; Sequence 6992, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC

Db      111 GYWS 115

RESULT 12
US-09-252-991A-29457
; Sequence 29457, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Search completed: April 18, 2005, 14:25:31
Job time : 18.6047 secs

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; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/107,532A
;   FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/085,598
;   FILING DATE: 14 May 1998
;   APPLICATION NUMBER: 60/051571
;   FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Ariniello, Pamela Deneke
;   REGISTRATION NUMBER: 40,489
;   REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (781)893-5007
;   TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6992:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 408 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     HYPOTHETICAL: YES
;     ORIGINAL SOURCE:
;       ORGANISM: Enterococcus faecium
;     FEATURE:
;       NAME/KEY: misc feature
;       LOCATION: (8) LOCATION 1...408
;   SEQUENCE DESCRIPTION: SEQ ID NO: 6992:
US-09-107-532A-6992
```

Query Match 90.9%; Score 30; DB 4; Length 408;
Best Local Similarity 80.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
Db 263 GYWMT 267

```

RESULT 15
US-09-949-016-6862
; Sequence 6862, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6862
;   LENGTH: 414
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-6862
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Query Match 90.9%; Score 30; DB 4; Length 414;
Best Local Similarity 80.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
Db 11 GYWLS 15

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:29:25 ; Search time 43 Seconds
(without alignments)
11.188 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 206

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	60.6	5	2 JH0253	gut pentapeptide -
2	16	48.5	5	2 A32516	cholecystokinin-5
3	13	39.4	4	2 S09478	globulin IV alpha
4	13	39.4	5	2 PT0308	Ig heavy chain CRD
5	11	33.3	3	3 F37196	bradykinin-potenti
6	11	33.3	4	2 A34626	RPCH-related neuro
7	11	33.3	4	2 B53284	T-cell receptor be
8	11	33.3	4	2 PT0661	T-cell receptor be
9	11	33.3	5	2 A60803	neuropeptide - sea
10	11	33.3	5	2 PT0281	Ig heavy chain CRD
11	11	33.3	5	2 PT0729	T-cell receptor be
12	11	33.3	5	2 PT0580	T-cell receptor be
13	11	33.3	5	3 G37196	bradykinin-potenti
14	9	27.3	3	3 I50412	gene p20K protein
15	9	27.3	4	2 A32480	achatin-1 - Giant
16	9	27.3	5	2 S70154	URF1 protein - Xan
17	9	27.3	5	2 B37325	pap fibrial regul
18	9	27.3	5	2 A37114	hypoxanthine phosph
19	9	27.3	5	2 B61445	Leu-enkephalin - b
20	9	27.3	5	2 A61445	Met-enkephalin - b
21	9	27.3	5	2 B61168	cocoonase (EC 3.4.
22	9	27.3	5	2 I40469	dnazX-like protein
23	8	24.2	3	3 GKHU	growth-modulating
24	8	24.2	4	2 I38888	COI intron 16 prot
25	8	24.2	4	2 PL0140	carbon-monoxide de
26	8	24.2	5	2 PT0278	Ig heavy chain CRD
27	8	24.2	5	2 S69237	surface protein te
28	7	21.2	3	3 A22565	R-phycoerythrin al
29	7	21.2	3	3 A43391	TRH-like tripeptid

30 7 21.2 3 3 S68328 blood cell protein
31 7 21.2 4 2 A37832 phenol 2-monooxyge
32 7 21.2 4 2 I61883 protamine PI - ora
33 7 21.2 4 2 PT0240 Ig heavy chain CRD
34 7 21.2 4 2 S43959 Ig mu chain V regi
35 7 21.2 4 2 I37013 protamine PI - Cer
36 7 21.2 4 2 I84439 tyrosine-melanocyt
37 7 21.2 4 2 A32039 protamine PI - sav
38 7 21.2 5 1 HOROHA proctolin - Americ
39 7 21.2 5 2 I39964 ribosomal protein
40 7 21.2 5 2 I39966 ribosomal protein
41 7 21.2 5 2 I39965 major protein anti
42 7 21.2 5 2 E60274 R-phycoerythrin ga
43 7 21.2 5 2 F22565 angiotensin-conver
44 7 21.2 5 2 PQ0009 photosystem I 10.4
45 7 21.2 5 2 PQ0689

ALIGNMENTS

RESULT 1

JH0253

gut pentapeptide - Japanese eel

C;Species: Anguilla japonica (Japanese eel)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995

C;Accession: JH0253

R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.

Biochem. Biophys. Res. Commun. 180, 828-832, 1991

A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.

A;Reference number: JH0253; MUID:92062113; PMID:1953755

A;Accession: JH0253

A;Molecule type: protein

A;Residues: 1-5 <UES>

A;Experimental source: gut

C;Comment: This peptide increased basal tone of the circular muscle of the esophagagast, and of the circular muscle of the gastro-intestinal junction.

Query Match 60.6%; Score 20; DB 2; Length 5;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3

Db 1 GFW 3

RESULT 2

A32516

cholecystokinin-5 - dog

N;Alternate names: CCK-5

C;Species: Canis lupus familiaris (dog)

C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000

C;Accession: A32516

R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H

Am. J. Physiol. 252, G272-G275, 1987

A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and inte

A;Reference number: A32516; MUID:87153871; PMID:3826354

A;Accession: A32516

A;Molecule type: protein

A;Residues: 1-5 <SHI>

C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecyst.

C;Superfamily: gastrin

C;Keywords: amidated carboxyl end; neuropeptide

F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 48.5%; Score 16; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WM 4

Db 2 WM 3

RESULT 3

S09478
 globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)
 N;Alternate names: IIS globulin alpha subunit gamma chain
 C;Species: Cucurbita sp. (cucurbit)
 C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996
 C;Accession: S09478
 R;Ohmura, M.; Hara, I.; Matsubara, H.
 Plant Cell Physiol. 21, 157-167, 1980
 A;Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and
 A;Reference number: S09066
 A;Accession: S09478
 A;Molecule type: protein
 A;Residues: 1-4 <OHM>

Query Match 39.4%; Score 13; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2
 ||
 3 GY 4

DB 3 GY 4

RESULT 4

PT0308
 Ig heavy chain CRD3 region (clone 6-88) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0308
 R;Ramada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A;Reference number: PT0222; MUID:91108337; PMID:1899102
 A;Accession: PT0308
 A;Molecule type: DNA
 A;Residues: 1-5 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match 39.4%; Score 13; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WMS 5
 ||
 2 WES 4

DB 2 WES 4

RESULT 5

F37196
 bradykinin-potentiating peptide 6 - island jararaca
 C;Species: Bothrops insularis (island jararaca)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: F37196
 R;Cintrá, A.C.O.; Vieira, C.A.; Giglio, J.R.
 J. Protein Chem. 9, 221-227, 1990
 A;Title: Primary structure and biological activity of bradykinin potentiating peptides
 A;Reference number: A37196; MUID:90351557; PMID:2386615
 A;Accession: F37196
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-3 <CIN>
 C;Keywords: pyroglutamic acid
 P;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 33.3%; Score 11; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3

DB 3 W 3

RESULT 6

A34626
 RPCH-related neuroptide - ferruginous spindle
 C;Species: Fuscus ferrugineus (ferruginous spindle)
 C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
 C;Accession: A34626
 R;Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;
 Blochem. Biophys. Res. Commun. 167, 273-279, 1990
 A;Title: A molluscan neuroptide related to the crustacean hormone, RPCH.
 A;Reference number: A34626; MUID:90179762; PMID:2310394
 A;Accession: A34626
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-4 <KUR>
 C;Keywords: neuroptide

Query Match 33.3%; Score 11; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
 ||
 4 W 4

DB 4 W 4

RESULT 7

B53284
 T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C;Accession: B53284
 R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
 Mol. Immunol. 28, 881-888, 1991
 A;Title: Evolutionarily conserved organization and sequences of germline diversity and
 A;Reference number: A53284; MUID:91342695; PMID:1678859
 A;Accession: B53284
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-4 <HAR>
 A;Cross-references: GB:S60737; NID:q233916; PIDN:AAB19518.1; PID:q233918
 A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
 C;Keywords: T-cell receptor

Query Match 33.3%; Score 11; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
 ||
 2 W 2

DB 2 W 2

RESULT 8

PT0661
 T-cell receptor beta chain V-D-J region (121-18V) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
 C;Accession: PT0661
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0661
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FE>
 A;Cross-references: UNIPROT:Q8BZQ7; UNIPROT:Q8CCN5
 A;Experimental source: day 4 postnatal thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 33.3%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
DB 3 W 3

RESULT 9
A60803
neuropeptide - sea anemone (Anthopleura elegantissima)
C;Species: Anthopleura elegantissima
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A60803
R;Graff, D.; Grimmelikhuijzen, C.J.P.
Brain Res. 442, 354-358, 1988
A;Title: Isolation of <Glu-Ser-Lu-Arg-Trp-NH-2, a novel neuropeptide from sea anemones.
A;Reference number: A60803; MUID:88222764; PMID:2897223
A;Accession: A60803
A;Molecule type: protein
A;Residues: 1-5 <GRA>
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 33.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
DB 5 W 5

RESULT 10
PT0281
Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0281
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0281
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
DB 4 W 4

RESULT 11
PT0729
T-cell receptor beta chain V-D-J region (120-1J) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0640; PT0685; PT0729
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0640
A;Status: translation not shown

Query Match 33.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
DB 4 W 4

Query Match 33.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
DB 4 W 4

A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: newborn thymus, strain BALB/c, clone 120-1J
A;Accession: PT0685
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-1C
A;Accession: PT0729
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE3>
A;Experimental source: newborn thymus, strain BALB/c, clone 135-1AG
C;Keywords: T-cell receptor

Query Match 33.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
DB 5 W 5

RESULT 12
PT0580
T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0580
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0580
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 33.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
DB 4 W 4

RESULT 13
G37196
bradykinin-potentiating peptide 7 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C;Accession: G37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Accession: G37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <CIN>
A;Cross-references: UNIPROT:P30425
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 33.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3

Db 3 W 3

RESULT 14

I50412
 gene p20K protein - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C/Accession: I50412
 R;Mao, P.L.; Beauchemin, M.; Bedard, P.A.
 J. Biol. Chem. 268, 8131-8139, 1993
 A;Title: Quiescence-dependent activation of the p20K promoter in growth-arrested chicken
 A;Reference number: A46643; MUID:93216790; PMID:8463325
 A;Accession: I50412
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-3 <MAO>
 A;Cross-references: GB:I02537; NID:G212616; PID:G212617
 C;Genetics:
 A;Gene: p20K

Query Match 27.3%; Score 9; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MS 5
 ||
 Db 1 MS 2

RESULT 15

A32480
 achatin-I - giant African snail
 N;Contains: achatin-II
 C;Species: Achatina fulica (giant African snail)
 C>Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 09-Jul-2004
 C/Accession: A32480
 R;Kamatani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.; Sun
 Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989
 A;Title: Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica feru
 A;Reference number: A32480; MUID:89273551; PMID:2597281
 A;Accession: A32480
 A;Molecule type: protein
 A;Residues: 1-4 <KAM>
 A;Cross-references: UNIPROT:P35904
 A;Note: stereochemistry of the active form confirmed by chemical synthesis
 R;Ishida, T.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nomoto
 FEBS Lett. 307, 253-256, 1992
 A;Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous neuro
 (H-Gly-Phe-Ala-Asp-OH).
 A;Reference number: A46691; MUID:92354723; PMID:1644179
 A;Contents: annotation; X-ray crystallography, 0.85 angstroms
 A;Note: achatin-II has L-phenylalanine
 C;Keywords: D-amino acid
 F;2/Modified site: D-phenylalanine (Phe) #status experimental

Query Match 27.3%; Score 9; DB 2; Length 4;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GY 2
 ||
 Db 1 GF 2

Search completed: April 18, 2005, 15:39:08
 Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:21:19 ; Search time 178 Seconds
(without alignments)
14.384 Million cell updates/sec

Title: US-09-674-716B-9
Perfect score: 33
Sequence: 1 GYMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 53

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	45.5	4	1 OCP3 OCTMI	P58649 octopus min
2	15	45.5	5	1 UF01 MOUSE	P38639 mus musculus
3	11	33.3	2	1 GWA SEPOF	P83570 sepiia offic
4	11	33.3	5	1 BpP7 BOTIN	P30425 bothrops in
5	10	30.3	5	1 PAP2 PARMA	P81864 pardachirus
6	10	30.3	5	1 RE32 LITRU	P82073 litoria rub
7	9	27.3	4	1 ACHI ACHFU	P35904 achatina fu
8	9	27.3	4	1 OCP1 OCTMI	P58648 octopus min
9	8	24.2	3	1 GRWV HUMAN	P01157 homo sapien
10	8	24.2	4	1 DCML PSECH	P19316 pseudomonas
11	7	21.2	4	1 FAR3 HIRME	P42562 hirudo medi
12	7	21.2	4	1 FAR3 HIRME	P42563 hirudo medi
13	7	21.2	4	1 FYRI ANTEL	P58706 anthopleura
14	7	21.2	4	2 Q96AT0	O96at0 homo sapien
15	7	21.2	5	1 AL14 CARMA	P81817 carcinus ma
16	7	21.2	5	1 FARP ARTTR	P41853 artiposthi
17	7	21.2	5	1 PRCT CARMA	P67857 carcinus ma
18	7	21.2	5	1 PRCT LIMPO	P67858 limulus pol
19	7	21.2	5	1 PRCT PERAM	P67859 periplaneta
20	7	21.2	5	1 PSK DAUCA	P58261 daucus caro
21	6	18.2	4	1 DCMS PSECH	P19318 pseudomonas
22	6	18.2	4	1 EOSI HUMAN	P02731 homo sapien
23	6	18.2	4	1 FMRF MACNI	P01162 macrocallis
24	6	18.2	5	1 AP21 EISFO	P84182 eisenia foe
25	6	18.2	5	1 BIOA CITFR	P13071 citrobacter
26	6	18.2	5	1 BIOB CITFR	P12997 citrobacter
27	6	18.2	5	1 TPIS CANFA	P54714 canis famli
28	6	18.2	5	1 UX4A CHLTR	P38005 chlamydia t
29	6	18.2	5	2 Q99007	Q99007 hordeum vul
30	5	15.2	4	1 ILME SEPOF	P83568 sepiia offic
31	5	15.2	5	1 EI03 LITRU	P82099 litoria rub

32	5	15.2	5	2 P83073	P83073 bacillus ce
33	4	12.1	4	1 FFKA ANTEL	P58705 anthopleura
34	4	12.1	4	1 YLMI YEAST	P36515 saccharomyc
35	4	12.1	5	1 MPA4 JUNVI	P81826 juniperus v
36	4	12.1	5	1 RE11 LITRU	P82070 litoria rub
37	4	12.1	5	1 RE21 LITRU	P82071 litoria rub
38	4	12.1	5	1 RE31 LITRU	P82072 litoria rub
39	4	12.1	5	1 UC22 MAIZE	P80628 zea mays (m
40	3	9.1	4	1 FLRF HIRME	P42561 hirudo medi
41	3	9.1	4	1 FLRN ANTEL	P58707 anthopleura
42	3	9.1	4	2 Q16047	Q16047 homo sapien
43	3	9.1	5	1 EI04 LITRU	P82100 litoria rub
44	3	9.1	5	1 FARP CHICK	P83308 gallus gall
45	3	9.1	5	1 SUGA_ACHDO	P19991 acheta dome

ALIGNMENTS

RESULT 1
OCP3 OCTMI STANDARD; PRT; 4 AA.
AC P58649;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cardioactive peptides Ocp-3/Ocp-4.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-4 is a 1000 time less active
CC than Ocp-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=WALDI; RANGE=1-4; NOTE=Ref.1.
KW D-amino acid; Direct protein sequencing; Hormone.
FT MOD RES 2 2 D-serine (in form Ocp-4).
SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 45.5%; Score 15; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYW 3
Db 1 GSW 3

RESULT 2
UF01 MOUSE STANDARD; PRT; 5 AA.
ID UF01 MOUSE
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;

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RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separative and sequencing of familial and novel murine proteins using
RT preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.6, its MW is: 19 kDa.
KW Direct protein sequencing.
FT NON_TER 5
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 45.5%; Score 15; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GW 3
DB 3 GRW 5

RESULT 3
ID GWA SEPOF STANDARD; PRT; 2 AA.
AC P83570;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neuropeptide GWA.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidae; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN (1)
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Optic lobe;
RX MEDLINE=98100358; PubMed=9437704; DOI=10.1016/S0196-9781(97)00241-6;
RA Henry J., Favrel P., Boucaud-Camou E.;
RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related
RT peptide inhibiting the motility of the mature oviduct in the
RT cuttlefish, Sepia officinalis.";
RL Peptides 18:1469-1474(1997).
CC -1- FUNCTION: Regulatory neuropeptide with myotropic activity
CC targeting the distal oviduct. Inhibits the motility of the oviduct
CC by decreasing tonus, frequency and amplitude of contractions.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI; RANGE=1-2; NOTE=Ref.1.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 2 2 Tryptophan amide.
SQ SEQUENCE 2 AA; 261 MW; 7378100000000000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
DB 2 W 2

RESULT 4
ID BPP7 BOTIN STANDARD; PRT; 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylidae; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;

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RN SEQUENCE.
RP TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it. It acts
CC as an indirect hypotensive agent.
DR PIR; G37196; G37196.
KW Direct protein sequencing; Hypotensive agent;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
DB 3 W 3

RESULT 5
ID PAP2 PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea mores sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleioidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN (1)
RP SEQUENCE.
RX TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea mores sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -1- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels in
CC membranes. At high concentration causes cell membrane lysis.
CC -1- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pardaxin family.
KW Direct protein sequencing; Toxin.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.6e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GW 3
DB 1 GFF 3

RESULT 6
ID RE32 LITRU STANDARD; PRT; 5 AA.
AC P82073;

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DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Rubellidin 3.2.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria rubella. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
 CC activity.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 KW Amphibian defense peptide; Direct protein sequencing.
 SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;
 Query Match 30.3%; Score 10; DB 1; Length 5;
 Best Local Similarity 33.3%; Pred. No. 1.6e+06;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYW 3
 |::
 Db 2 GFF 4

RESULT 7
 ACH1 ACHFU
 ID ACH1 ACHFU STANDARD; PRT; 4 AA.
 AC P35904;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Achatin-I.
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE CHARACTERIZATION, AND SYNTHESIS.
 RC STRAIN=Perussac; TISSUE=Ganglion;
 RX MEDLINE=89273551; PubMed=2597281;
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
 RT fulica Perussac containing a D-amino acid residue.";
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN=Perussac; TISSUE=Heart atrium;
 RX MEDLINE=91264856; PubMed=1675568;
 RA Fujimoto K., Kubota A., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
 RA Yoshida M., Harada I., Muneoka Y., Kobayashi M.;
 RT "Purification of achatin-I from the atria of the African giant snail,
 RT Achatina fulica, and its possible function.";
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
 RN [3]
 RP CRYSTALLIZATION.
 RX MEDLINE=93014529; PubMed=1399265;
 RA Ihida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
 RA Iwashita T., Nomoto K.;
 RT "Crystal structure and molecular conformation of achatin-I (H-Gly-D-
 RT Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid
 RT residue.";
 RL Int. J. Pept. Protein Res. 39:258-264(1992).

CC -1- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency
 CC and produces a spike broadening of the identified heart excitatory
 CC neuron (PON); also enhances the amplitude and frequency of the
 CC heart beat. Has also an effect on several other muscles.
 DR PIR; A32480; A32480.
 KW D-amino acid; Direct protein sequencing; Hormone.
 FT MOD RES 2 2 D-phenylalanine.
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;
 Query Match 27.3%; Score 9; DB 1; Length 4;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GY 2
 |:
 Db 1 GF 2

RESULT 8
 OCP1 OCTMI
 ID OCP1 OCTMI STANDARD; PRT; 4 AA.
 AC P58678;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cardioactive peptides Ocp-1/Ocp-2.
 OS Octopus minor (Octopus).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
 OX NCBI_TaxID=89766;
 RN [1]
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
 RC TISSUE=Brain;
 RX MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;
 RA Iwakoshi E., Hisada M., Minakata H.;
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
 RT Octopus minor.";
 RL Peptides 21:623-630(2000).
 CC -1- FUNCTION: Cardioactive; has both positive chronotropic and
 CC inotropic effects on the heart. Ocp-2 is a 1000 time less active
 CC than Ocp-1.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Ocp-2 has L-Phe instead of D-Phe.
 CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
 KW D-amino acid; Direct protein sequencing; Hormone.
 FT MOD RES 2 2 D-phenylalanine (in form Ocp-1).
 SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;
 Query Match 27.3%; Score 9; DB 1; Length 4;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GY 2
 |:
 Db 1 GF 2

RESULT 9
 GRWM HUMAN
 ID GRWM HUMAN STANDARD; PRT; 3 AA.
 AC P01157;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Growth-modulating peptide.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77162369; PubMed=858356;
 RA Schlesinger D.H., Pickart L., Thaler M.M.;

RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
 RL Experientia 33:324-325(1977).
 CC -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate
 CC growth of some cell types and to inhibit other types in vitro.
 CC GO: GO:0001558; P:regulation of cell growth; NAS.
 KW Direct protein sequencing.
 SQ SEQUENCE 3 AA; 340 MW; 6331E810000000000 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 3;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2
 |:
 Db 1 GH 2

RESULT 10
 DCML_PSECH STANDARD; PRT; 4 AA.
 AC P19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
 DE dehydrogenase subunit L) (CO-DH L) (Fragment).
 GN Name-cuL;
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae.
 ON NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydohydrophic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
 CC -!- COFACTOR: Binds 1 copper(I) ion, 1 molybdenum(VI) ion and 1
 CC molybdopterin cytosine dinucleotide (MCD) per subunit.
 CC -!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small
 CC subunit.
 DR PIR; P10140; P10140.
 KW Direct protein sequencing; Molybdenum; Oxidoreductase.
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F00000000 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 4;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2
 |:
 Db 2 GH 3

RESULT 11
 FAR3_HIRME STANDARD; PRT; 4 AA.
 ID FAR3_HIRME STANDARD; PRT; 4 AA.
 AC P42562;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FMRPamide-like neuropeptide YLRP-amide.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
 ON NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)
 CC family.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 4 4 Phenylalanine amide.
 SQ SEQUENCE 4 AA; 598 MW; 69D4073B300000000 CRC64;

Query Match 21.2%; Score 7; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2
 |:
 Db 1 Y 1

RESULT 12
 FAR4_HIRME STANDARD; PRT; 4 AA.
 ID FAR4_HIRME STANDARD; PRT; 4 AA.
 AC P42563;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FMRPamide-like neuropeptide YMRP-amide.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
 ON NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)
 CC family.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 4 4 Phenylalanine amide.
 SQ SEQUENCE 4 AA; 616 MW; 69D4068B300000000 CRC64;

Query Match 21.2%; Score 7; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2
 |:
 Db 1 Y 1

RESULT 13
 FVRI_ATEL STANDARD; PRT; 4 AA.
 ID FVRI_ATEL STANDARD; PRT; 4 AA.
 AC P58706;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Antho-Riamide I [Contains: Antho-Riamide II].
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthaeae; Actiniidae; Anthopleura.
 ON NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=92270459; PubMed=1821096; DOI=10.1016/0196-9781(91)90190-Z;
 RA Notherker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
 RA Grimmeikhuijzen C.J.P.;
 RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
 RT biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its des-

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RT phenyllactyl fragment Tyr-Arg-Ile-NH2." ;
RL Peptides 12:1165-1173(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Notherker H.-P., Gimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Rhamide and Antho-Rhamide." ;
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron specific.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT CHAIN 1 4 Antho-Rhamide I.
FT CHAIN 2 4 Antho-Rhamide II.
FT MOD_RES 1 1 3-phenyllactic acid.
FT MOD_RES 4 4 Isoleucine amide.
SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 21.2%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2
DB 2 Y 2

RESULT 14
Q96ATO PRELIMINARY; PRT; 4 AA.
AC Q96ATO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FLJ30656 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
TISSUE=Lung;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016791; AAI16791.2;
SQ SEQUENCE 4 AA; 512 MW; 633DCB56F0000000 CRC64;
```

```
Query Match 21.2%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2
DB 2 Y 2

RESULT 15
AL14_CARMA STANDARD; PRT; 5 AA.
ID AL14_CARMA
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carcinustatin 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
TISSUE=Cerebral ganglion, and Thoracic ganglion;
RC MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas." ;
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -1- SIMILARITY: Belongs to the allatostatin family.
KW Amidation; Direct protein sequencing; Multigene family; Neuropeptide.
FT MOD_RES 5 5 Leucine amide (Potential).
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 21.2%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2
DB 1 Y 1

Search completed: April 18, 2005, 15:38:14
Job time : 180 secs
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:20:24 ; Search time 167 Seconds
(without alignments)
11.580 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYVMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 45841

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	33	100.0	5	3	AAY32257
2	29	87.9	5	2	AAR62882
3	27	81.8	5	2	AAR97316
4	27	81.8	5	2	AAY05038
5	27	81.8	5	4	AAB61293
6	27	81.8	5	5	AAU75739
7	27	81.8	5	5	AAOI17609
8	27	81.8	5	6	ABU11259
9	27	81.8	5	7	ADC82794
10	27	81.8	5	8	ADL27482
11	27	81.8	5	8	ADM95105
12	27	81.8	5	8	ADM98314
13	27	81.8	5	8	ADO36523
14	27	81.8	5	8	ADO36535
15	27	81.8	5	8	ADO15171
16	27	81.8	5	8	ADR15143
17	25	75.8	5	2	AAR76079
18	24	72.7	4	5	AAE22200
19	24	72.7	4	8	ADJ38912
20	24	72.7	5	2	AAR85499
21	24	72.7	5	2	AAW23429
22	24	72.7	5	2	AAW93474
23	24	72.7	5	4	AAB62861
24	24	72.7	5	5	ABB07357
25	24	72.7	5	8	ADM10172

26	24	72.7	5	8	ADM10201
27	24	72.7	5	8	ADR19265
28	24	72.7	5	8	ADR71367
29	24	72.7	5	8	ADR71338
30	23	69.7	5	2	AAR74931
31	23	69.7	5	2	AAR74929
32	23	69.7	5	2	AAW24546
33	23	69.7	5	2	AAW83024
34	23	69.7	5	2	AAW62192
35	23	69.7	5	2	AAW57588
36	23	69.7	5	2	AAW44181
37	23	69.7	5	2	AAW02550
38	23	69.7	5	2	AAW89632
39	23	69.7	5	2	AAW05045
40	23	69.7	5	3	AAB14741
41	23	69.7	5	3	AAW90891
42	23	69.7	5	3	AAV77518
43	23	69.7	5	3	AAW80139
44	23	69.7	5	3	AAB12174
45	23	69.7	5	3	AAW92158

ALIGNMENTS.

RESULT 1

AAW32257

ID AAY32257 standard; peptide; 5 AA.

XX

AC AAY32257;

XX

DT 15-FEB-2000 (first entry)

XX

DE Light chain CDR H1 of mouse anti-CD23 Mab C11.

XX

KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;

KW monoclonal antibody; chimeric antibody; humanised antibody;

KW complementarity determining region; CDR; autoimmune disease;

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;

KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

KW urticaria; nephrotic syndrome; glomerulonephritis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;

KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;

KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;

XX therapy.

XX

OS Mus musculus.

XX

PN WO958679-A1.

XX

PD 18-NOV-1999.

XX

PF 07-MAY-1999; 99WO-GB001434.

XX

PR 09-MAY-1998; 98GB-00009839.

XX

PA (GLAX) GLAXO GROUP LTD.

XX

PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX

DR WPI; 2000-053101/04.

XX

DR N-PSDB; AA234742.

XX

PT Cell receptor specific antibodies useful for treating e.g. arthritis,

XX diabetes, multiple sclerosis and psoriasis.

XX

PS Claim 1; Page 40; 81pp; English.

XX

CC This sequence represents complementarity determining region 1 (CDR H1)

CC of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11

CC (see also AAY32263). The invention provides altered antibodies, such as

CC chimeric or humanised antibodies, which comprise sufficient of the amino

CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on
 CC haematopoietic cells. The antibodies are used to block soluble CD23
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They
 CC are also useful for studying interactions between CD23 and various
 CC ligands and determining the binding agents
 XX
 SQ Sequence 5 AA;

Query Match 100.0%; Score 33; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
 |||||
 DB 1 GYWMS 5

RESULT 2

AAR62882
 ID AAR62882 standard; peptide; 5 AA.

XX AAR62882;

XX 25-MAR-2003 (revised)

DT 18-JUL-1995 (first entry)

XX Murine anti-human atherosclerotic plaque MAb Z2D3 VH CDR1.

DE Atherosclerosis; atherosclerotic plaque; anti-hydroxysteroid antibody;
 KW murine monoclonal antibody; heavy chain variable region: CDR1;
 KW complementarity determining region; imaging; plaque ablation.
 XX

OS Mus musculus.

XX Key Location/Qualifiers
 FH Region 1..5
 FT /label= CDR1

XX WO9425053-A1.

XX 10-NOV-1994.

XX 26-APR-1994; 94WO-US004641.

XX 26-APR-1993; 93US-00053451.

XX (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.

XX Ditlow CC, Chen FW, Calenoff B;

XX WPI; 1994-357904/44.

DR N-PSDB; AAQ78734.

XX New antigen comprising hydroxy:steroid and quat. ammonium salt - and
 PT related antibodies, useful e.g. for imaging, ablating or treating
 PT atherosclerotic plaque, and detecting plaque specific antibodies.

XX Claim 199; Page 147; 288pp; English.

XX Mice were immunised with an extract of human atherosclerotic plaque, then
 CC spleen cells were fused with SP2/01-Ag-14 myeloma cells. Hybridomas were
 CC screened by ELISA for reactivity with the immunogen and clone Z2D3 was
 CC isolated. The Z2D3 antibody reacts specifically with atherosclerotic
 CC tissue; it recognises a non-protein antigen containing cholesterol (or
 CC similar steroid that is a substrate for cholesterol oxidase) and a
 CC quaternary ammonium salt (pref. a phosphatidylcholine or related compound

CC that is a substrate for phospholipase C). The CDR sequences for the heavy
 CC and light chains of Z2D3 were determined; peptides comprising the CDRs
 CC are claimed, including chimeric (CDR-grafted) murine-human antibodies.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 5 AA;

Query Match 87.9%; Score 29; DB 2; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
 |||||
 DB 1 GFWMS 5

RESULT 3

AAR97316
 ID AAR97316 standard; peptide; 5 AA.

XX AAR97316;

XX 15-OCT-1996 (first entry)

XX Humanised monoclonal antibody heavy chain CDR.

XX Monoclonal antibody; humanised; mouse; framework region; FR; CDR;

KW complementary determining region; anti-carcinoembryonic antigen; CEA;
 KW diagnosis; imaging; therapy; immune response.

XX Mus musculus.

XX WO9611013-A1.

XX 18-APR-1996.

XX 28-SEP-1995; 95WO-US011964.

XX 05-OCT-1994; 94US-00318157.

XX (IMMU-) IMMUNOMEDICS INC.

XX Hansen HJ, Armour KL;

XX WPI; 1996-209653/21.

XX New humanised anti-CEA monoclonal antibody - having engrafted murine
 PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.

XX Claim 5; Page 38; 62pp; English.

XX New humanised monoclonal antibodies (MAbs) comprising the complementary
 CC determining regions (CDRs) of a parental murine class III anti-
 CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
 CC heterologous antibody which can be derived from any species including
 CC human, retain the anti-CEA binding specificity of the parental murine MAb
 CC but are less immunogenic in a human subject than the parental MAb. The
 CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
 CC -producing cancers and patients receiving the humanised antibodies and
 CC conjugates show improved therapeutic results, decreased immune responses
 CC and decreased immune-mediated adverse effects compared to the parent
 CC antibody. This sequence is a murine derived CDR region which corresponds
 CC to CDR 1 in the heavy chain of the humanised MAb. See AAR97313-97333

XX Sequence 5 AA;

Query Match 81.8%; Score 27; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
 |||||
 DB 2 YWMS 5

XX	Human; antibody; scFv; CDR; complementarity determining region; TANGO 268; cadiant; cerebroprotective; cytosatic; anticoagulant; thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW	platelet membrane glycoprotein receptor; bleeding disorder;
KW	blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW	ischaemia; cardiovascular disease; immunological disease; liver disorder
KW	cancer.
XX	
OS	Homo sapiens.
XX	
PN	WO200100810-A1.
XX	
XX	04-JAN-2001.
PD	
XX	30-JUN-2000; 2000WO-US018152.
XX	
XX	30-JUN-1999; 99US-00345468.
PR	06-DEC-1999; 99US-00454824.
PR	14-FEB-2000; 2000US-00503387.
PR	
XX	(MILL-) MILLENNIUM PHARM INC.
PA	
XX	
PI	Busfield SJ, Vilelalel J, Jandrot-Perrus M, Vainchenker W;
PI	Gill DS, Qian MD, Kingsbury G;
XX	
XX	WPI; 2001-080877/09.
XX	
PT	New genes encoding human platelet-expressed collagen receptor.
PT	glycoprotein VI, and its modulators, useful for preventing, treating and
PT	diagnosing hemorrhagic disorders, thrombotic diseases and immunological
PT	disorders.
XX	
XX	Claim 31; Page 102; 227pp; English.
XX	
CC	The present sequence is given in a specification relating to an isolated
CC	nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC	glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
CC	and polypeptides and their modulators, e.g. antisense nucleic acids,
CC	ribozymes and antibodies, are useful for preventing, treating and
CC	diagnosing disorders associated with aberrant expression or activity of
CC	GPVI. These disorders include bleeding disorders (e.g.
CC	thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.
CC	thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
CC	coronary artery and cerebral artery diseases (e.g. stroke and ischaemia)
CC	cardiovascular diseases (e.g. atherosclerosis and myocardial infarction)
CC	immunological diseases (e.g. platelet disorder) and embryonic liver
CC	disorders. Preferably they are used to prevent acute cardiac ischaemia
CC	following angioplasty and metastatic cancers, especially of the colon and
CC	liver
XX	
SQ	Sequence 5 AA;
Query Match	81.8%; Score 27; DB 4; Length 5;
Best Local Similarity	100.0%; Pred.No.1.8e+06;
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	2 YWMS 5
Db	2 YWMS 5
RESULT 6	
AAU75739	
ID	AAU75739 standard; peptide; 5 AA.
XX	
AC	AAU75739;
XX	
XX	
DT	08-MAY-2002 (first entry)
XX	
DE	Anti-(MCP)-1 antibody heavy chain protein hypervariable region CDR1.
XX	
KW	Human; antibody; MCP; monocyte chemoattractant; antiasthmatic;

KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KW cardiovascular disease; angina pectoris; myocardial infarction;
 KW coronary restenosis; atherosclerosis; immunological disorder;
 KW developmental disorder; embryonic disorder; liver disorder;
 KW cerebral vascular disease; venous thromboembolism disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200280968-A1.
 XX
 XX 17-OCT-2002.
 XX
 XX
 XX 09-APR-2002; 2002WO-US011122.
 XX
 XX 09-APR-2001; 2001US-00829495.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Busfield SJ, Valleval J, Jandrot-Perrus M, Vainchencker W;
 PI Gill DS, Qian DM, Kingsbury G;
 XX
 XX WPI; 2003-058477/05.
 XX
 XX Novel substantially purified antibody immunospecifically binding to TANGO
 PT 268 antigen, useful for treating bleeding disorders such as
 PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.
 XX
 PS Disclosure; Page 111; 236pp; English.
 XX
 CC This invention relates to a novel purified antibody comprising a variable
 CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
 CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
 CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
 CC The antibodies of the invention act to decrease or block TANGO 268
 CC binding to extracellular matrix components, or as a collagen or platelet
 CC release and aggregation blocker. The antibodies of the invention are
 CC useful for modulating proliferation, migration, morphology,
 CC differentiation and/or function of megakaryocytes and platelets,
 CC including during development e.g. embryogenesis, modulating leukocyte-
 CC platelet and platelet-endothelium interactions in inflammation and/or
 CC thrombosis, and modulating platelet aggregation and degranulation. They
 CC are also useful for modulating disorders associated with abnormal or
 CC aberrant megakaryocyte and/or platelet proliferation, migration,
 CC morphology, differentiation and/or function, e.g. bleeding disorders such
 CC as thrombocytopenia. Other diseases which may be modulated by these
 CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
 CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
 CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
 CC coronary diseases (e.g. cardiovascular diseases including angina
 CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
 CC etc); immunological disorders, developmental disorders, embryonic
 CC disorders, liver disorders, cerebral vascular diseases, venous
 CC thromboembolism disease, coronary diseases, and metastatic cancers. The
 CC antibodies of the invention only causes a transient decrease in platelet
 CC counts, platelet aggregation, and/or platelet activation and so have some
 CC advantages over prior art methods. The present sequence represents a
 CC peptide sequence used to generate the antibodies of the invention
 XX
 SQ Sequence 5 AA;
 Query Match 81.8%; Score 27; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YNWS 5
 Db |||||
 2 YNWS 5
 RESULT 9
 ADC82794
 ID ADC82794 standard; peptide; 5 AA.

XX ADC82794;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE CDR region #3 in heavy chain of human Fab fragment.
 XX
 KW Binding molecule; selective affinity; ligand;
 KW anti-immunoglobulin reagent; phage expressed antibody library;
 KW tumour antigen; complementarity determining region; CDR; human disease;
 KW cellular pathology; human; Fab; heavy chain.
 XX
 OS Homo sapiens.
 XX
 XX US2003044772-A1.
 XX
 XX 06-MAR-2003.
 XX
 XX 15-OCT-2001; 2001US-00977797.
 XX
 XX 04-AUG-1997; 97US-0113667P.
 PR
 PR 04-AUG-1998; 98US-00129026.
 XX
 XX (MOLE-) APPLIED MOLECULAR EVOLUTION.
 PA
 XX Watkins JD, Huse WD, Wu H;
 PI
 PI WPI; 2003-625402/59.
 DR
 DR N-PSDB; ADC82793.
 XX
 XX
 PT Identifying binding molecules having selective affinity for ligands for
 PT discovering reagents for treating diseases, by contacting solid support
 PT coated with anti-immunoglobulin reagent, to a phage expressed antibody
 PT library.
 XX
 XX Example 5; Page 16; 26pp; English.
 PS
 CC The present invention relates to a method for identifying a binding
 CC molecule having selective affinity for a ligand. The method involves
 CC providing a solid support coated with an anti-immunoglobulin reagent, and
 CC a phage expressed antibody library, and contacting the solid support to
 CC the phage expressed antibody library. The invention also discloses a
 CC method for identifying an antibody having selective affinity for a
 CC tumour, and a complementarity determining region (CDR) of an antibody
 CC selective for a tumour antigen. The methods of the invention are useful
 CC for identifying a binding molecule having selective affinity for a
 CC ligand, for the discovery of specific reagents for diagnosis and
 CC treatment of human diseases, for identifying binding molecules to, for
 CC example tumour cells or other cellular pathologies for the selective
 CC targeting of therapeutic agents, or for the identification of binding
 CC molecules to normal or diseased tissues for the selective targeting of,
 CC for example diagnostic agents such as imaging reagents. The methods are
 CC rapid and efficient for the identification of binding molecules which
 CC exhibit selective affinity for one or more ligands of interest. The
 CC methods allow the simultaneous screening of multiple binding molecules
 CC against multiple ligands of interest. Moreover, very little information
 CC is required regarding the identity or function of either the binding
 CC molecule or the ligand. For example diverse populations of binding
 CC molecules can be simultaneously screened against diverse populations of
 CC ligands to rapidly identify numerous molecules exhibiting a desired
 CC binding specificity. The methods provide improved sensitivity and
 CC specificity of detection through the selective immobilisation of the
 CC binding molecule population on a solid support. The present sequence
 CC represents a CDR region in the heavy chain of human Fab fragment.
 XX
 SQ Sequence 5 AA;
 Query Match 81.8%; Score 27; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YNWS 5
 |||||

Db 2 YWMS 5

RESULT 10
ADL27482
ID ADL27482 standard; peptide; 5 AA.
XX
AC ADL27482;
XX
DT 20-MAY-2004 (first entry)
XX
DE CDR from the heavy chain of antibody EGP16D8-1-2.
XX
KW glycoprotein; EGP6D8-1-1; EGP13F6-1-2; EGP13C6-1-1;
KW Ebola virus infection; antibody; heavy chain;
KW Complementarity determining region; CDR.
XX
OS Mus sp.
XX
PN WO2004018649-A2.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-US027450.
XX
PR 23-AUG-2002; 2002US-00226795.
XX
PA (USSA) US ARMY MEDICAL RES INST INFECTIOUS DISE.
XX
PI Hart MK, Wilson JA;
XX
DR WPI; 2004-226835/21.
XX
PT New isolated monoclonal antibody that binds Ebola virus GP, which
PT monoclonal antibody comprises a heavy chain variable region, useful for
PT treating or ameliorating Ebola virus infection.
XX
PS Claim 31; Page 64; 68pp; English.
XX
CC The specification describes monoclonal antibodies that bind Ebola virus
CC glycoprotein. The antibodies are EGP6D8-1-1, EGP13F6-1-2, and EGP13C6-1-
CC 1. The monoclonal antibodies of the invention are useful for treating or
CC ameliorating an Ebola virus infection. The antibodies were found to be
CC effective when administered 2 days after challenge. After significant
CC viral replication had occurred. ADL27482-ADL27484 represents
CC complementarity determining regions (CDRs) from the heavy chain of a
CC monoclonal antibody of the invention.
XX
SQ Sequence 5 AA;

Query Match 81.8%; Score 27; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
Db 2 YWMS 5
|||

RESULT 11
ADM95105
ID ADM95105 standard; peptide; 5 AA.
XX
AC ADM95105;
XX
DT 15-JUL-2004 (first entry)
XX
DE Murine MN-14 Mab heavy chain variable region CDR1.
XX
KW non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW complementarity determining region; pancreatic cancer; breast cancer;
KW ovarian cancer.
XX

OS Mus sp.
XX
PN WO2004032962-A1.
XX
PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-364813/34.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Claim 6; SEQ ID NO 23; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the CDR1 of
CC the murine MN-14 antibody heavy chain variable region and used to
CC generate the humanised/chimeric antibody of the invention.
XX
SQ Sequence 5 AA;

Query Match 81.8%; Score 27; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
Db 2 YWMS 5
|||

RESULT 12
ADM98314
ID ADM98314 standard; peptide; 5 AA.
XX
AC ADM98314;
XX
DT 15-JUL-2004 (first entry)
XX
DE Humanised murine MN-14 antibody heavy chain variable region CDR1 peptide.
XX
KW carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; humanised;
KW murine; mouse; antibody; MN-14; non-medullary thyroid carcinoma;
KW medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW hepatocellular carcinoma; breast cancer; lung cancer;
KW antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW apoptosis.
XX
OS Mus sp.
XX
DT Synthetic.
XX
PN WO2004032857-A2.
XX
PD 22-APR-2004.
XX
PF 08-OCT-2003; 2003WO-US031801.
XX
PR 08-OCT-2002; 2002US-0416531P.

```

PR 11-OCT-2002; 2002WO-US032307.
XX 02-MAY-2003; 2003US-0467161P.
PA (IMMU-) IMMUNOMEDICS INC.
XX Goldenberg DM, Hansen HJ;
XX WPI; 2004-340797/31.
XX
XX Treating non-medullary or medullary thyroid carcinoma, involves
PT administering to subject, either concurrently or sequentially, anti-
PT carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
XX Claim 8; Page 76; 122pp; English.
XX
XX This invention relates to methods for treating cancers that express
XX carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
XX therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
XX antibodies that can be used following administration of an agent that
XX will increase antibody effector functions or following administration of
XX an amount of interferon effective to upregulate CEA expression in tumour
XX cells. The present invention describes the anti-CEA antibody as a class
XX III humanised murine monoclonal antibody that retains specificity for CEA
XX binding and is preferably an MN-14 antibody or fragment thereof.
XX Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
XX composition useful for the treatment of non-medullary or medullary
XX thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
XX carcinoma, as well as breast or lung cancer. Furthermore, it can
XX stimulate antibody-dependent cell-mediated cytotoxicity, complement-
XX mediated lysis and apoptosis as well as inhibit cell cycle progression,
XX cell growth and angiogenesis. This peptide sequence is a CDR region of
XX the humanised murine MN-14 antibody of the invention.
XX
XX Sequence 5 AA;
XX
XX Query Match 81.8%; Score 27; DB 8; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 YWMS 5
XX DB |||||
XX 2 YWMS 5
XX
XX RESULT 13
XX ADO36523
XX ID ADO36523 standard; peptide; 5 AA.
XX AC ADO36523;
XX XX
XX DT 12-AUG-2004 (first entry)
XX XX
XX DE Human anti-heparanase 13B2 VH CDR1 SEQ ID NO:37.
XX
XX human; monoclonal antibody; heparanase; heparanase inhibitor;
XX anti-heparanase antibody; cytostatic; immunosuppressive; antiarthritic;
XX antiasthmatic; antiinflammatory; dermatological; antiarteriosclerotic;
XX neuroprotective; nontropic; heparanase antagonist; cancer; tumour;
XX melanoma; lymphoma; prostate carcinoma; pancreatic carcinoma;
XX bladder carcinoma; fibrosarcoma; rhabdomyosarcoma; mastocytoma;
XX mammary adenocarcinoma; leukaemia; rheumatoid fibroblast;
XX autoimmune disease; arthritis; asthma; lupus erythematosus;
XX allograft rejection; vascular restenosis; atherosclerosis;
XX Alzheimer's disease.
XX
XX Homo sapiens.
XX OS
XX XX
XX PN WO2004043989-A2.
XX XX
XX PD 27-MAY-2004.
XX XX
XX PF 05-NOV-2003; 2003WO-US035464.
XX XX
XX PR

```

```

PR 07-NOV-2002; 2002US-0424803P.
XX (MEDA-) MEDAREX INC.
XX (CELL-) CELLTECH R & D.
XX
XX Huang H, Holmes S, Mason S;
XX WPI; 2004-411694/38.
XX
XX New human monoclonal antibody to heparanase, for use in treating or
PT preventing cancer, autoimmune disease, arthritis, asthma, lupus
PT erythematosus, allograft rejection, atherosclerosis, and Alzheimer's
PT disease.
XX
XX Claim 14; SEQ ID NO 37; 108pp; English.
XX
XX The present invention describes an isolated human monoclonal antibody
XX which binds to and inhibits activity of human heparanase. Human anti-
XX heparanase antibodies of the present invention have cytostatic,
XX immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,
XX dermatological, antiarteriosclerotic, neuroprotective and nontropic
XX activities, and can be used as heparanase antagonists. The antibody,
XX methods and compositions of the present invention are useful in treating
XX or preventing cancer or tumours, e.g. melanoma, lymphoma, prostate
XX carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,
XX rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a
XX rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus
XX erythematosus, allograft rejection, vascular restenosis, atherosclerosis,
XX and Alzheimer's disease. The present sequence represents a human anti-
XX heparanase CDR amino acid sequence, which is used in the exemplification
XX of the present invention.
XX
XX Sequence 5 AA;
XX
XX Query Match 81.8%; Score 27; DB 8; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 YWMS 5
XX DB |||||
XX 2 YWMS 5
XX
XX RESULT 14
XX ADO36535
XX ID ADO36535 standard; peptide; 5 AA.
XX AC ADO36535;
XX XX
XX DT 12-AUG-2004 (first entry)
XX XX
XX DE Human anti-heparanase IE7 VH CDR1 SEQ ID NO:49.
XX
XX human; monoclonal antibody; heparanase; heparanase inhibitor;
XX anti-heparanase antibody; cytostatic; immunosuppressive; antiarthritic;
XX antiasthmatic; antiinflammatory; dermatological; antiarteriosclerotic;
XX neuroprotective; nontropic; heparanase antagonist; cancer; tumour;
XX melanoma; lymphoma; prostate carcinoma; pancreatic carcinoma;
XX bladder carcinoma; fibrosarcoma; rhabdomyosarcoma; mastocytoma;
XX mammary adenocarcinoma; leukaemia; rheumatoid fibroblast;
XX autoimmune disease; arthritis; asthma; lupus erythematosus;
XX allograft rejection; vascular restenosis; atherosclerosis;
XX Alzheimer's disease.
XX
XX Homo sapiens.
XX OS
XX XX
XX PN WO2004043989-A2.
XX XX
XX PD 27-MAY-2004.
XX XX
XX PF 05-NOV-2003; 2003WO-US035464.
XX XX
XX PR 07-NOV-2002; 2002US-0424803P.
XX

```

XX PA (MEDA-) MEDAREX INC.
 XX PA (CELL-) CELLTECH R & D.
 XX PI Huang H, Holmes S, Mason S;
 XX XX WPI; 2004-411694/38.
 XX DR
 XX XX
 XX PT New human monoclonal antibody to heparanase, for use in treating or
 PT preventing cancer, autoimmune disease, arthritis, asthma, lupus
 PT erythematous, allograft rejection, atherosclerosis, and Alzheimer's
 PT disease.
 XX PT
 XX PS Claim 14; SEQ ID NO 49; 108pp; English.
 XX XX
 XX CC The present invention describes an isolated human monoclonal antibody
 CC which binds to and inhibits activity of human heparanase. Human anti-
 CC heparanase antibodies of the present invention have cytostatic,
 CC immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,
 CC dermatological, antiarteriosclerotic, neuroprotective and neurotropic
 CC activities, and can be used as heparanase antagonists. The antibody,
 CC methods and compositions of the present invention are useful in treating
 CC or preventing cancer or tumors, e.g. melanoma, lymphoma, prostate
 CC carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,
 CC rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a
 CC rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus
 CC erythematous, allograft rejection, vascular restenosis, atherosclerosis,
 CC and Alzheimer's disease. The present sequence represents a human anti-
 CC heparanase CDR amino acid sequence, which is used in the exemplification
 CC of the present invention.
 XX CC
 XX SQ Sequence 5 AA;

Query Match 81.8%; Score 27; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
 ||||
 Db 2 YWMS 5

RESULT 15

ADR15171
 ID ADR15171 standard; peptide; 5 AA.
 XX AC ADR15171;
 XX DT 21-OCT-2004 (first entry)
 XX DE Anti-protein C inhibitor antibody heavy chain CDR1 peptide #2.
 XX KW anti-protein C inhibitor antibody; anti-PCI antibody;
 KW activated protein C; aPC; sepsis; disseminated intravascular coagulation;
 KW arterial thrombosis; protein C inhibitor; heavy chain; CDR1.
 XX OS Unidentified.
 XX FN WO2004065418-A1.
 XX PD 05-AUG-2004.
 XX PF 20-JAN-2004; 2004WO-JP000429.
 XX PR 20-JAN-2003; 2003JP-00011529.
 XX XX (CHUS) CHUGAI SEIYAKU KK.
 XX PI Koga T, Kimura N, Yoshino T, Ono K;
 XX WPI; 2004-593430/57.
 XX PT New anti-protein C inhibitor (PCI) antibody, inhibiting PCI with respect

PT to activation protein C (apc) activity, and apc production by
 PT thrombin/thrombomodulin composite, useful for treating sepsis, arterial
 PT thrombosis.
 XX PS Claim 4; SEQ ID NO 52; 105pp; Japanese.
 XX CC The invention comprises anti-protein C inhibitor (PCI) antibody. The anti-
 CC -PCI antibody of the invention is useful for treating or preventing a
 CC disease which develops and/or progresses due to reduced activated protein
 CC C (apc) activity. Such diseases include: sepsis, disseminated
 CC intravascular coagulation, and arterial thrombosis. The present amino
 CC acid sequence represents an anti-protein C inhibitor antibody peptide of
 CC the invention.

XX SQ Sequence 5 AA;

Query Match 81.8%; Score 27; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
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 Db 2 YWMS 5

Search completed: April 18, 2005, 15:35:15
 Job time : 179 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:38:19 ; Search time 130 Seconds
(without alignments)
12.783 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370693 residues

Total number of hits satisfying chosen parameters: 22949

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	5	17 US-10-783-311-283	Sequence 283, App
2	33	100.0	5	17 US-10-783-311-315	Sequence 315, App
3	27	81.8	5	9 US-09-832-312-61	Sequence 61, Appl
4	27	81.8	5	9 US-09-253-794-23	Sequence 23, Appl
5	27	81.8	5	10 US-09-977-797A-76	Sequence 76, Appl
6	27	81.8	5	11 US-09-829-495-61	Sequence 61, Appl
7	27	81.8	5	15 US-10-226-795-23	Sequence 23, Appl
8	27	81.8	5	16 US-10-703-714-37	Sequence 37, Appl
9	27	81.8	5	16 US-10-703-714-49	Sequence 49, Appl
10	27	81.8	5	16 US-10-680-734-23	Sequence 23, Appl
11	27	81.8	5	17 US-10-842-011-15	Sequence 15, Appl
12	27	81.8	5	17 US-10-842-011-30	Sequence 30, Appl
13	24	72.7	4	10 US-09-948-004-32	Sequence 32, Appl

14	24	72.7	5	9 US-09-192-854-151	Sequence 151, App
15	24	72.7	5	9 US-09-968-561A-265	Sequence 265, App
16	24	72.7	5	10 US-09-155-106-1	Sequence 1, Appli
17	24	72.7	5	10 US-09-968-744A-265	Sequence 265, App
18	24	72.7	5	11 US-09-968-561A-265	Sequence 265, App
19	24	72.7	5	15 US-10-436-549-496	Sequence 496, App
20	24	72.7	5	15 US-10-436-549-525	Sequence 525, App
21	24	72.7	5	16 US-10-297-371A-4	Sequence 4, Appli
22	24	72.7	5	16 US-10-745-102-2	Sequence 2, Appli
23	24	72.7	5	16 US-10-712-425-496	Sequence 496, App
24	24	72.7	5	16 US-10-712-425-525	Sequence 525, App
25	24	72.7	5	17 US-10-783-311-91	Sequence 91, Appl
26	24	72.7	5	17 US-10-842-011-9	Sequence 9, Appli
27	24	72.7	5	17 US-10-879-994-70	Sequence 70, Appl
28	24	72.7	5	17 US-10-808-538-1	Sequence 1, Appli
29	24	72.7	5	17 US-10-773-032-496	Sequence 496, App
30	24	72.7	5	17 US-10-773-032-525	Sequence 525, App
31	24	72.7	5	17 US-10-903-858-19	Sequence 19, Appl
32	23	69.7	5	9 US-09-748-960-12	Sequence 12, Appl
33	23	69.7	5	9 US-09-832-312-49	Sequence 49, Appl
34	23	69.7	5	9 US-09-770-002-1	Sequence 1, Appli
35	23	69.7	5	9 US-09-423-800-62	Sequence 62, Appl
36	23	69.7	5	10 US-09-977-797A-90	Sequence 90, Appl
37	23	69.7	5	10 US-09-269-921-6	Sequence 6, Appli
38	23	69.7	5	10 US-09-509-098-8	Sequence 8, Appli
39	23	69.7	5	11 US-09-829-495-49	Sequence 49, Appl
40	23	69.7	5	14 US-10-182-018-62	Sequence 62, Appl
41	23	69.7	5	14 US-10-216-484-2	Sequence 2, Appli
42	23	69.7	5	14 US-10-169-003-62	Sequence 62, Appl
43	23	69.7	5	14 US-10-218-253-6	Sequence 6, Appli
44	23	69.7	5	14 US-10-337-981-62	Sequence 62, Appl
45	23	69.7	5	14 US-10-384-933-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-783-311-283
; Sequence 283, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10783,311
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-283

Query Match 100.0%; Score 33; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
|||
Db 1 GYWS 5

RESULT 2
US-10-783-311-315
; Sequence 315, Application US/10783311
; Publication No. US20050009136A1

GENERAL INFORMATION:
APPLICANT: Nixon, Andrew
TITLE OF INVENTION: PAPP-A LIGANDS
FILE REFERENCE: 10280-059001
CURRENT APPLICATION NUMBER: US/10/783,311
CURRENT FILING DATE: 2004-02-19
PRIOR APPLICATION NUMBER: US 60/448,515
PRIOR FILING DATE: 2003-02-19
NUMBER OF SEQ ID NOS: 394
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 315
LENGTH: 5
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-315

Query Match 100.0%; Score 33; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|||||
Db 1 GYWMS 5

RESULT 3
US-09-832-312-61
Sequence 61, Application US/09832312
Patent No. US20010049829A1
GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 61
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
US-09-832-312-61

Query Match 81.8%; Score 27; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
|||||
Db 2 YWMS 5

RESULT 4
US-09-253-794-23
Sequence 23, Application US/09253794
Patent No. US20020018750A1
GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CBA HUMANIZED
MOUSE MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,794
FILING DATE: 22-Feb-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,157
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-253-794-23

Query Match 81.8%; Score 27; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
|||||
Db 2 YWMS 5

RESULT 5
US-09-977-797A-76
Sequence 76, Application US/09977797A
Publication No. US2003004472A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffrey D.
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
FILE REFERENCE: AME-06805
CURRENT APPLICATION NUMBER: US/09/977,797A
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: 09/129,026
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 08/905,825
PRIOR FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 136
SOFTWARE: PatentIn version 3.1
SEQ ID NO 76
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
US-09-977-797A-76

Query Match 81.8%; Score 27; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
|
|
|
|
Db 2 YWMS 5

RESULT 6

US-09-829-495-61
; Sequence 61, Application US/09829495
; Publication No. US2004001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-61

Query Match 81.8%; Score 27; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
|
|
|
|
Db 2 YWMS 5

RESULT 7

US-10-226-795-23
; Sequence 23, Application US/10226795
; Publication No. US20040053865A1
; GENERAL INFORMATION:
; APPLICANT: HART, MARY KATE
; APPLICANT: WILSON, JULIE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
; FILE REFERENCE: ARMY 166
; CURRENT APPLICATION NUMBER: US/10/226,795
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 23
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
; OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence
US-10-226-795-23

Query Match 81.8%; Score 27; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
|
|
|
|
Db 2 YWMS 5

RESULT 8

US-10-703-714-37
; Sequence 37, Application US/10703714
; Publication No. US20040170630A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Haichun
; APPLICANT: Holmes, Steven
; APPLICANT: Mason, Sean
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE
; FILE REFERENCE: MXI-294
; CURRENT APPLICATION NUMBER: US/10/703,714
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 60/424803
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-703-714-37

Query Match 81.8%; Score 27; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
|
|
|
|
Db 2 YWMS 5

RESULT 9

US-10-703-714-49
; Sequence 49, Application US/10703714
; Publication No. US20040170630A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Haichun
; APPLICANT: Holmes, Steven
; APPLICANT: Mason, Sean
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE
; FILE REFERENCE: MXI-294
; CURRENT APPLICATION NUMBER: US/10/703,714
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 60/424803
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-703-714-49

Query Match 81.8%; Score 27; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
|
|
|
|
Db 2 YWMS 5

RESULT 10

US-10-680-734-23
; Sequence 23, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
; APPLICANT: GOLDENBERG, DAVID M.

```
; APPLICANT: HANSEN, HANS J.
; TITLE OF INVENTION: ANTIBODY THERAPY
; FILE REFERENCE: 40923-0051US5
; CURRENT APPLICATION NUMBER: US/10/680,734
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: 60/467,161
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: PCT/US02/32307
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/416,531
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 23
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus sp.
;
US-10-680-734-23

Query Match      81.8%; Score 27; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 YWMS 5
      ||||
Db      2 YWMS 5

RESULT 11
US-10-842-011-15
; Sequence 15, Application US/10842011
; Publication No. US20050025763A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
; FILE REFERENCE: 05882.0110.NPUS04
; CURRENT APPLICATION NUMBER: US/10/842,011
; CURRENT FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo Sapiens
;
US-10-842-011-15

Query Match      81.8%; Score 27; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 YWMS 5
      ||||
Db      2 YWMS 5

RESULT 12
US-10-842-011-30
; Sequence 30, Application US/10842011
; Publication No. US20050025763A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
; FILE REFERENCE: 05882.0110.NPUS04
; CURRENT APPLICATION NUMBER: US/10/842,011
; CURRENT FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo Sapiens
;
US-10-842-011-30

Query Match      81.8%; Score 27; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 YWMS 5
      ||||
Db      2 YWMS 5

RESULT 13
US-09-948-004-32
; Sequence 32, Application US/09948004
; Publication No. US20030017979A1
; GENERAL INFORMATION:
; APPLICANT: MACK, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
;
US-09-948-004-32

Query Match      72.7%; Score 24; DB 10; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 YWMS 5
      |||
Db      1 YWMN 4

RESULT 14
US-09-192-854-151
; Sequence 151, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 151
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-192-854-151

Query Match      72.7%; Score 24; DB 9; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYMS 5
      |||
Db      1 GYMS 5

RESULT 15
US-09-968-561A-265
; Sequence 265, Application US/09968561A
; Patent No. US2002016462A1
```

GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 265
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-265

Query Match 72.7%; Score 24; DB 9; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5
Db 1 GYWS 5

Search completed: April 18, 2005, 15:50:47
Job time : 131 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:31:43 ; Search time 40 Seconds
(without alignments)
9.331 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 27945

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	87.9	5	2	US-08-480-434-22
2	29	87.9	5	2	US-08-480-434-31
3	29	87.9	5	2	US-08-053-451B-22
4	29	87.9	5	2	US-08-053-451B-31
5	27	81.8	5	1	US-08-244-626-12
6	27	81.8	5	2	US-08-480-434-32
7	27	81.8	5	2	US-08-318-157B-23
8	27	81.8	5	2	US-08-053-451B-32
9	27	81.8	5	4	US-09-253-794-23
10	25	75.8	5	1	US-08-353-400-27
11	24	72.7	4	4	US-09-948-004-32
12	24	72.7	5	4	US-08-753-750B-38
13	24	72.7	5	4	US-09-508-413A-28
14	24	72.7	5	4	US-09-192-854-151
15	24	72.7	5	4	US-09-155-106-1
16	24	72.7	5	6	5185431-15
17	24	72.7	5	6	5185431-15
18	23	69.7	5	1	US-08-318-970B-1
19	23	69.7	5	1	US-08-318-370B-3
20	23	69.7	5	3	US-09-406-532-5
21	23	69.7	5	3	US-08-479-089A-7
22	23	69.7	5	4	US-07-669-545B-7
23	23	69.7	5	4	US-09-091-071-6
24	23	69.7	5	4	US-09-269-921-6
25	20	60.6	4	1	US-07-869-933-21
26	20	60.6	4	3	US-09-103-663-21
27	20	60.6	5	2	US-08-476-176B-50

28 20 60.6 5 3 US-08-127-721A-50 Sequence 50, Appl
29 20 60.6 5 3 US-08-485-246A-50 Sequence 50, Appl
30 20 60.6 5 4 US-09-424-712-20 Sequence 20, Appl
31 20 60.6 5 4 US-09-688-188B-40 Sequence 40, Appl
32 20 60.6 5 4 US-09-628-665-8 Sequence 8, Appl
33 20 60.6 5 4 US-09-291-417D-40 Patent No. 5217869
34 20 60.6 5 6 5217869-8 Patent No. 5217869
35 20 60.6 5 6 5217869-8 Patent No. 5217869
36 19 57.6 4 4 US-09-069-827A-173 Sequence 173, Appl
37 19 57.6 5 3 US-08-469-141A-64 Sequence 64, Appl
38 19 57.6 5 3 US-07-987-264-1 Sequence 1, Appl
39 19 57.6 5 3 US-09-382-689A-4 Sequence 4, Appl
40 19 57.6 5 4 US-08-877-605-9 Sequence 9, Appl
41 19 57.6 5 4 US-08-877-605-14 Sequence 14, Appl
42 19 57.6 5 4 US-09-254-180C-1 Sequence 1, Appl
43 19 57.6 5 5 PCT-US95-13794-64 Sequence 64, Appl
44 19 57.6 5 6 5217869-44 Patent No. 5217869
45 19 57.6 5 6 5217869-44 Patent No. 5217869

ALIGNMENTS

RESULT 1
US-08-480-434-22
; Sequence 22, Application US/08480434
; Patent No. 5811248
; GENERAL INFORMATION:
; APPLICANT: Charles C. Ditlow, et al.
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,434
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-053
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-480-434-22

Query Match 87.9%; Score 29; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYWS 5
|:|

Db 1 GFWMS 5

RESULT 2

US-08-480-434-31
; Sequence 31, Application US/08480434
; Patent No. 5811248
; GENERAL INFORMATION:
; APPLICANT: Charles C. Ditlow, et al.
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,434
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; US-08-480-434-31

Query Match 87.9%; Score 29; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5

Db 1 GFWMS 5

RESULT 3

US-08-053-451B-22
; Sequence 22, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Ditlow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

Query Match 87.9%; Score 29; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5

Db 1 GFWMS 5

; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
; US-08-053-451B-22

Query Match 87.9%; Score 29; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5

Db 1 GFWMS 5

RESULT 4

US-08-053-451B-31
; Sequence 31, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Ditlow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEX: 66141 PENNIE

US-08-053-451B-31
; Sequence 31, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Ditlow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEX: 66141 PENNIE

US-08-053-451B-31
; Sequence 31, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Ditlow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-053-451B-31

Query Match 87.9%; Score 29; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
|:|
Db 1 GFWMS 5

RESULT 5
US-08-244-626-12
Sequence 12, Application US/08244626
Patent No. 5502167
GENERAL INFORMATION:
APPLICANT: Waldmann, Herman
APPLICANT: Walsh, Louise
APPLICANT: Crowe, James Scott
APPLICANT: Lewis, Alan Peter
TITLE OF INVENTION: CDR GRAFTED HUMANISED CHIMERIC T-CELL
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c.
STREET: 555 Thirteenth Street, N. W.
CITY: Washington
STATE: D. C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,626
FILING DATE: July 15, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02251
FILING DATE: December 4, 1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-153A
TELEPHONE: (202) 763-6040
TELEFAX: (202) 763-6031
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-244-626-12

Query Match 81.8%; Score 27; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
||||

Db 2 YWMS 5

RESULT 6
US-08-480-434-32
Sequence 32, Application US/08480434
Patent No. 5811248
GENERAL INFORMATION:
APPLICANT: Charles C. Dittlow, et al.
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
ANTIBODIES THEREOF, AND USES THEREOF
TITLE OF INVENTION: 88
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,434
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-053
TELEPHONE: (415) 854-3660
TELEFAX: (415) 854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-480-434-32

Query Match 81.8%; Score 27; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
||||
Db 2 YWMS 5

RESULT 7
US-08-318-157B-23
Sequence 23, Application US/08318157B
Patent No. 5874540
GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
APPLICANT: ARMOUR, Kathryn L.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
ANTIBODIES
TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/318,157B
;; FILING DATE: 05-OCT-1994
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SAXE, Bernhard D.
;; REGISTRATION NUMBER: 28,665
;; REFERENCE/DOCKET NUMBER: 18733/464
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; TYPE: amino acid
;; LENGTH: 5 amino acids
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-318-157B-23

Query Match 81.8%; Score 27; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
Db 2 YWMS 5

RESULT 8
US-08-053-451B-32
; Sequence 32, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Ditlow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acids
; LENGTH: 5 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: DNA
;; HYPOTHETICAL: N
;; ANTI-SENSE: N
;; US-08-053-451B-32

Query Match 81.8%; Score 27; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
Db 2 YWMS 5

RESULT 9
US-09-253-794-23
; Sequence 23, Application US/09253794
; Patent No. 6676924
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-253-794-23

Query Match 81.8%; Score 27; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
Db 2 YWMS 5

```
RESULT 10
US-08-353-400-27
; Sequence 27, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-353-400-27

Query Match 75.8%; Score 25; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWM 4
Db 1 GYWI 4

RESULT 11
US-09-948-004-32
; Sequence 32, Application US/09948004
; Patent No. 6723538
; GENERAL INFORMATION:
; APPLICANT: MACK, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE OF INVENTION: immunological disorders
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
; US-09-948-004-32

Query Match 72.7%; Score 24; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
Db 1 YWMN 4

RESULT 12
US-08-753-750B-38
; Sequence 38, Application US/08753750B
; Patent No. 6610506
; GENERAL INFORMATION:
; APPLICANT: Lo, Reggie Y. C.
; APPLICANT: Schryvers, Anthony B.
; TITLE OF INVENTION: PASTEURELLA BINDING PROTEINS OF
; TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; FILE REFERENCE: A34762 021645.0105
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
; PRIOR FILING DATE: 1995-12-01
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Pasteurella haemolytica
; US-08-753-750B-38

Query Match 72.7%; Score 24; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3
Db 3 GYW 5

RESULT 13
US-09-508-413A-2
; Sequence 2, Application US/09508413A
; Patent No. 6667035
; GENERAL INFORMATION:
; APPLICANT: von Eichel-Streiber, Christoph
; APPLICANT: Moos, Michael
; TITLE OF INVENTION: AMINO ACID SEQUENCES FOR THERAPEUTIC AND
; TITLE OF INVENTION: PROPHYLACTIC USE AGAINST DISEASES DUE TO CLOSTRIDIUM
; TITLE OF INVENTION: DIFFICILE TOXINS
; FILE REFERENCE: 415142000200
; CURRENT APPLICATION NUMBER: US/09/508,413A
; CURRENT FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: PCT/EP98/05759
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-508-413A-2

Query Match 72.7%; Score 24; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
Db 2 YWMN 5

RESULT 14
US-09-192-854-151
; Sequence 151, Application US/09192854
; Patent No. 6696245
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
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; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 151
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-192-854-151

Query Match      72.7%; Score 24; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWMS 5
      |||.||
Db      1 GYWS 5

RESULT 15
US-09-155-106-1
; Sequence 1, Application US/09155106
; Patent No. 6730300
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,106
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/04696
; FILING DATE: 19-MAR-1997
; APPLICATION NUMBER: US 60/013,708
; FILING DATE: 20-MAR-1996
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-155-106-1

Query Match      72.7%; Score 24; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 YWMS 5
      |||.
Db      2 YWMT 5

Search completed: April 18, 2005, 15:39:49
Job time : 41 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:59:59 ; Search time 37.5581 Seconds
(without alignments)
48.674 Million cell updates/sec

Title: US-09-674-716B-11
Perfect score: 98
Sequence: 1 EIRLKSNDYATHYAESVKG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	100.0	101	2 S26460	Ig heavy chain V r
2	98	100.0	115	2 S38714	Ig heavy chain V r
3	93	94.9	106	2 S24521	Ig heavy chain V r
4	93	94.9	115	1 AVMS06	Ig heavy chain V-I
5	91	92.9	113	1 AVMS09	Ig heavy chain V-I
6	91	92.9	113	1 AVMS61	Ig heavy chain V-I
7	91	92.9	113	1 AVMSAB	Ig heavy chain V-I
8	91	92.9	113	1 AVMSB7	Ig heavy chain V-I
9	91	92.9	115	1 AVMS82	Ig heavy chain V-I
10	89	90.8	115	2 A25803	Ig heavy chain V r
11	86	87.8	113	1 AVMS57	Ig heavy chain V-I
12	85	86.7	113	1 HVMSAM	Ig heavy chain V-I
13	75.5	77.0	111	1 MHMS76	Ig heavy chain V-I
14	73	74.5	139	2 PC1213	Ig heavy chain pre
15	68	69.4	64	2 I77394	Ig heavy chain V r
16	68	69.4	121	2 S09958	Ig heavy chain V-D
17	67	68.4	100	2 S26462	Ig heavy chain V r
18	67	68.4	110	2 PH1092	Ig heavy chain V r
19	67	68.4	110	2 PH1091	Ig heavy chain V r
20	67	68.4	119	2 A27630	Ig heavy chain pre
21	67	68.4	121	2 A41940	Ig heavy chain V r
22	67	68.4	141	2 I32513	Ig heavy chain pre
23	66	67.3	125	2 S67945	Ig heavy chain BrE
24	65	66.3	139	2 G29380	Ig heavy chain pre
25	64	65.3	110	2 PH1093	Ig heavy chain V r
26	63	64.3	220	2 S68211	Ig heavy chain (Ma
27	63	64.3	444	2 FC4436	monoclonal antibod
28	61	62.2	119	2 PH1293	Ig heavy chain pre
29	61	62.2	137	2 S42467	Ig heavy chain V r

30 58 59.2 55 2 S46466 Ig heavy chain V r
31 58 59.2 100 2 PL0122 Ig heavy chain V-I
32 58 59.2 126 2 S44107 Ig heavy chain V-D
33 58 59.2 132 2 PH1289 Ig heavy chain pre
34 57 58.2 116 2 H29380 Ig heavy chain pre
35 57 58.2 118 2 A31485 Ig heavy chain V r
36 57 58.2 137 2 B34903 Ig heavy chain pre
37 57 58.2 137 2 A34903 Ig heavy chain pre
38 57 58.2 137 2 D34903 Ig heavy chain pre
39 57 58.2 137 2 F34903 Ig heavy chain pre
40 57 58.2 142 1 EVTR2 Ig heavy chain pre
41 56 57.1 127 2 S58213 Ig heavy chain V r
42 56 57.1 133 2 PH1288 Ig heavy chain pre
43 55 56.1 100 2 S26926 Ig heavy chain V r
44 55 56.1 119 2 PH1290 Ig heavy chain pre
45 55 56.1 119 2 PH1292 Ig heavy chain pre

ALIGNMENTS

RESULT 1
S26460

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S26460

R;Kavaler, J.

submitted to the EMBL Data Library, April 1991

A;Reference number: S26459

A;Accession: S26460

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-101 <KAV>

A;Cross-references: EMBL:X59106; NID:G51707; PIDN:CAA41832.1; PID:951708

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 98; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 9.2e-09; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDYATHYAESVKG 19

Db 32 EIRLKSNDYATHYAESVKG 50

RESULT 2
S38714

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000

C;Accession: S38714

R;Cimanis, A.Y.

submitted to the EMBL Data Library, November 1993

A;Reference number: S38713

A;Accession: S38714

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-115 <CIM>

A;Cross-references: EMBL:X76014; NID:G416092; PIDN:CAA53601.1; PID:gl334076

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;14-99/Domain: immunoglobulin homology <IMV>

Query Match 100.0%; Score 98; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.1e-08; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDYATHYAESVKG 19

Db 49 EIRLKSNDYATHYAESVKG 67

RESULT 3

S24521
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S24521
R:Kaartinen, M.

submitted to the EMBL Data Library, October 1991

A:Reference number: S24490
A:Accession: S24521
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <KAA>
A:Cross-references: EMBL:X66664; NID:G51247; PIDN:CAA47226.1; PID:G51248
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:21-106/Domain: immunoglobulin homology <IMM>

Query Match 94.9%; Score 93; DB 2; Length 106;
Best Local Similarity 94.7%; Pred. No. 6.3e-08; Indels 0; Gaps 0;
Matches 18; Conservative 1; Mismatches 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 56 EIRLKSNNYATHYAESVKG 74

RESULT 4

AVMS06
Ig heavy chain V-III region (J606) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: C92811; A02072
R:Johnson, N.; Slankard, J.; Paul, L.; Hood, L.
J. Immunol. 128, 302-307, 1982
A:Title: The complete V domain amino acid sequences of two myeloma inulin-binding proteins
A:Reference number: A92811; MUID:82099361; PMID:6798111

A:Accession: C92811
A:Molecule type: protein
A:Residues: 1-115 <JOH>
A:Cross-references: UNIPROT:P01801
C:Comment: This chain was isolated from a myeloma protein that binds inulin.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Query Match 94.9%; Score 93; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 6.9e-08; Indels 0; Gaps 0;
Matches 18; Conservative 1; Mismatches 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 5

AVMS09
Ig heavy chain V-III region (E109) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: C93818; A02072
R:Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A:Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A:Reference number: A93818; MUID:78158406; PMID:417344

A:Accession: C93818
A:Molecule type: protein
A:Residues: 1-113 <VRA>
A:Cross-references: UNIPROT:P01798
C:Comment: This chain was isolated from a myeloma protein that binds inulin.
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 1.4e-07; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 1;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 6

AVMS61
Ig heavy chain V-III region (U61) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: B93818; A02072
R:Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A:Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A:Reference number: A93818; MUID:78158406; PMID:417344

A:Accession: B93818
A:Molecule type: protein
A:Residues: 1-113 <VRA>
A:Cross-references: UNIPROT:P01797
C:Comment: This chain was isolated from a myeloma protein that binds inulin.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 1.4e-07; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 1;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 7

AVMSAB
Ig heavy chain V-III region (A4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 24-Apr-1984 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: A93818; A02072
R:Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A:Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A:Reference number: A93818; MUID:78158406; PMID:417344

A:Accession: A93818
A:Molecule type: protein
A:Residues: 1-113 <VRA>

A:Cross-references: UNIPROT:P01796
C:Comment: This chain was isolated from a myeloma protein that binds inulin.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 1.4e-07; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 1;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 8

AVMSB7

RESULT 13
MHMS76
Ig heavy chain V-III region (HPC76) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1980 #sequence_revision 30-Sep-1980 #te
C;Accession: A02074

Search completed: April 18, 2005, 14:23:34
Job time : 41.5581 secs

```

Query Match          69.4%; Score 68; DB 2; Length 64;
Best Local Similarity 72.2%; Pred. No. 0.00042;
Matches 13: Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:57:43 ; Search time 172.767 seconds
(without alignments)
56.316 Million cell updates/sec

Title: US-09-674-716B-11
Perfect score: 98
Sequence: 1 EIRLKSNDNYATHAESVKG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	94.9	115	1 HV32_MOUSE	P01801 mus musculus
2	92	93.9	464	2 Q6PIP8	Q6PIP8 mus musculus
3	91	92.9	113	1 HV27_MOUSE	P01796 mus musculus
4	91	92.9	113	1 HV28_MOUSE	P01797 mus musculus
5	91	92.9	113	1 HV29_MOUSE	P01798 mus musculus
6	91	92.9	113	1 HV30_MOUSE	P01799 mus musculus
7	91	92.9	115	1 HV33_MOUSE	P01802 mus musculus
8	90	91.8	487	2 Q80Z17	Q80Z17 mus musculus
9	86	87.8	113	1 HV31_MOUSE	P01800 mus musculus
10	85	86.7	113	1 HV34_MOUSE	P01803 mus musculus
11	75.5	77.0	111	1 HV35_MOUSE	P01804 mus musculus
12	68	69.4	64	2 Q61750	Q61750 mus musculus
13	67	68.4	471	2 Q66K04	Q66K04 mus musculus
14	64	65.3	458	2 Q65ZQ1	Q65ZQ1 homo sapien
15	57	58.2	142	1 HV01_RAT	P01805 rattus norv
16	57	58.2	479	2 Q7TMK4	Q7TMK4 mus musculus
17	52	53.1	493	2 Q6GMX2	Q6GMX2 homo sapien
18	51	52.0	480	2 Q91XB1	Q91XB1 mus musculus
19	49	50.0	357	2 Q6J2D0	Q6J2D0 pseudomonas
20	49	50.0	361	2 Q9RBZ2	Q9RBZ2 pseudomonas
21	49	50.0	614	2 Q6DDQ7	Q6DDQ7 xenopus lae
22	48	49.0	122	1 HV21_MOUSE	P01790 mus musculus
23	48	49.0	123	1 HV18_MOUSE	P01787 mus musculus
24	48	49.0	123	1 HV19_MOUSE	P01788 mus musculus
25	48	49.0	123	1 HV22_MOUSE	P01791 mus musculus
26	48	49.0	123	1 HV25_MOUSE	P01794 mus musculus
27	47.5	48.5	754	2 Q8CGQ1	Q8CGQ1 mus musculus
28	47	48.0	357	2 Q9RBZ3	Q9RBZ3 pseudomonas
29	47	48.0	398	2 Q88ZK4	Q88ZK4 lactobacill
30	46	46.9	122	1 HV20_MOUSE	P01789 mus musculus
31	46	46.9	144	1 HV26_MOUSE	P01795 mus musculus

32 46 46.9 163 2 Q68WS1
33 46 46.9 2910 2 Q9FND5
34 45.5 46.4 703 2 Q8COV3
35 45.5 46.4 756 2 Q6IMH7
36 45 45.9 121 2 Q9UL71
37 45 45.9 300 2 Q8ID86
38 45 45.9 422 2 Q8WR61
39 45 45.9 450 2 Q8U651
40 45 45.9 485 1 HUNB_CLOAL
41 45 45.9 593 2 Q6INM5
42 44 44.9 123 1 HV23_MOUSE
43 44 44.9 253 2 Q8DZT9
44 44 44.9 253 2 Q8ESI6
45 44 44.9 270 2 Q7VLX9

Q68ws1 rickettsia
Q9fnd5 arabidopsis
Q8cov3 mus musculus
Q6imh7 mus musculus
Q9ul71 homo sapien
Q8id86 plasmodium
Q8wr61 lymantria d
Q8u651 agrobacteri
Q96785 clogmia alb
Q6inm5 xenopus lae
P01792 mus musculus
Q8dz7 streptococc
Q8esi6 streptococc
Q7vlx9 haemophilus

ALIGNMENTS

RESULT 1
HV32_MOUSE STANDARD; PRT; 115 AA.
AC P01801;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG heavy chain V-III region J606.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RX MEDLINE-8209361; PubMed-6798111;
RA Johnson N., Stankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-binding proteins."
RL J. Immunol. 128:302-307(1982).
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein that binds inulin.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; C92811; AVMS06.
DR HSSP; P01852; INFED.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig, 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 114 IG-like.
FT DISULFID 22 98 By similarity.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12810 MW; B67AD6638A121A5F CRC64;

Query Match 94.9%; Score 93; DB 1; Length 115;

Best Local Similarity 94.7%; Pred. No. 3.3e-07;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHAESVKG 19

|||||:|||||

Db 50 EIRLKSNNYATHAESVKG 68

RESULT 2

ID Q6PIP8 PRELIMINARY; PRT; 464 AA.
AC Q6PIP8;

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DE Hypothetical protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=Czech II; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=1247732; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klauener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.P., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,
 RA Stapleton M.J., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnarlatne P.H.,
 RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Czech II; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC031470; AAH31470.1; -
 DR HSSP; P01865; 1KB5.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG.c1.
 DR InterPro; IPR003006; IG.MHC.
 DR InterPro; IPR003596; IG.v.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00230; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 464 AA; 51246 MW; FDAC40A45B5E1443 CRC64;

Query Match 93.9%; Score 92; DB 2; Length 464;
 Best Local Similarity 89.5%; Pred. No. 2.2e-06;
 Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
 :||:|||||
 Db 69 QIRLRSDNYATHYAESVKG 87

RESULT 3
 HV27_MOUSE
 ID HV27_MOUSE STANDARD; PRT; 113 AA.
 AC P01796;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V-III region A4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=78158406; PubMed=417344;
 RA Vrana M., Rudikoff S., Potter M.;
 RT "Sequence variation among heavy chains from inulin-binding myeloma

RT proteins";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
 CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
 binds inulin.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A33818; AVMSAB.
 DR HSSP; P01783; 1IGC.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG.v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 >113 Ig-like.
 FT DISULFID 22 98 By similarity.
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;
 Query Match 92.9%; Score 91; DB 1; Length 113;
 Best Local Similarity 94.7%; Pred. No. 6.9e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
 :|||||
 Db 50 EIRLKSHNYATHYAESVKG 68

RESULT 4
 HV28_MOUSE
 ID HV28_MOUSE STANDARD; PRT; 113 AA.
 AC P01797;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V-III region U61.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=78158406; PubMed=417344;
 RA Vrana M., Rudikoff S., Potter M.;
 RT "Sequence variation among heavy chains from inulin-binding myeloma
 proteins";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
 CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
 binds inulin.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; B93818; AVMS61.
 DR HSSP; P01783; 1IGC.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG.v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 >113 Ig-like.
 FT DISULFID 22 98 By similarity.
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;

Query Match 92.9%; Score 91; DB 1; Length 113;
 Best Local Similarity 94.7%; Pred. No. 6.9e-07;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
 :|||||
 Db 50 EIRLKSHNYATHYAESVKG 68

RESULT 5
 HV29_MOUSE

```

ID HV29_MOUSE STANDARD; PRT; 113 AA.
AC P01798;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region E109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RL proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC -1- binds inulin.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; C93818; AVMS09.
DR HSSP; P01783; 1IGC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 >113
FT DISULFID 22 98
FT NON TER 113 113
FT SEQUENCE 113 AA; 12647 MW; BE50F2F20EBD129B CRC64;

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 6.9e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
DB 50 EIRLKSHNYATHYAESVKG 68

RESULT 6
HV30_MOUSE STANDARD; PRT; 113 AA.
ID HV30_MOUSE PRT; 113 AA.
AC P01799;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region ABE-47N.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=77134726; PubMed=402936;
RA Vrana M., Rudikoff S., Potter M.;
RT "Heavy-chain variable-region sequence from an inulin-binding myeloma
RL protein."
RL Biochemistry 16:1170-1175(1977).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC -1- binds inulin.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90400; AVMSB7.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 >113
FT SEQUENCE 113 AA; 12647 MW; BE50F2F20EBD129B CRC64;

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 6.9e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
DB 50 EIRLKSHNYATHYAESVKG 68

RESULT 7
HV33_MOUSE STANDARD; PRT; 115 AA.
ID HV33_MOUSE PRT; 115 AA.
AC P01802;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region W3082.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RL binding proteins."
RL J. Immunol. 128:302-307(1982).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC -1- binds inulin.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; D92811; AVMS82.
DR HSSP; P01852; 1NFD.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 114
FT DISULFID 22 98
FT NON TER 115 115
FT SEQUENCE 115 AA; 12887 MW; 9B4517648C121C5A CRC64;

Query Match 92.9%; Score 91; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 7e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
DB 50 EIRLKSHNYATHYAESVKG 68

RESULT 8
Q80Z17 PRELIMINARY; PRT; 487 AA.
ID Q80Z17
AC Q80Z17;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
```

```

FT DISULFID 22 98 By similarity.
SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 6.9e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
DB 50 EIRLKSHNYATHYAESVKG 68

RESULT 7
HV33_MOUSE STANDARD; PRT; 115 AA.
ID HV33_MOUSE PRT; 115 AA.
AC P01802;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region W3082.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RL binding proteins."
RL J. Immunol. 128:302-307(1982).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC -1- binds inulin.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; D92811; AVMS82.
DR HSSP; P01852; 1NFD.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 114
FT DISULFID 22 98
FT NON TER 115 115
FT SEQUENCE 115 AA; 12887 MW; 9B4517648C121C5A CRC64;

Query Match 92.9%; Score 91; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 7e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
DB 50 EIRLKSHNYATHYAESVKG 68

RESULT 8
Q80Z17 PRELIMINARY; PRT; 487 AA.
ID Q80Z17
AC Q80Z17;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	DR	Pfam: PF00047; ig: 1.
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	DR	SMART; SM00406; IGV: 1.
RA	Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	DR	PROSITE; PS00835; IG LIKE; 1.
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	KW	Direct protein sequencing; Immunoglobulin V region.
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	FT	DOMAIN 22 >113
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	FT	DISULFID 22 98
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	FT	NON TER 113 113
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	SQ	SEQUENCE 113 AA; 12732 MW; 26618F626B59859E CRC64;
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		Query Match 87.8%; Score 86; DB 1; Length 113;
RA	Richards S.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		Best Local Similarity 89.5%; Pred. No. 4.5e-06;
RA	Villalon D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,		Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
RA	Fahay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,	QY	1 EIRLKSNDNYATHYAESVKG 19
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	DB	50 EIRLKSHNYETHYAESVKG 68
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		RESULT 10
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	HV34_MOUSE	STANDARD; PRT; 113 AA.
RA	Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,	ID HV34_MOUSE	
RA	Jones S.J., Marra M.A.;	AC P01803;	
RT	"Generation and initial analysis of more than 15,000 full-length human	DT 21-JUL-1986 (Rel. 01, Created)	
RT	and mouse cDNA sequences.";	DT 21-JUL-1986 (Rel. 01, Last sequence update)	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	DT 05-JUL-2004 (Rel. 44, Last annotation update)	
RN	[2]	DE IG heavy chain V region AMPC1.	
RP	SEQUENCE FROM N.A.	OS Mus musculus (Mouse)	
RC	STRAIN=FVB/N; TISSUE=Colon;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
RA	Strausberg R.;	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.	RN	NCBI_TaxID=10090;
DR	EMBL; BC049143; AAH49143.1; -	RP	SEQUENCE.
DR	HSSP; P01789; IMCP.	RX	MEDLINE=81216632; PubMed=6787122;
DR	InterPro; IPR007110; IG-like.	RA	Rudikoff S., Potter M.;
DR	InterPro; IPR003597; IG cl.	RT	"Immunoglobulin heavy chains from anti-inulin myeloma proteins:
DR	InterPro; IPR003006; IG_MHC.	RT	evidence for a new heavy chain joining segment.";
DR	InterPro; IPR003596; IG_V.	RL	J. Immunol. 127:191-194(1981).
DR	Pfam; PF07654; CI-set; 2.	CC	-!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
DR	SMART; SM00406; IGV: 1.	CC	binds inulin.
DR	PROSITE; PS00835; IG LIKE; 4.	CC	-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.	DR	PIR; A02073; HVMSAM.
KW	Hypothetical protein_2.	DR	HSSP; P01783; IIGC.
SQ	SEQUENCE 487 AA; 53019 MW; 31F2C893900A4D80 CRC64;	DR	InterPro; IPR007110; IG-like.
	Query Match 91.8%; Score 90; DB 2; Length 487;	DR	InterPro; IPR003596; IG_V.
	Best Local Similarity 89.5%; Pred. No. 4.9e-06;	DR	Pfam; PF00047; ig: 1.
	Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	DR	SMART; SM00406; IGV: 1.
QY	1 EIRLKSNDNYATHYAESVKG 19	DR	PROSITE; PS00835; IG LIKE; 1.
DB	69 EIRLRSNNYATHYAESVKG 87	KW	Direct protein sequencing; Immunoglobulin V region.
	RESULT 9	FT	DOMAIN 1 >113
HV31_MOUSE	STANDARD; PRT; 113 AA.	FT	DISULFID 22 98
ID HV31_MOUSE		FT	NON TER 113 113
AC P01800;		SQ	SEQUENCE 113 AA; 12691 MW; 7A6D906AAA966E9E CRC64;
DT 21-JUL-1986 (Rel. 01, Created)			Query Match 86.7%; Score 85; DB 1; Length 113;
DT 01-OCT-1993 (Rel. 27, Last sequence update)			Best Local Similarity 89.5%; Pred. No. 6.6e-06;
DT 05-JUL-2004 (Rel. 44, Last annotation update)			Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DE IG heavy chain V-III region T957.		QY	1 EIRLKSNDNYATHYAESVKG 19
OS Mus musculus (Mouse)		DB	50 EIRLKSHNYATHYAESVKG 68
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			RESULT 11
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		HV35_MOUSE	STANDARD; PRT; 111 AA.
RN	NCBI_TaxID=10090;	ID HV35_MOUSE	
RP	SEQUENCE.	AC P01804;	
RX	MEDLINE=81216632; PubMed=6787122;	DT 21-JUL-1986 (Rel. 01, Created)	
RA	Rudikoff S., Potter M.;	DT 21-JUL-1986 (Rel. 01, Last sequence update)	
RT	"Immunoglobulin heavy chains from anti-inulin myeloma proteins:	DT 10-OCT-2003 (Rel. 42, Last annotation update)	
RT	evidence for a new heavy chain joining segment.";	DE IG heavy chain V-III region HPC76 (fragment).	
RL	J. Immunol. 127:191-194(1981).	OS Mus musculus (Mouse)	
CC	-!- MISCELLANEOUS: This chain was isolated from a myeloma protein that	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
CC	binds inulin.	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like domain.		
DR	PIR; A02810; AVMS57.		
DR	HSSP; P01783; IIGC.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003596; IG_V.		

```

OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81013937; PubMed=6251474;
RA Bernard O., Gough N.M.;
RT "Nucleotide sequence of immunoglobulin heavy chain joining segments
between translocated VH and mu constant regions genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).
CC -1- MISCELLANEOUS: The sequence of the first 197 residues of the C
region was also determined and differs in only 3 positions from
the corresponding portion of the mouse MOPC 104e mu chain.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02074; MMS76.
DR HSSP; P01852; INFD.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT NON_TER 1 1
FT DOMAIN <1 110 Ig-like.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12304 MW; 0ED98EC7348056A CRC64;

Query Match 77.0%; Score 75.5; DB 1; Length 111;
Best Local Similarity 89.5%; Pred. No. 0.00023;
Matches 17; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 EIRLSDNYATHYAESVKG 19
Db 45 EIRLKS-GYATHYAESVKG 62
||||| |||||||
||||| |||||||

RESULT 12
Q61750 PRELIMINARY; PRT; 64 AA.
AC Q61750;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE JH-Cdelta locus, partial cds. (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92017847; PubMed=1922069;
RA Owens J.D.Jr., Finkelman F.D., Mountz J.D., Mushinski J.F.;
RT "Nonhomologous recombination at sites within the mouse JH-C delta
locus accompanies C mu deletion and switch to immunoglobulin D
secretion.";
RL Mol. Cell. Biol. 11:5660-5670(1991).
DR EMBL; M64568; AAA39341.1; -.
DR PIR; I77394; I77394.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
FT NON_TER 64
SQ SEQUENCE 64 AA; 7594 MW; FE83625079AC3F28 CRC64;

Query Match 69.4%; Score 68; DB 2; Length 64;
Best Local Similarity 72.2%; Pred. No. 0.0021;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IRLKSDNYATHYAESVKG 19
Db 9 ITVKSDNYGANYAESVKG 26
|:|||||:|||||
|:|||||:|||||

RESULT 13
Q66K04

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ID Q66K04 PRELIMINARY; PRT; 471 AA.
AC Q66K04;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CZECH II; TISSUE=Mammary tumor;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maizra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CZECH II; TISSUE=Mammary tumor;
RX Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC080671; AAH80671.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 52258 MW; 81B57C3228315AC2 CRC64;

Query Match 68.4%; Score 67; DB 2; Length 471;
Best Local Similarity 76.5%; Pred. No. 0.027;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRLKSDNYATHYAESVKG 18
Db 70 IRKSDNYATYVADSVK 86
||:|||||:|||||
||:|||||:|||||

RESULT 14
Q65ZQ1 PRELIMINARY; PRT; 458 AA.
AC Q65ZQ1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Anti-colorectal carcinoma heavy chain.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93383497; PubMed=8372513;
 RA Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
 RT "Cloning and characterization of 116NS19.9 heavy and light chain
 cDNAs and expression of antibody fragments in *Escherichia coli*."
 RL Year Immunol. 7:56-62(1993).
 DR EMBL; S65761; AAB28159.1; -.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR Pfam; PF00047; IG; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 458 AA; 50602 MW; 4AE29F9981D8DFF CRC64;

Query Match 65.3%; Score 64; DB 2; Length 458;
 Best Local Similarity 68.4%; Pred. No. 0.08;
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 EIRKSDNYATHYAESVKG 19
 ||| |::||| :|:|
 Db 69 EIGNKGNHATYAESVKG 87

Oy 1 EIRKSDNYATHYAESVKG 19
 ||| |::||| :|:|
 Db 69 EIRKANNVYVYGRSLKG 87

Search completed: April 18, 2005, 14:21:57
 Job time : 174.767 secs

RESULT 15
 HV01_RAT
 ID HV01_RAT STANDARD; PRT; 142 AA.
 AC P01805;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region IR2 precursor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83064537; PubMed=6292865;
 RA Hellman L., Pettersson U., Engstrom A., Karlsson T., Bennich H.;
 RT "Structure and evolution of the heavy chain from rat immunoglobulin
 E."
 RL Nucleic Acids Res. 10:6041-6049(1982).
 CC -!- MISCELLANEOUS: The mRNA was isolated from an IgE-secreting
 immunocytoma that arises spontaneously in LOU/CwSL rats.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02075; EVRIR2.
 DR HSP; P01789; IMCP.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 19
 FT CHAIN 20 142 Ig heavy chain V region IR2.
 FT DOMAIN 20 133 Ig-like.
 FT NON_TER 142 142
 SQ SEQUENCE 142 AA; 16024 MW; DE29E6CFE745DF3B CRC64;

Query Match 58.2%; Score 57; DB 1; Length 142;
 Best Local Similarity 52.6%; Pred. No. 0.32;
 Matches 10; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:32:07 ; Search time 200.163 Seconds
(without alignments)
36.712 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRLKSDNVATHYAESVKG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	19	3 AAY32258	Aay32258 Light cha
2	98	100.0	123	6 ABO10742	Abol0742 Variable
3	98	100.0	123	6 ABR44686	Abra44686 Murine Mu
4	98	100.0	123	8 ADQ90820	Adq90820 Kabat sub
5	98	100.0	137	3 AAY32260	Aay32260 Mouse ant
6	98	100.0	286	4 AAB50426	Aab50426 Antibody
7	98	100.0	444	3 AAY32263	Aay32263 Humanised
8	95	96.9	100	4 AAE06973	Aae06973 Mouse ger
9	95	96.9	100	8 ADQ89258	Adq89258 Mouse imm
10	95	96.9	299	4 AAB50425	Aab50425 Mouse ant
11	93	94.9	115	2 AAR34018	Aar34018 BW 835 VH
12	93	94.9	116	2 AAY03869	Aay03869 SM3 heavy
13	93	94.9	119	2 AAW46958	Aaw46958 Amino aci
14	93	94.9	119	7 ABR82775	Abra82775 Hybridoma
15	93	94.9	119	7 ABR82885	Abra82885 Hybridoma
16	93	94.9	120	2 AAW01589	Aaw01589 Lead bind
17	93	94.9	122	3 AAY90812	Aay90812 2G3 Hybri
18	93	94.9	142	2 AAW06212	Aaw06212 MAB Br-3
19	93	94.9	142	2 AAW85059	Aaw85059 Mouse Br-
20	93	94.9	142	6 ABUS5893	Abus5893 Mouse ant
21	93	94.9	143	2 AAR09423	Aar09423 Br-3 Heavy
22	93	94.9	255	5 AAR072870	Aar072870 PS-23 sin
23	93	94.9	256	5 AAU72866	Aau72866 PS-3 sing
24	93	94.9	503	5 AAU72874	Aau72874 3B10xP5-2
25	93	94.9	570	2 AAY39451	Aay39451 Antibody

ALIGNMENTS

RESULT 1

AAY32258

ID AAY32258 standard; peptide; 19 AA.

XX AC AAY32258;

XX XX

DT 15-FEB-2000 (first entry)

XX XX

DE Light chain CDR H2 of mouse anti-CD23 MAb C11.

XX XX

KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;

KW monoclonal antibody; chimeric antibody; humanised antibody;

KW complementarity determining region; CDR; autoimmune disease;

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;

KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

KW urticaria; nephrotic syndrome; glomerulonephritis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;

KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;

KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;

XX KW

OS Mus musculus.

XX XX

PN WO9558679-A1.

XX XX

PD 18-NOV-1999.

XX XX

PF 07-MAY-1999; 99WO-GB001434.

XX XX

PR 09-MAY-1998; 98GB-00009839.

XX XX

PA (GLAX) GLAXO GROUP LTD.

XX XX

PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX XX

DR WPI; 2000-053101/04.

XX XX

XX N-PSDB; AA234743.

XX XX

PT Cell receptor specific antibodies useful for treating e.g. arthritis,

XX XX

PT diabetes, multiple sclerosis and psoriasis.

XX XX

PS Claim 1; Page 40; 81pp; English.

XX XX

CC This sequence represents complementarity determining region 2 (CDR H2)

CC of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11

CC (see also AAY32263). The invention provides altered antibodies, such as

CC chimeric or humanised antibodies, which comprise sufficient of the amino

CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on
 CC haematopoietic cells. The antibodies are used to block soluble CD23
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They
 CC are also useful for studying interactions between CD23 and various
 CC ligands and determining the binding agents
 XX
 XX Sequence 19 AA;

Query Match 100.0%; Score 98; DB 3; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
 |||||
 DB 1 EIRLSDNYATHYAESVKG 19

RESULT 2
 ABO10742
 ID ABO10742 standard; protein; 123 AA.

XX
 AC ABO10742;

XX 20-AUG-2003 (first entry)

XX Variable region of murine antibody MuVHIIIC.

XX Modified antibody; deimmunised antibody; anti-PSMA antibody;
 KW prostate specific membrane antigen; immunogenic; CDR; murine;
 KW complementarity determining region; J591; J415; J533; E99; mouse;
 KW prostatic disorder; cancerous disorder; genitourinary inflammation;
 KW prostatitis; benign enlargement; prostatic cancer; testicular cancer;
 KW solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic;
 KW antiinflammatory; cytostatic; framework region; variable heavy chain;
 KW variable light chain; VH; VL; variable region.
 XX
 XX Mus musculus.

XX WO200298897-A2.

XX 12-DEC-2002.

XX 30-MAY-2002; 2002WO-US017068.

XX 01-JUN-2001; 2001US-0295214P.

XX 20-SEP-2001; 2001US-0323585P.

XX 08-MAR-2002; 2002US-0362810P.

XX (CORR) CORNELL RES FOUND INC.

XX Bander N, Carr FJ, Hamilton A;

XX WPI; 2003-156839/15.

XX New modified anti-prostate specific membrane antigen (PSMA)
 PT immunoglobulins, useful for treating or preventing a prostatic or
 PT cancerous disorder, e.g. genitourinary inflammation, prostatitis, or
 PT prostatic or testicular cancer.

PS Disclosure; Fig 7C; 254pp; English.

XX The present invention relates to modified (e.g. deimmunised) antibodies
 CC to prostate specific membrane antigen (PSMA). The modified anti-PSMA
 CC antibodies are less immunogenic compared to the unmodified anti-PSMA
 CC antibodies. The modified antibodies comprise complementarity determining
 CC regions (CDRs) from a non-human antibody (e.g. murine antibody J591, J415,

CC J533 or E99), and framework sequences that are less immunogenic in humans
 CC (e.g. less antigenic than the murine frameworks in which a murine CDR
 CC naturally occurs). The modified antibodies bind with PSMA, preferably
 CC human PSMA, with high affinity and specificity. The anti-PSMA antibodies
 CC are useful for treating or preventing a prostatic or cancerous disorder,
 CC e.g. genitourinary inflammation, prostatitis, benign enlargement,
 CC prostatic cancer or testicular cancer, or solid tumours, soft tissue
 CC tumours or metastatic lesions, and its associated pain. The present
 CC sequence represents a variable region from a murine antibody
 XX
 XX Sequence 123 AA;

Query Match 100.0%; Score 98; DB 6; Length 123;
 Best Local Similarity 100.0%; Pred. No. 3e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
 |||||
 DB 50 EIRLSDNYATHYAESVKG 68

RESULT 3

ABR44686

ID ABR44686 standard; protein; 123 AA.

XX ABR44686;

XX 25-JUL-2003 (first entry)

XX Murine MuVHIIIC amino acid sequence SEQ ID NO:69.

XX Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic;
 KW prostate specific membrane antigen; antipsoriatic; antiarthritic;
 KW dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;
 KW epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;
 KW neoplastic disorder.

XX Mus musculus.

XX WO2003024388-A2.

XX 27-MAR-2003.

XX 30-MAY-2002; 2002WO-US017204.

XX 20-SEP-2001; 2001US-0324100P.

XX 08-MAR-2002; 2002US-0362612P.

XX (CORR) CORNELL RES FOUND INC.

XX Bander N;

XX WPI; 2003-313319/30.

XX Ablating/killing aberrant prostate specific membrane antigen-expressing
 PT cells for treating skin disorders, by contacting the cell with an
 PT antibody that binds to the extracellular domain of prostate specific
 PT membrane antigen.

XX Disclosure; Page 37; 225pp; English.

XX The present invention describes a method (M1) for ablating or killing an
 CC aberrant prostate specific membrane antigen (PSMA)-expressing cell (e.g.
 CC an epidermal and a dermal cell). M1 comprises contacting the cell, or a
 CC vascular endothelial cell proximate to the cell, with an antibody (or its
 CC antigen-binding fragment), which binds specifically to the extracellular
 CC domain of PSMA in an amount sufficient to ablate or kill the cell. The
 CC antibodies have antipsoriatic, antiarthritic, dermatological, cytostatic,
 CC antiinflammatory and antiallergic activities, and can be used in
 CC vaccines. M1 is useful for treating a skin disorder in a subject, by
 CC administering to the subject, an amount of an antibody which binds
 CC specifically to the extracellular domain of PSMA (the subject is a
 CC mammal, preferably human and is having, or at risk of, a skin disorder).

CC The skin disorder is a dermal or an epidermal disorder, and is selected
 CC from psoriasis (preferably chronic stationary psoriasis, psoriasis
 CC vulgaris, eruptive (glutamate) psoriasis, psoriatic erythroderma,
 CC generalised pustular psoriasis (Von Zumbusch), annular pustular
 CC psoriasis, and localised pustular psoriasis), psoriatic arthritis,
 CC exfoliative dermatitis, pityriasis rubra pilaris, pityriasis rosea,
 CC parapsoriasis, pityriasis lichenoides, lichen planus, lichen nitidus,
 CC ichthyosiform dermatosis, keratodermas, dermatosis, and prokeratosis,
 CC preferably psoriasis. M1 is useful for treating a skin disorder such as
 CC an inflammatory or neoplastic disorder of the epidermis or dermis,
 CC preferably an epidermal precancerous or cancerous lesion. M1 is also
 CC useful to treat or prevent disorders involving aberrant activity of PSMA-
 CC expressing cell, e.g. kidney, liver or brain cell. ACC69816 to ACC69837
 CC and ABR44613 to ABR44733 represent sequences used in the exemplification
 CC of the present invention

XX SQ Sequence 123 AA;

Query Match 100.0%; Score 98; DB 6; Length 123;
 Best Local Similarity 100.0%; Pred. No. 3e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19

Db 50 EIRLKSDNYATHYAESVKG 68

RESULT 4

ADQ90820
 ID ADQ90820 standard; protein; 123 AA.

XX AC

ADQ90820;

XX DT 07-OCT-2004 (first entry)

XX DE Kabat subgroup murine VHIIIC.

XX XX

KW insulin-related disorder; prostate specific membrane antigen; PSMA;
 KW obesity; hyperglycaemia; hypoglycaemia; hyperinsulinaemia;
 KW insulin-resistance; impaired glucose tolerance; impaired fasting glucose;
 KW Type 1 diabetes mellitus; Type 2 diabetes mellitus; gestational diabetes;
 KW antibody; mouse.

XX OS Mus musculus.

XX PN US2004136998-A1.

XX XX

PD 15-JUL-2004.

XX PF 17-OCT-2003; 2003US-00688015.

XX XX

PR 30-OCT-2002; 2002US-0422396P.

XX XX

PA (BAND/) BANDER N H.

XX PI Bander NH;

XX XX

DR WPI; 2004-533338/51.

XX XX

PT Use of anti-prostate specific membrane antigen antibodies for treating or
 PT preventing insulin-related disorders, e.g. obesity, hyperglycemia,
 PT hypoglycemia, hyperinsulinemia, insulin-resistance, or Type 1 or 2
 PT diabetes mellitus.

XX XX

PS Disclosure; SEQ ID NO 69; 89pp; English.

XX XX

CC The invention relates to a method of treating or preventing an insulin-
 CC related disorder in a subject which comprises administering an antibody
 CC or its antigen-binding portion specific for prostate specific membrane
 CC antigen (PSMA). The method is useful for treating an insulin-related
 CC disorder, including obesity, hyperglycaemia, hypoglycaemia,
 CC hyperinsulinaemia, insulin-resistance, impaired glucose tolerance,
 CC impaired fasting glucose, Type 1 diabetes mellitus, Type 2 diabetes

CC mellitus, and gestational diabetes. The present sequence represents Kabat
 CC subgroup murine VHIIIC.

XX SQ Sequence 123 AA;

Query Match 100.0%; Score 98; DB 8; Length 123;
 Best Local Similarity 100.0%; Pred. No. 3e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19

Db 50 EIRLKSDNYATHYAESVKG 68

RESULT 5

AAV32260

ID AAV32260 standard; protein; 137 AA.

XX AC

AAV32260;

XX DT 15-FEB-2000 (first entry)

XX XX

DE Mouse anti-CD23 Mab C11 heavy chain variable region.

XX XX

KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
 KW therapy.

XX OS Mus musculus.

XX XX

FH Key Location/Qualifiers

FT Region 59..63

FT /note= "CDR H1"

FT Region

FT /note= "CDR H2"

FT Region 78..96

FT /note= "CDR H3"

FT Region 129..131

FT /note= "CDR H3"

XX PN WO9558679-A1.

XX XX

PD 18-NOV-1999.

XX XX

PF 07-MAY-1999; 99WO-GB001434.

XX XX

PR 09-MAY-1998; 98GB-00009839.

XX XX

PA (GLAX) GLAXO GROUP LTD.

XX XX

PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX XX

DR WPI; 2000-053101/04.

XX XX

DR N-PSDB; AAZ34745.

XX XX

PT Cell receptor specific antibodies useful for treating e.g. arthritis,

PT diabetes, multiple sclerosis and psoriasis.

XX XX

PS Claim 8; Fig 1; 81pp; English.

XX XX

CC This sequence represents the heavy chain variable region (VH) of murine
 CC anti-CD23 (FCERII) monoclonal antibody C11. The invention provides
 CC altered antibodies, such as chimeric or humanised antibodies (see
 CC AAV32262 and AAV32263), which comprise sufficient of the amino acid
 CC sequences of the C11 light and heavy chain complementarity determining
 CC regions (see AAV32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies are
 CC used to block soluble CD23 formation in human therapy, for the treatment

CC of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
 CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
 CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
 CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
 CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
 CC malignancies (claimed). They are also useful for studying interactions
 CC between CD23 and various ligands and determining the binding agents
 XX
 SQ Sequence 137 AA;

Query Match 100.0%; Score 98; DB 3; Length 137;

Best Local Similarity 100.0%; Pred. No. 3.4e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0;

Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19

DB 78 EIRLKSNDNYATHYAESVKG 96

RESULT 6

AAB50426

ID AAB50426 standard; protein; 286 AA.

AC AAB50426;

XX

DT 13-MAR-2001 (first entry)

XX

DE Antibody 33F12 catalytic fragment.

XX

KW Antibody 33F12; ketone compound; antitumour; cytotoxic;

KW targeted drug delivery.

XX

OS Unidentified.

XX

PN WO200071556-A1.

XX

PD 30-NOV-2000.

XX

PF 24-MAY-2000; 2000WO-US014366.

XX

PR 25-MAY-1999; 99US-00318661.

XX

PA (SCRI) SCRIPPS RES INST.

XX

PI Barbas CF, Shabat D, Rader C, List B, Lerner RA;

XX

DR WPI: 2001-0611339/07.

XX

DR N-PSDB; AAC90472.

XX

PT New ketone compounds containing active agents useful as carriers for e.g.

PT antitumor agents, antibiotics or fluorescent molecules.

XX

PS Disclosure; Fig 10; 45pp; English.

XX

CC The present sequence may be used in the activation of new ketone produg

CC compounds containing active agents. The ketone derivatives are useful as

CC carriers for antitumor agents such as cytotoxic agents, where the

CC antitumor agent is a microtubule stabilising agent such as paclitaxel,

CC epothilone or its therapeutically active analogue or an anthracycline

CC antibiotic such as doxorubicin or its therapeutically active analogue.

CC The ketone derivatives are useful for targeted drug delivery. The

CC inactive molecules in the ketone compounds are converted to active

CC molecules by retro-Michael reaction. The antibody has bifunctional

CC activity and specifically immunoreacts with cell surface antigen of a

CC target cell. The active ingredients can be mixed effectively with

CC excipients as per desired amount along with the buffering agent to

CC enhance the effectiveness and activity of the compound

XX

SQ Sequence 286 AA;

Query Match 100.0%; Score 98; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 8.2e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19

DB 203 EIRLKSNDNYATHYAESVKG 221

RESULT 7

AAAY32263

ID AAY32263 standard; protein; 444 AA.

XX

AC AAY32263;

XX

DT 15-FEB-2000 (first entry)

XX

DE Humanised anti-CD23 MAb C11 heavy chain.

XX

KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human;

KW monoclonal antibody; chimeric antibody; humanised antibody;

KW complementarity determining region; CDR; autoimmune disease;

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;

KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

KW urticaria; nephrotic syndrome; glomerulonephritis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;

KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;

KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;

KW therapy.

XX

OS Homo sapiens.

XX

OS Synthetic.

XX

PH Key

FT Region

FT Location/Qualifiers

FT 1..30

FT /note= "framework region 1"

FT 31..35

FT /note= "CDR 1"

FT 36..49

FT /note= "framework region 2"

FT 50..68

FT /note= "CDR 2"

FT 69..100

FT /note= "framework region 3"

FT 101..103

FT /note= "CDR 3"

FT 104..111

FT /note= "framework region 4"

FT 112..444

FT /note= "constant region"

XX

PN WO9598679-A1.

XX

PD 18-NOV-1999.

XX

PF 07-MAY-1999; 99WO-GB001434.

XX

PR 09-MAY-1998; 98GB-00009839.

XX

PA (GLAX) GLAXO GROUP LTD.

XX

PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX

DR WPI: 2000-053101/04.

XX

DR N-PSDB; AA234748.

XX

CC Cell receptor specific antibodies useful for treating e.g. arthritis,

CC diabetes, multiple sclerosis and psoriasis.

XX

PS Claim 9; Fig 4; 81pp; English.

XX

CC This amino acid sequence represents the heavy chain of humanised anti-

CC CD23 (FCERII) monoclonal antibody C11, composed of a human framework

CC (HSGKVII) and the heavy chain complementarity determining regions (see

CC AAY32257-59) of murine antibody C11. The DNA was constructed by splice
CC overlap PCR. The invention provides altered antibodies, such as chimeric
CC or humanised antibodies, which comprise sufficient of the amino acid
CC sequences of the C11 light and heavy chain complementarity determining
CC regions to render them capable of binding to the CD23 type II molecule
CC expressed on haematopoietic cells. The antibodies are used to block
CC soluble CD23 formation in human therapy, for the treatment of arthritis,
CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,
CC glomerulonephritis, inflammatory bowel disease, ulcerative colitis,
CC Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
CC bronchitis) or diabetes (particularly type I diabetes), and B-cell
CC malignancies (claimed). They are also useful for studying interactions
CC between CD23 and various ligands and determining the binding agents
xx Sequence 444 AA;
SQ

CC portion of an immunoglobulin of human origin. The humanised antibodies
CC are useful for inhibiting the interaction of a cell expressing CCR2. They
CC are useful for inhibiting or treating HIV infection. The proteins of the
CC invention are useful for inhibiting leukocyte trafficking, for treating
CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
CC disorders such as rheumatoid arthritis and multiple sclerosis,
CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They
CC are useful in therapy or diagnosis, and in the manufacture of a
CC medicament for treating CCR-2 mediated disease. They are also useful for
CC treating allergy, anaphylaxis, malignancy, chronic and acute
CC inflammation, histamine and IgE- mediated allergic reaction, shock,
CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
CC associated with vascular intervention, including angioplasty and/or stent
CC placement in a mammal. Humanised antibodies are also useful for
CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
CC neointimal hyperplasia of a vessel in a mammal, preferably associated
CC with vascular intervention. The present sequence is mouse germline heavy
CC chain variable (VH) region, V(H)22.1
xx
SQ Sequence 100 AA;

CC	AA32257-59) of murine antibody C11. The DNA was constructed by splice overlap PCR. The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of the C11 light and heavy chain complementarity determining regions to render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23 formation in human therapy, for the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease, COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes (particularly type I diabetes), and B-cell malignancies (claimed). They are also useful for studying interactions between CD23 and various ligands and determining the binding agents
XX	
SQ	Sequence 444 AA;
	Query Match 100.0%; Score 98; DB 3; Length 444;
	Best Local Similarity 100.0%; Pred. No. 1.4e-07;
	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 EIRLXSDNYATHYAESVKG 19
DB	50 EIRLXSDNYATHYAESVKG 68
RESULT 8	
AA506973	
ID	AAE06973 standard; protein; 100 AA.
XX	AAE06973;
AC	
XX	
DT	16-OCT-2001 (first entry)
DE	Mouse germline heavy chain variable (VH) region, V(H)22.1.
XX	
KW	Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; neurotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; neointimal hyperplasia; VH; heavy chain variable region.
OS	Mus sp.
XX	
WO	2000157226-A1.
PX	
PN	
XX	
PD	09-AUG-2001.
XX	
PF	02-FEB-2001; 2001WO-US003537.
XX	
PR	03-FEB-2000; 2000US-00497625.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
XX	
PI	Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
DR	WPI; 2001-488888/53.
XX	
PT	Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin.
PS	Disclosure; Page 152-153; 183pp; English.
XX	
CC	The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a

CC immunoglobulin or its antigen binding fragment comprising the chains. The
 CC humanised immunoglobulin or its antigen binding fragment preferably
 CC comprises two heavy chains and two light chains. The humanised
 CC immunoglobulin and its heavy and light chains are useful for the
 CC diagnosis, prevention and/or treatment of diseases or conditions
 CC associated with aberrant expression or activity of the CCR2 polypeptide,
 CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV
 CC infection and atherosclerosis. This sequence represents a mouse
 CC immunoglobulin protein of the invention.

XX SQ Sequence 100 AA;

Query Match 96.9%; Score 95; DB 8; Length 100;

Best Local Similarity 94.7%; Pred. No. 7.5e-08;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19

Db 50 QIRLSDNYATHYAESVKG 68

RESULT 10

AAB50425

ID AAB50425 standard; protein; 299 AA.

AC AAB50425;

DT 13-MAR-2001 (first entry)

DE Mouse antibody 38C2 catalytic fragment.

KW Mouse; antibody 38C2; ketone compound; antitumour; cytotoxic;
 KW targeted drug delivery.

OS Mus sp.

PN WO200071556-A1.

PD 30-NOV-2000.

PF 24-MAY-2000; 2000WO-US014366.

PR 25-MAY-1999; 99US-00318661.

PA (SCRI) SCRIPPS RES INST.

PI Barbas CF, Shabat D, Rader C, List B, Lerner RA;

DR WPI; 2001-061339/07.

DR N-PSDB; AAC90471.

PT New ketone compounds containing active agents useful as carriers for e.g.
 PT antitumor agents, antibiotics or fluorescent molecules.

PS Disclosure; Fig 9; 45pp; English.

CC The present sequence may be used in the activation of new ketone produg
 CC compounds containing active agents. The ketone derivatives are useful as
 CC carriers for antitumour agents such as cytotoxic agents, where the
 CC antitumour agent is a microtubule stabilising agent such as paclitaxel,
 CC epothilone or its therapeutically active analogue or an anthracycline
 CC antibiotic such as doxorubicin or its therapeutically active analogue.
 CC The ketone derivatives are useful for targeted drug delivery. The
 CC inactive molecules in the ketone compounds are converted to active
 CC molecules by retro-Michael reaction. The antibody has bifunctional
 CC activity and specifically immunoreacts with cell surface antigen of a
 CC target cell. The active ingredients can be mixed effectively with
 CC excipients as per desired amount along with the buffering agent to
 CC enhance the effectiveness and activity of the compound

XX SQ Sequence 299 AA;

Query Match 96.9%; Score 95; DB 4; Length 299;

Best Local Similarity 94.7%; Pred. No. 2.7e-07;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19

Db 205 EIRLSDNYATHYAESVKG 223

RESULT 11

AAR34018

ID AAR34018 standard; protein; 115 AA.

AC AAR34018;

DT 25-MAR-2003 (revised)

DT 02-AUG-1993 (first entry)

DE BW 835 VH.

KW Monoclonal antibody; Mab; hybridoma; lung; adenocarcinoma; mammary;
 KW ovary; prostate; polymorphic epithelial mucin; PEM.

OS Synthetic.

PN DE4133791-A1.

PD 15-APR-1993.

PF 11-OCT-1991; 91DE-04133791.

PR 11-OCT-1991; 91DE-04133791.

PA (BEHW) BEHRINGWERKE AG.

PI Bosslet K, Pfeleiderer P, Seemann G;

DR WPI; 1993-127068/16.

DR N-PSDB; AAQ40046.

PT New monoclonal antibody BW835 specific for tumour antigens - useful for
 PT diagnosis and treatment of tumours affecting the breasts, ovaries,
 PT prostate and lungs.

PS Disclosure; Fig 1a; 24pp; German.

CC Monoclonal antibody BW 835 is produced by hybridoma cell line BW 835. The
 CC antibody strongly reacts with lung adenocarcinomas and human mammary-
 CC ovary- and prostate carcinomas. It additionally reacts with polymorphic
 CC epithelial mucin (PEM) but does not react with normal human tissue.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 115 AA;

Query Match 94.9%; Score 93; DB 2; Length 115;

Best Local Similarity 94.7%; Pred. No. 1.9e-07;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19

Db 46 EIRLSDNYATHYAESVKG 64

RESULT 12

AAV03869

ID AAV03869 standard; protein; 116 AA.

AC AAV03869;

DT 16-JUN-1999 (first entry)

DE SM3 heavy chain variable region.

XX SM3 antibody; epitope; mimic; crystal; tumour; MUC1 epitope; allergy;

KW immune response; arthritis; multiple sclerosis; asthma; diabetes;
 KW inflammatory disorder; transplant rejection; graft versus host disease.
 OS Unidentified.
 XX WO9910379-A1.
 PN
 XX 04-MAR-1999.
 PD
 XX 24-AUG-1998; 98WO-GB002542.
 PF
 XX 22-AUG-1997; 97GB-00017946.
 PR
 XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 PA
 XX Freemont PS, Snary D, Sternberg MJE, Bates PA, Dokurno P;
 PI WPI; 1999-204650/17.
 XX N-PSDB; AAX31971.
 DR
 XX New SM3 antibody crystal structures - used to develop agents for treating
 PT e.g. tumors, autoimmune disorders, allergies, inflammatory disorders or
 PT transplant rejection.
 PT

PS Disclosure; Page 279-280; 316pp; English.
 XX

CC The invention relates to a process for preparing a crystal using cadmium.
 CC Structure factors or structural coordinates obtained from the crystal of
 CC SM3 antibody bound to an epitope can be used to design mimics of the
 CC antibody or the epitope. The crystals comprise at least an epitope
 CC binding fragment of the SM3 antibody bound to a peptide recognised by the
 CC epitope binding site of SM3. The products and methods can be used to
 CC develop agents for the detection of tumour cells and for therapy against
 CC tumours. MUC1 epitope mimics can also be used to prevent or decrease an
 CC immune response, e.g. in the therapy of diseases caused by autoimmune
 CC responses (such as arthritis, multiple sclerosis, asthma or diabetes),
 CC allergies, inflammatory disorders or transplant rejections such as graft
 CC versus host disease. The present sequence represents the amino acid
 CC sequence of a heavy chain variable region of SM3 antibody
 XX

SQ Sequence 116 AA;

Query Match 94.9%; Score 93; DB 2; Length 116;
 Best Local Similarity 94.7%; Pred. No. 1.9e-07;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
 |||||:|||||
 DB 50 EIRLKSNVYATHYAESVKG 68

RESULT 13
 AAW46958
 ID AAW46958 standard; protein; 119 AA.
 XX
 AC AAW46958;

DT 06-JUL-1998 (first entry)
 XX

DE Amino acid sequence of a synthetic branched mucin type glycolipid.
 XX Branched mucin type glycolipid; V region; heavy chain; antibody;
 KW cancer treatment; diagnosis.
 XX

OS Synthetic.
 XX

PN JP10084963-A.
 XX

PD 07-APR-1998.
 XX

PF 12-SEP-1996; 96JP-00241725.
 XX

PR 12-SEP-1996; 96JP-00241725.
 XX

XX (TOYJ) TOSOH CORP.
 PA
 XX WPI; 1998-264850/24.
 DR N-PSDB; AAV22331.
 XX
 PT Recognising branched mucin type synthetic glycolipid - using gene
 PT fragment of an antibody, useful in cancer treatment and diagnosis.
 XX
 PS Disclosure; Page 4-5; 6pp; Japanese.
 XX

CC The present sequence represents a branched mucin type synthetic
 CC glycolipid. A gene fragment encoding the V region of the heavy chain of
 CC an antibody recognising the present protein is claimed. The antibody gene
 CC fragment is useful for the development of cancer treatments and
 CC diagnosing agents
 CC

SQ Sequence 119 AA;

Query Match 94.9%; Score 93; DB 2; Length 119;
 Best Local Similarity 94.7%; Pred. No. 2e-07;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
 |||||:|||||
 DB 50 EIRLKSNVYATHYAESVKG 68

RESULT 14
 ABR82775
 ID ABR82775 standard; protein; 119 AA.
 XX

AC ABR82775;

XX 18-DEC-2003 (first entry)
 DT

XX Hybridoma HB22-23 anti-CD22 MAb heavy chain Vh-D-Jh junction sequence.
 DE

XX CD22; B-cell malignancy; anti-CD22 antibody; cytostatic; human; HB22-23.
 KW

XX Homo sapiens.
 OS

XX WO2003072036-A2.
 PN

XX 04-SEP-2003.
 PD

XX 20-FEB-2003; 2003WO-US005323.
 PF

XX 21-FEB-2002; 2002US-0359419P.
 PR

XX 21-OCT-2002; 2002US-0420472P.
 PR

XX (UYDU-) UNIV DUKE.
 PA

PA (REGC) UNIV CALIFORNIA.
 XX

XX Tedder T, Tuscano J;
 PI

XX WPI; 2003-712652/67.
 DR

DR N-PSDB; ACF36425.
 XX

PT Treating a human patient diagnosed with a B-cell malignancy by
 PT administering a blocking anti-CD22 monoclonal antibody binding to the
 PT first two Ig-like domains of native human CD22 (hCD22).
 XX

PS Claim 31; Fig 14; 72pp; English.
 XX

CC The invention relates to treating a human patient diagnosed with a B-cell
 CC malignancy. The method involves (a) administering to the human patient a
 CC blocking anti-CD22 monoclonal antibody binding to the first two Ig-like
 CC domains, or to an epitope within the first two Ig-like domains of native
 CC human CD22 (hCD22) (ABR82771) and (b) monitoring the response of the
 CC malignancy to the treatment. The method is useful for treating a human
 CC patient diagnosed with a B-cell malignancy comprising Hodgkin's lymphoma,
 CC Burkitt's lymphoma, multiple myeloma, chronic lymphocytic leukemia, hairy

Db 50 EIRLKSNNYATHYAESVKG 68
Search completed: April 18, 2005, 14:15:21
Job time : 202.163 secs

CC cell leukemia or polymphocytic leukemia. The present sequence represents
CC the amino acid sequence for heavy chain Vh-D-Jh junction for anti-CD22
CC antibody from hybridoma HB22-23
XX
SQ Sequence 119 AA;

Query Match 94.9%; Score 93; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNNYATHYAESVKG 19
|||||:|||||
DB 50 EIRLKSNNYATHYAESVKG 68

RESULT 15
ABR82885
ID ABR82885 standard; protein; 119 AA.
XX
AC ABR82885;
XX
DT 18-DEC-2003 (first entry)
XX
DE Hybridoma HB22-23 anti-CD22 Mab heavy chain (VH) fragment.
XX
KW CD22; autoimmune disease; anti-CD22 antibody; immunosuppressive;
KW cytostatic; nephrotropic; dermatological; antiinflammatory; anti-ulcer;
KW antirheumatic; antiarthritic; antipsoriatic; thyromimetic; antianemic;
KW antidiabetic; antiallergic; gene therapy; HB22-23.
XX
OS Homo sapiens.

XX WO2003072736-A2.
XX
XX 04-SEP-2003.
XX
XX 21-FEB-2003; 2003WO-US005549.
XX
XX 21-FEB-2002; 2002US-0359419P.
XX 21-OCT-2002; 2002US-0420472P.
XX
XX (UYDU-) UNIV DUKE.
XX
XX Tedder TF;
XX
XX WFI; 2003-721765/68.
XX N-PSDB; ACF36493.
XX
XX Treating an autoimmune disease or a B-cell malignancy in a human patient
XX comprises administering an amount of an anti-CD22 monoclonal antibody to
XX the patient and monitoring the response of the disease to the treatment.
XX
XX Claim 1; Fig 14; 69pp; English.

XX The invention relates to treating a human patient diagnosed with an
XX autoimmune disease. The method involves administering to the patient an
XX amount of a blocking anti-CD22 monoclonal antibody and monitoring the
XX response of the autoimmune disease to the treatment. The method is useful
XX in treating autoimmune diseases (e.g. glomerulonephritis, systemic lupus
XX erythematosus, rheumatoid arthritis, psoriasis, ulcerative colitis,
XX Hashimoto's thyroiditis, autoimmune haemolytic anemias, diabetes or
XX allergies) or B-cell malignancies (e.g. lymphomas or leukemias). The
XX present sequence represents the amino acid sequence for heavy chain Vh-D-
XX Jh junction for anti-CD22 antibody from hybridoma HB22-23
XX
XX Sequence 119 AA;

Query Match 94.9%; Score 93; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNNYATHYAESVKG 19
|||||:|||||

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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:22:17 ; Search time 143.605 Seconds
(without alignments)
43.975 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRLKSDNYATHYAESVKG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10D_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	100.0	123	14	US-10-160-506-69
2	98	100.0	123	16	US-10-449-379-69
3	98	100.0	123	16	US-10-688-015-69
4	98	100.0	285	9	US-09-883-758-4
5	95	96.9	100	9	US-09-840-459-36
6	95	96.9	100	16	US-10-766-773-36
7	95	96.9	100	16	US-10-766-610-36
8	95	96.9	100	16	US-10-733-563-36
9	95	96.9	298	9	US-09-883-758-2
10	93	94.9	119	15	US-10-372-481-15
11	93	94.9	119	15	US-10-371-797-15
12	93	94.9	122	17	US-10-879-994-66
13	93	94.9	255	15	US-10-239-656-69

14	93	94.9	256	15	US-10-239-656-61	Sequence 61, Appl
15	93	94.9	503	15	US-10-239-656-77	Sequence 77, Appl
16	91	92.9	19	16	US-10-769-308-32	Sequence 32, Appl
17	91	92.9	19	17	US-10-769-074-32	Sequence 32, Appl
18	91	92.9	151	9	US-09-564-329A-15	Sequence 15, Appl
19	91	92.9	151	9	US-09-855-153-15	Sequence 15, Appl
20	91	92.9	151	9	US-09-854-811-15	Sequence 15, Appl
21	91	92.9	151	9	US-09-934-773-15	Sequence 15, Appl
22	91	92.9	151	9	US-09-963-620-15	Sequence 15, Appl
23	91	92.9	151	10	US-09-855-632-15	Sequence 15, Appl
24	91	92.9	151	14	US-10-225-784-15	Sequence 15, Appl
25	91	92.9	151	14	US-10-224-720-15	Sequence 15, Appl
26	91	92.9	151	14	US-10-225-779-15	Sequence 15, Appl
27	91	92.9	151	15	US-10-374-381-15	Sequence 15, Appl
28	91	92.9	151	15	US-10-446-542-15	Sequence 15, Appl
29	91	92.9	151	16	US-10-769-308-27	Sequence 27, Appl
30	91	92.9	151	17	US-10-769-074-27	Sequence 70, Appl
31	90	91.8	123	14	US-10-160-506-70	Sequence 70, Appl
32	90	91.8	123	16	US-10-449-379-70	Sequence 70, Appl
33	90	91.8	123	16	US-10-688-015-70	Sequence 11, Appl
34	85	86.7	114	14	US-10-422-049-11	Sequence 12, Appl
35	85	86.7	114	14	US-10-422-049-12	Sequence 68, Appl
36	82	83.7	17	17	US-10-879-994-68	Sequence 7, Appl
37	82	83.7	117	14	US-10-277-471A-5	Sequence 5, Appl
38	82	83.7	262	14	US-10-277-471A-5	Sequence 30, Appl
39	79	80.6	19	14	US-10-160-506-30	Sequence 30, Appl
40	79	80.6	19	16	US-10-449-379-30	Sequence 30, Appl
41	79	80.6	19	16	US-10-688-015-30	Sequence 47, Appl
42	79	80.6	116	14	US-10-160-506-47	Sequence 49, Appl
43	79	80.6	116	14	US-10-160-506-49	Sequence 60, Appl
44	79	80.6	116	14	US-10-160-506-60	Sequence 61, Appl
45	79	80.6	116	14	US-10-160-506-61	

ALIGNMENTS

RESULT 1
US-10-160-506-69
; Sequence 69, Application US/10160506
; Publication No. US20030161832A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR PROSTATE SPECIFIC MEMBRANE ANTIGEN
; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR PROSTATE SPECIFIC MEMBRANE ANTIGEN
; FILE REFERENCE: 10448-162001
; CURRENT APPLICATION NUMBER: US/10/160,506
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/324,100
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,612
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-160-506-69

Query Match 100.0%; Score 98; DB 14; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
|||||
Db 50 EIRLKSDNYATHYAESVKG 68

RESULT 2
US-10-449-379-69
; Sequence 69, Application US/10449379

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; Publication No. US20040120958A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 10448-163002
; CURRENT APPLICATION NUMBER: US/10/449,379
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 10/160,505
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/323,585
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,810
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/295,214
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-449-379-69

Query Match      100.0%; Score 98; DB 16; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLXSDNYATHYAESVKG 19
Db 50 EIRLXSDNYATHYAESVKG 68

RESULT 3
US-10-688-015-69
; Sequence 69, Application US/10688015
; Publication No. US20040136998A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; TITLE OF INVENTION: INSULIN-RELATED DISORDERS USING BINDING AGENTS SPECIFIC FOR
; FILE REFERENCE: 10448-196001
; CURRENT APPLICATION NUMBER: US/10/688,015
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/422,396
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-688-015-69

Query Match      100.0%; Score 98; DB 16; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLXSDNYATHYAESVKG 19
Db 50 EIRLXSDNYATHYAESVKG 68

RESULT 4
US-09-883-758-4
; Sequence 4, Application US/09883758
; Patent No. US20020058804A1
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
```

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; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF0011S
; CURRENT APPLICATION NUMBER: US/09/883,758
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/318,661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment
US-09-883-758-4

Query Match      100.0%; Score 98; DB 9; Length 285;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLXSDNYATHYAESVKG 19
Db 203 EIRLXSDNYATHYAESVKG 221

RESULT 5
US-09-840-459-36
; Sequence 36, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-840-459-36

Query Match      96.9%; Score 95; DB 9; Length 100;
Best Local Similarity 94.7%; Pred. No. 2.9e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLXSDNYATHYAESVKG 19
Db 50 EIRLXSDNYATHYAESVKG 68

RESULT 6
US-10-766-773-36
; Sequence 36, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
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APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
FILE REFERENCE: 1855.1052-028
CURRENT APPLICATION NUMBER: US/10/766,773
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 100
TYPE: PRT
ORGANISM: Mus musculus
US-10-766-773-36

Query Match 96.9%; Score 95; DB 16; Length 100;
Best Local Similarity 94.7%; Pred. No. 2.9e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
DB 50 QIRLSDNYATHYAESVKG 68

RESULT 7
US-10-766-610-36
Sequence 36, Application US/10766610
Publication No. US20040132980A1
GENERAL INFORMATION:
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
FILE REFERENCE: 1855.1052-029
CURRENT APPLICATION NUMBER: US/10/766,610
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: 09/840,459
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 100
TYPE: PRT
ORGANISM: Mus musculus
US-10-766-610-36

Query Match 96.9%; Score 95; DB 16; Length 100;
Best Local Similarity 94.7%; Pred. No. 2.9e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19

DB 50 QIRLSDNYATHYAESVKG 68

RESULT 8
US-10-733-563-36
Sequence 36, Application US/10733563
Publication No. US20040151721A1
GENERAL INFORMATION:
APPLICANT: O'Keefe, Theresa
APPLICANT: Ponath, Paul
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
FILE REFERENCE: 10448-213001
CURRENT APPLICATION NUMBER: US/10/733,563
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: US 10/272,899
PRIOR FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 60/392,364
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/350,166
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 100
TYPE: PRT
ORGANISM: Mus musculus
US-10-733-563-36

Query Match 96.9%; Score 95; DB 16; Length 100;
Best Local Similarity 94.7%; Pred. No. 2.9e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
DB 50 QIRLSDNYATHYAESVKG 68

RESULT 9
US-09-883-758-2
Sequence 2, Application US/09883758
Patent No. US20020059804A1
GENERAL INFORMATION:
APPLICANT: Barbas III, Carlos F.
APPLICANT: Shabat, Doron
APPLICANT: Rader, Christoph
APPLICANT: List, Benjamin
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
FILE REFERENCE: PLF00115
CURRENT APPLICATION NUMBER: US/09/883,758
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US/09/318,661
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 298
TYPE: PRT
ORGANISM: Mus musculus
US-09-883-758-2

Query Match 96.9%; Score 95; DB 9; Length 298;
Best Local Similarity 94.7%; Pred. No. 9.6e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
DB 205 EIRLSDNYATHYAESVKG 223

RESULT 10

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US-10-372-481-15
; Sequence 15, Application US/10372481
; Publication No. US20030202975A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas P.
; TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 5405,306
; CURRENT APPLICATION NUMBER: US/10/372,481
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/US03/05549
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-372-481-15

Query Match          94.9%; Score 93; DB 15; Length 119;
Best Local Similarity 94.7%; Pred. No. 7.3e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
Db 50 EIRKSNYYATHYAESVKG 68

RESULT 11
US-10-371-797-15
; Sequence 15, Application US/10371797
; Publication No. US20040001828A1
; GENERAL INFORMATION:
; APPLICANT: TUSCANO, Joseph
; APPLICANT: TEDDER, Thomas
; TITLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22
; FILE REFERENCE: 39754-0951
; CURRENT APPLICATION NUMBER: US/10/371,797
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 119
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-371-797-15

Query Match          94.9%; Score 93; DB 15; Length 119;
Best Local Similarity 94.7%; Pred. No. 7.3e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
Db 50 EIRKSNYYATHYAESVKG 68

RESULT 12
US-10-879-994-66
; Sequence 66, Application US/10879994
; Publication No. US20050032175A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Yancopoulos, George D.
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; APPLICANT: Karow, Margaret
; APPLICANT: Smith, Eric
; TITLE OF INVENTION: HIGH AFFINITY FUSION PROTEINS AND THERAPEUTIC AND DIAGNOSTIC METH
; FILE REFERENCE: REG 203E2
; CURRENT APPLICATION NUMBER: US/10/879,994
; CURRENT FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: 10/610,452
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 122
; TYPE: PRT
; ORGANISM: mus musculus
; US-10-879-994-66

Query Match          94.9%; Score 93; DB 17; Length 122;
Best Local Similarity 94.7%; Pred. No. 7.5e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
Db 50 EIRKSNYYATHYAESVKG 68

RESULT 13
US-10-239-656-69
; Sequence 69, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTERBEUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HORMEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-11 single
; OTHER INFORMATION: chain Fv
; US-10-239-656-69

Query Match          94.9%; Score 93; DB 15; Length 255;
Best Local Similarity 94.7%; Pred. No. 1.7e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
Db 51 EIRKSNYYATHYAESVKG 69

RESULT 14
US-10-239-656-61
; Sequence 61, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
```

Db 298 EIRLKSNNYATHYAESVKG 316
Search completed: April 18, 2005, 14:54:43
Job time : 144.605 secs

; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFMEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-2 single
; OTHER INFORMATION: chain Fv
; US-10-239-656-61

Query Match 94.9%; Score 93; DB 15; Length 256;
Best Local Similarity 94.7%; Pred. No. 1.7e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNNYATHYAESVKG 19
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Db 51 EIRLKSNNYATHYAESVKG 69

RESULT 15
US-10-239-656-77
; Sequence 77, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUPER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFMEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic 3B10XP5-
; OTHER INFORMATION: 2 bispecific single chain Fv
; US-10-239-656-77

Query Match 94.9%; Score 93; DB 15; Length 503;
Best Local Similarity 94.7%; Pred. No. 3.5e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNNYATHYAESVKG 19
|||||:|||||

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:01:43 ; Search time 51.6977 Seconds
(without alignments)
27.435 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98
Sequence: 1 EIRLKSNDVATHYAESVKG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	285	3	US-09-318-661-4
2	98	100.0	285	4	US-09-883-758-4
3	95	96.9	100	4	US-09-840-459-36
4	95	96.9	100	4	US-09-497-625A-36
5	95	96.9	298	3	US-09-318-661-2
6	95	96.9	298	4	US-09-883-758-2
7	93	94.9	115	1	US-08-468-661-1
8	93	94.9	115	1	US-08-466-722A-1
9	93	94.9	115	1	US-08-478-857-1
10	93	94.9	115	2	US-08-471-771-1
11	93	94.9	115	3	US-09-130-783-1
12	93	94.9	120	3	US-08-767-128-28
13	93	94.9	122	3	US-08-483-749A-2
14	91	92.9	151	4	US-09-564-329A-15
15	91	92.9	151	4	US-09-963-620-15
16	91	92.9	151	4	US-09-855-632-15
17	91	92.9	151	4	US-09-934-773-15
18	85	86.7	114	3	US-08-483-749A-10
19	80.5	82.1	119	3	US-08-767-128-26
20	74	75.5	119	1	US-08-192-102-5
21	74	75.5	119	1	US-08-324-799-5
22	74	75.5	119	2	US-08-192-861A-5
23	74	75.5	119	3	US-09-133-119-5
24	74	75.5	119	3	US-08-192-093A-5
25	74	75.5	119	4	US-09-756-301B-5
26	74	75.5	119	4	US-09-756-398B-5
27	72	73.5	119	1	US-08-442-542-45

28	72	73.5	119	3	US-08-765-469-45	Sequence 45, Appli
29	71	72.4	227	1	US-08-681-432-2	Sequence 2, Appli
30	68	69.4	19	2	US-08-737-085A-4	Sequence 4, Appli
31	68	69.4	19	3	US-09-246-258-4	Sequence 4, Appli
32	68	69.4	19	3	US-09-532-106-4	Sequence 4, Appli
33	68	69.4	19	4	US-09-839-666-4	Sequence 4, Appli
34	68	69.4	27	2	US-08-737-085A-21	Sequence 21, Appli
35	68	69.4	27	3	US-09-246-258-21	Sequence 21, Appli
36	68	69.4	27	4	US-09-532-106-21	Sequence 21, Appli
37	68	69.4	27	4	US-09-839-666-21	Sequence 21, Appli
38	67	68.4	110	3	US-08-767-128-24	Sequence 24, Appli
39	67	68.4	115	3	US-08-767-128-36	Sequence 24, Appli
40	66	67.3	19	1	US-07-977-696C-78	Sequence 78, Appli
41	66	67.3	19	1	US-08-129-930B-78	Sequence 78, Appli
42	66	67.3	19	3	US-08-976-288A-78	Sequence 78, Appli
43	66	67.3	100	4	US-09-840-459-35	Sequence 35, Appli
44	66	67.3	100	4	US-09-497-625A-35	Sequence 35, Appli
45	66	67.3	134	1	US-07-977-696C-13	Sequence 13, Appli

ALIGNMENTS

RESULT 1
US-09-318-661-4
; Sequence 4, Application US/09318661
; Patent No. 6268488
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/318,661
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment
US-09-318-661-4

Query Match 100.0%; Score 98; DB 3; Length 285;
Best Local Similarity 100.0%; Pred. No. 5.2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDVATHYAESVKG 19
|||
DB 203 EIRLKSNDVATHYAESVKG 221

RESULT 2
US-09-883-758-4
; Sequence 4, Application US/09883758
; Patent No. 6677435
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/883,758
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/318,661
; PRIOR FILING DATE: 1999-05-25

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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment
US-09-883-758-4

Query Match          100.0%; Score 98; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 5.2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EIRLKSNDNYATHYAESVKG 19
Db      203 EIRLKSNDNYATHYAESVKG 221

RESULT 3
US-09-840-459-36
; Sequence 36, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-36

Query Match          96.9%; Score 95; DB 4; Length 100;
Best Local Similarity 94.7%; Pred. No. 5e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 EIRLKSNDNYATHYAESVKG 19
Db      50 QIRLKSNDNYATHYAESVKG 68

RESULT 4
US-09-497-625A-36
; Sequence 36, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
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; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-497-625A-36

Query Match          96.9%; Score 95; DB 4; Length 100;
Best Local Similarity 94.7%; Pred. No. 5e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 EIRLKSNDNYATHYAESVKG 19
Db      50 QIRLKSNDNYATHYAESVKG 68

RESULT 5
US-09-318-661-2
; Sequence 2, Application US/09318661
; Patent No. 6268488
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/318,661
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-318-661-2

Query Match          96.9%; Score 95; DB 3; Length 298;
Best Local Similarity 94.7%; Pred. No. 1.7e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 EIRLKSNDNYATHYAESVKG 19
Db      205 EIRLKSNDNYATHYAESVKG 223

RESULT 6
US-09-883-758-2
; Sequence 2, Application US/09883758
; Patent No. 6677435
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/883,758
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/318,661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
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/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 298
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-883-758-2

Query Match          96.9%; Score 95; DB 4; Length 298;
Best Local Similarity 94.7%; Pred. No. 1.2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHYAESVKG 19
   |||||:|||||
Db 205 EIRLSDNYATHYAESVKG 223

RESULT 7
US-08-468-661-1
/ Sequence 1, Application US/08468661
/ Patent No. 5639621
/ GENERAL INFORMATION:
/ APPLICANT: Bosslet, Klaus
/ APPLICANT: Pfeleiderer, Peter
/ APPLICANT: Seeman, Gerhard
/ TITLE OF INVENTION: Monoclonal Antibodies Against
/ TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the
/ TITLE OF INVENTION: Preparation Thereof and the Use Thereof
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE: 06-JUNE-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION NUMBER: US 07/957,827
/ FILING DATE: 08-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Forman, David S.
/ REGISTRATION NUMBER: 35,694
/ REFERENCE/DOCKET NUMBER: 05552-1227-02000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 115 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-468-661-1

Query Match          94.9%; Score 93; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 1.2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHYAESVKG 19
   |||||:|||||
Db 46 EIRLSDNYATHYAESVKG 64

RESULT 8
US-08-466-272A-1
/ Sequence 1, Application US/08466272A
/ Patent No. 5674994
/ GENERAL INFORMATION:
/ APPLICANT: Bosslet, Klaus
/ APPLICANT: Pfeleiderer, Peter
/ APPLICANT: Seeman, Gerhard
/ TITLE OF INVENTION: Monoclonal Antibodies Against
/ TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the Preparation
/ TITLE OF INVENTION: Thereof and the Use Thereof
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/957,827
/ FILING DATE: 08-OCT-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bugalsky, Lawrence B.
/ REGISTRATION NUMBER: 35,086
/ REFERENCE/DOCKET NUMBER: 02481-1227-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 115 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-466-272A-1

Query Match          94.9%; Score 93; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 1.2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHYAESVKG 19
   |||||:|||||
Db 46 EIRLSDNYATHYAESVKG 64

RESULT 9
US-08-478-857-1
/ Sequence 1, Application US/08478857
/ Patent No. 5695758
/ GENERAL INFORMATION:
/ APPLICANT: Bosslet, Klaus
/ APPLICANT: Pfeleiderer, Peter
/ APPLICANT: Seeman, Gerhard
/ TITLE OF INVENTION: Monoclonal Antibodies Against
/ TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the Preparation
/ TITLE OF INVENTION: Thereof and the Use Thereof
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
/ STREET: 1300 I Street, N.W., Suite 700
/ CITY: Washington
```

STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,857
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/957,827
FILING DATE: 08-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 02481-1227-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-478-857-1

Query Match 94.9%; Score 93; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 1.2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHVAESVKG 19
Db 46 EIRKSNYYATHVAESVKG 64

RESULT 10
US-08-471-771-1
Sequence 1, Application US/08471771
Patent No. 5837824
GENERAL INFORMATION:
APPLICANT: Bosset, Klaus
APPLICANT: Pfeleiderer, Peter
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Monoclonal Antibodies Against
TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the
TITLE OF INVENTION: Preparation Thereof and the Use Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,771
FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/957,827
FILING DATE: 08-OCT-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:

NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552-1227-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-471-771-1

Query Match 94.9%; Score 93; DB 2; Length 115;
Best Local Similarity 94.7%; Pred. No. 1.2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHVAESVKG 19
Db 46 EIRKSNYYATHVAESVKG 64

RESULT 11
US-09-130-783-1
Sequence 1, Application US/09130783
Patent No. 6030797
GENERAL INFORMATION:
APPLICANT: Bosset, Klaus
APPLICANT: Pfeleiderer, Peter
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Monoclonal Antibodies Against
TITLE OF INVENTION: Tumor-Associated Antigens, Processes for the
TITLE OF INVENTION: Preparation Thereof and the Use Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,783
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/471,771
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552-1227-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-130-783-1

Query Match 94.9%; Score 93; DB 3; Length 115;
Best Local Similarity 94.7%; Pred. No. 1.2e-07;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 46 EIRLKSNNYATHYAESVKG 64

RESULT 12
US-08-767-128-28
; Sequence 28, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSWALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-28

Query Match 94.9%; Score 93; DB 3; Length 120;
Best Local Similarity 94.7%; Pred. No. 1.3e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 13
US-08-483-749A-2
; Sequence 2, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-749A-2

Query Match 94.9%; Score 93; DB 3; Length 122;
Best Local Similarity 94.7%; Pred. No. 1.3e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 14
US-09-564-329A-15
; Sequence 15, Application US/09564329A
; Patent No. 6541212
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/564,329A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675

Tue Apr 19 06:14:46 2005

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; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-564-329A-15

Query Match          92.9%; Score 91; DB 4; Length 151;
Best Local Similarity 89.5%; Pred. No. 3.5e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 EIRLKSDNYATHYAESVKG 19
      |||||:|||||
Db      69 EIRLRSENYATHYAESVKG 87
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RESULT 15
US-09-963-620-15
; Sequence 15, Application US/09963620
; Patent No. 6756036
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Safran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/963,620
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
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; ORGANISM: SCID Mice
US-09-963-620-15
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Query Match          92.9%; Score 91; DB 4; Length 151;
Best Local Similarity 89.5%; Pred. No. 3.5e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 EIRLKSDNYATHYAESVKG 19
      |||||:|||||
Db      69 EIRLRSENYATHYAESVKG 87
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Search completed: April 18, 2005, 14:25:39
Job time : 59.6977 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:48:01 ; Search time 44 Seconds
(without alignments)
41.548 Million cell updates/sec

Title: US-09-674-716B-11
Perfect score: 98
Sequence: 1 EIRLKSNDNYATHVAESVKG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3436

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26.5	27.0	16	2 A39109	hypothetical prote
2	25	25.5	10	2 S77990	cytochrome-c oxida
3	24	24.5	19	2 S39387	protein kinase GSK
4	23	23.5	15	2 PH1631	Ig H chain V-D-J r
5	23	23.5	16	2 B60278	24K antigen - Myco
6	22	22.4	10	2 D46285	formaldehyde dehyd
7	22	22.4	14	2 S59495	formate dehydrogen
8	22	22.4	15	2 PA0046	protein OA100044
9	22	22.4	15	2 I67325	CD33 antigen homol
10	22	22.4	18	2 F49215	urease (EC 3.5.1.5
11	22	22.4	18	2 PQ0072	T-cell receptor be
12	22	22.4	19	2 A41077	protein-disulfide
13	21	21.4	9	2 B24362	chloramphenicol O-
14	21	21.4	9	2 S30494	cat gene leader pe
15	21	21.4	12	2 PH1587	Ig H chain V-D-J r
16	21	21.4	14	2 PH1471	T-cell receptor be
17	21	21.4	16	2 A29520	amino-acid racemas
18	21	21.4	17	2 A61334	trypsin (EC 3.4.21
19	21	21.4	18	2 PH0768	T-cell receptor be
20	21	21.4	18	4 I56393	lacZ/IS1 mutant fu
21	20	20.4	9	2 PT0238	Ig heavy chain CRD
22	20	20.4	10	2 S65388	cytochrome-c oxida
23	20	20.4	11	2 PT0301	Ig heavy chain CRD
24	20	20.4	12	2 S26546	T-cell receptor be
25	20	20.4	12	4 PC2122	aminotransferase c
26	20	20.4	13	2 PH1595	Ig H chain V-D-J r
27	20	20.4	14	2 A47421	leukotriene B-4 12
28	20	20.4	15	2 I78838	flt3 ligand isofor
29	20	20.4	15	2 A30330	neuropeptide pep -

ribulose-bisphosph
hypothetical prote
Ig H chain V-D-J r
Ig H chain V-D-J r
hypothetical prote
Ig H chain V-D-J r
Tha p 1 - Thaumeto
26K kidney and gal
leucosulfakinin-II
leucosulfakinin II
ranatachykinin B -
hypothetical prote
hypothetical prote
Ig gamma-2b chain
proteinase E - bla
serine proteinase

ALIGNMENTS

RESULT 1

A39109
hypothetical protein 1 - hepatitis C virus
C;Species: hepatitis C virus
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 18-Jun-1993
C;Accession: A39109
R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A;Title: Characterization of the terminal regions of hepatitis C viral RNA: identificat
A;Reference number: A39109; MUID:91156678; PMID:1705704
A;Accession: A39109
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-16 <HAN>
A;Cross-references: GB:M58406

Query Match 27.0%; Score 26.5; DB 2; Length 16;
Best Local Similarity 70.0%; Pred. No. 5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 8 NYATHVAESV 17
||| |||||
Db 8 NYCLH-AESV 16

RESULT 2

S77990
cytochrome-c oxidase (EC 1.9.3.1) chain VIIc - bigeye tuna (fragment)
C;Species: Thunnus obesus (bigeye tuna)
C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: S77990
R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A;Reference number: S77980
A;Accession: S77990
A;Molecule type: protein
A;Residues: 1-10 <ARN>
A;Cross-references: UNIPROT:P80982
A;Experimental source: heart; liver
C;Genetics:
A;Genome: nuclear
C;Function:
A;Pathway: oxidative phosphorylation; respiratory chain
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membran

Query Match 25.5%; Score 25; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 THYAE 15
:|||||
Db 1 SHYAE 5

RESULT 3

S39387
 protein kinase GSK-3-beta (EC 2.7.1.1) - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 07-May-1999
 C:Accession: S39387
 R:Sutherland, C.; Leighton, I.A.; Cohen, P.
 Biochem. J. 296, 15-19, 1993
 A>Title: Inactivation of glycogen synthase kinase-3-beta by phosphorylation: new kinase
 A:Reference number: S39387; MUID:94071817; PMID:8250835
 A:Accession: S39387
 A:Molecule type: protein
 A:Residues: 1-19 <SUT>
 A:Superfamily: Kinase-related transforming protein; protein kinase homology
 C:Keywords: phosphotransferase; protein kinase

Query Match 24.5%; Score 24; DB 2; Length 19;
 Best Local Similarity 62.5%; Pred. No. 1.6e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 THYAESVK 18
 | : || |
 DB 2 TSPAESXK 9

RESULT 4

PH1631
 IG H chain V-D-J region (clone B-less 202) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1631
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A>Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:Reference number: PH1580; MUID:93301609; PMID:8315387
 A:Accession: PH1631
 A:Molecule type: DNA
 A:Residues: 1-15 <LEV>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Keywords: immunoglobulin

Query Match 23.5%; Score 23; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 SDNYATHY 13
 | : || |
 DB 8 TDGYAMDY 15

RESULT 5

B60278
 24K antigen - Mycobacterium bovis (fragment)
 C:Species: Mycobacterium bovis
 C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
 C:Accession: B60278
 R:Fiifis, T.; Costopoulos, C.; Radford, A.J.; Bacic, A.; Wood, P.R.
 Infect. Immun. 59, 800-807, 1991
 A>Title: Purification and characterization of major antigens from a Mycobacterium bovis
 A:Reference number: A60278; MUID:91147217; PMID:1900061
 A:Accession: B60278
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-16 <FIF>
 A:Cross-references: UNIPROT:Q7M199

Query Match 23.5%; Score 23; DB 2; Length 16;
 Best Local Similarity 57.1%; Pred. No. 1.9e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 YAESVKG 19

DB 5 YKELKG 11
 | : || |

RESULT 6

D46285
 formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1) class III low activity form - Atle
 C:Species: Gadus morhua (Atlantic cod)
 C>Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: D46285
 R:Danielsson, O.; Jornvall, H.
 Proc. Natl. Acad. Sci. U.S.A. 89, 9247-9251, 1992
 A>Title: "Enzymogenesis": classical liver alcohol dehydrogenase origin from the glutathione
 A:Reference number: A46285; MUID:93028441; PMID:1409630
 A:Accession: D46285
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <DAN>
 A:Cross-references: UNIPROT:Q9PSQ8
 A>Note: sequence extracted from NCBI backbone (NCBI:116272)
 C:Keywords: NAD; oxidoreductase

Query Match 22.4%; Score 22; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 DNYATH 12
 | : || |
 DB 1 DEFVTH 6

RESULT 7

S59495
 formate dehydrogenase delta chain - Alcaligenes eutrophus (fragment)
 C:Species: Alcaligenes eutrophus
 C>Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S59495
 R:Friedebold, J.; Mayer, F.; Bill, E.; Trautwein, A.X.; Bowien, B.
 Biol. Chem. Hoppe-Seyler 376, 561-568, 1995
 A>Title: Structural and immunological studies on the soluble formate dehydrogenase from
 A:Reference number: S59492; MUID:96145736; PMID:8561915
 A:Accession: S59495
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <FRI>
 A:Cross-references: UNIPROT:Q7M0N7

Query Match 22.4%; Score 22; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 2.3e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 LKSDNYATH 12
 | : || |
 DB 1 MKIDNIITY 9

RESULT 8

PA0046
 protein QA100044 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C:Accession: PA0046; PA0042
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Teugita, A.
 submitted to JIPID, July 1994
 A>Description: Separation and characterization of Arabidopsis proteins by two-dimensional
 A:Reference number: PA0001
 A:Accession: PA0046
 A:Molecule type: protein
 A:Residues: 1-15 <KAM>
 A:Experimental source: stem

Query Match 22.4%; Score 22; DB 2; Length 15;
 Best Local Similarity 83.3%; Pred. No. 2.5e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 AESVKG 19
|||
Db 1 AESKKG 6

RESULT 9
I67525
CD33 antigen homolog - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I67525
R;Chies, J.A.; Lembezat, M.P.; Freitas, A.A.
Eur. J. Immunol. 24, 1657-1664, 1994
A:Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is
A:Reference number: I53392; MUID:94298870; PMID:8026526
A:Accession: I67525
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-15 <RES>
A:Cross-references: UNIPROT:Q7M0G8; GB:S71349; NID:g550037
C:Genetics:
A:Gene: I9 VH7183

Query Match 22.4%; Score 22; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 2.5e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 KSDNYATHY 13
:|:|:
Db 4 RRDHYGSSY 12

RESULT 10
F49215
urease (EC 3.5.1.5) small chain UreA - Helicobacter mustelae (ATCC 43772) (fragment)
C:Species: Helicobacter mustelae
C:Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: F49215
R;Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.
Infect. Immun. 60, 5259-5266, 1992
A:Title: Purification and characterization of the urease enzymes of Helicobacter species
A:Reference number: A49215; MUID:93084378; PMID:14522359
A:Cross-references: UNIPROT:Q9R5F6
C:Superfamily: urease, fused gamma/beta subunit; urease 11K chain homology; urease 12K
C:Keywords: hydrolase

Query Match 22.4%; Score 22; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 DNYATHYA 14
|
Db 7 DKMLHYA 14

RESULT 11
PQ0072
T-cell receptor beta chain (BTB98) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
C:Accession: PQ0072
R;Tanaka, A.; Ishiguro, N.; Shinagawa, M.
submitted to JIPID, May 1990
A:Description: Sequence analysis of bovine T-cell receptor beta chain genes.
A:Reference number: JQ0472
A:Accession: PQ0072

A:Molecule type: mRNA
A:Residues: 1-18 <TAN>
A:Experimental source: T cell
C:Genetics:
A:Gene: BTB98
C:Keywords: receptor

Query Match 22.4%; Score 22; DB 2; Length 18;
Best Local Similarity 38.5%; Pred. No. 3.1e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 6 SDNYATHYAESVK 18
||:|:
Db 4 SDDY--HFGPGTK 14

RESULT 12

A41077
protein-disulfide reductase (glutathione) (EC 1.8.4.2) Q-5 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 23-Jun-1993
C:Accession: A41077
R;Srivastava, S.P.; Chen, N.; Liu, Y.; Holtzman, J.L.
J. Biol. Chem. 266, 20337-20344, 1991
A:Title: Purification and characterization of a new isozyme of thiol:protein-disulfide
fic phospholipase C form 1A.
A:Reference number: A41077; MUID:92041865; PMID:1657921
A:Accession: A41077
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <SRI>
C:Keywords: oxidoreductase

Query Match 22.4%; Score 22; DB 2; Length 19;
Best Local Similarity 57.1%; Pred. No. 3.3e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 LKSDNYA 10
|||:
Db 12 LKKSNEFA 18

RESULT 13

B24362
chloramphenicol O-acetyltransferase leader peptide - Staphylococcus aureus plasmid PUB1
C:Species: Staphylococcus aureus
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C:Accession: B24362
R;Bruckner, R.; Matzura, H.
EMBO J. 4, 2295-2300, 1985
A:Title: Regulation of the inducible chloramphenicol acetyltransferase gene of the Staphy-
lococcus aureus plasmid PUB1
A:Reference number: A24362; MUID:86081739; PMID:3865770
A:Accession: B24362
A:Molecule type: DNA
A:Residues: 1-9 <BRU>
A:Cross-references: UNIPROT:P36884; GB:X02872; NID:g46536; PIDN:CAA26630.1; PID:g581555
C:Comment: Ribosome stalling in the translation of this leader peptide, caused by the e-
nslation of the chloramphenicol O-acetyltransferase from a ribosome binding site locate.

C:Genetics:
A:Genome: plasmid
C:Superfamily: unassigned leader peptides

Query Match 21.4%; Score 21; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 KSDNYAT 11
||:|:
Db 3 KSEDYSS 9

RESULT 14

S30494

cat gene leader peptide - Streptococcus agalactiae plasmid pIP501
C;Species: Streptococcus agalactiae
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 16-Aug-2004
C;Accession: S30494
R;Trieu-Quot, P.; de Cespedes, G.; Haraud, T.
Plasmid 28, 272-276, 1992
A;Title: Nucleotide sequence of the chloramphenicol resistance determinant of the Streptococcus agalactiae plasmid pIP501
A;Reference number: JQ1950; MUID:93096867; PMID:1461942
A;Accession: S30494
A;Molecule type: DNA
A;Residues: 1-9 <TRI>
A;Cross-references: UNIPROT:P36884; EMBL:X65462; NID:G49071; PIDN:CAA46454.1; PID:G58153
C;Genetics:
A;Genome: plasmid pIP501

Query Match 21.4%; Score 21; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 5 KSDNYAT 11
Db 3 KSEDYSS 9

RESULT 15
PHI587
IG H chain V-D-J region (wild-type clone 11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1587
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1587
A;Molecule type: DNA
A;Residues: 1-12 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 21.4%; Score 21; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 2.9e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 5 KSDNYATHY 13
Db 4 RGDLYAMDY 12

Search completed: April 18, 2005, 15:57:40
Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:39:55 ; Search time 178 Seconds
(without alignments)
54.660 Million cell updates/sec

Title: US-09-674-716B-11
Perfect score: 98
Sequence: 1 EIRLKSNDYATHYAESVKG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 10410

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	32.7	19	2	Q73129
2	29	29.6	15	2	Q91BM5
3	28	28.6	13	2	Q9UC27
4	27	27.6	14	1	NEJ2_FASHE
5	27	27.6	15	2	Q7BVD9
6	27	27.6	17	2	Q7BVD5
7	27	27.6	19	2	Q9L434
8	26	26.5	13	2	Q9KHJ4
9	26	26.5	14	2	Q85CA1
10	26	26.5	15	2	Q9UWH6
11	26	26.5	15	2	Q9TRT4
12	26	26.5	15	2	Q9TRT6
13	26	26.5	19	2	Q84863
14	25	25.5	10	1	COXO_THUOB
15	25	25.5	17	2	Q9V2K3
16	25	25.5	19	2	Q86DB6
17	24	24.5	13	2	Q9TWR4
18	24	24.5	14	2	Q93057
19	24	24.5	14	2	P70319
20	23	23.5	9	2	Q93LE4
21	23	23.5	10	2	P96423
22	23	23.5	14	2	P96347
23	23	23.5	15	2	Q8UF12
24	23	23.5	16	2	Q7MI99
25	23	23.5	17	2	Q9R4H9
26	23	23.5	18	2	Q9UWJ7
27	23	23.5	18	2	Q70ZU6
28	23	23.5	18	2	Q9PRX1
29	22	22.4	9	2	Q7RHC2
30	22	22.4	10	2	Q67B26
31	22	22.4	12	1	LOSK_LOCM1

32 22 22.4 14 2 Q7MON7
33 22 22.4 15 2 Q6SLH8
34 22 22.4 15 2 Q6QOR4
35 22 22.4 15 2 Q7M0G8
36 22 22.4 16 2 Q9R4J4
37 22 22.4 17 2 Q7RGD8
38 22 22.4 17 2 Q9R4P9
39 22 22.4 18 2 Q7TRF1
40 22 22.4 18 2 Q78379
41 22 22.4 18 2 Q9R5F6
42 22 22.4 18 2 Q7ZFR2
43 21 21.4 7 2 Q8K3H6
44 21 21.4 9 1 LPCA_STAAU
45 21 21.4 9 2 Q6LDI6

ALIGNMENTS

RESULT 1

Q73129 PRELIMINARY; PRT; 19 AA.
AC Q73129
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Wolinsky S.M., Korber B.T.M., Neumann A.U., Daniels M., Kunstman K.J., Whetzel A.J., Cao Y., Ho D.D., Saffrit J.T., Koup R.A.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA McDonald D.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U36027; AA97722.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2066 MW; E117102D52800EF4 CRC64;

Query Match 32.7%; Score 32; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSNDYNA 10
| : : : : : |
Db 7 EVVIRSDNFA 16

RESULT 2

Q91BM5 PRELIMINARY; PRT; 15 AA.
AC Q91BM5
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Envelope glycoprotein, V3 region (Fragment).
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]

```

RP SEQUENCE FROM N.A.
RX MEDLINE=95115054; PubMed=7815476;
RA Ahmad N., Baroudy B.M., Baker R.C., Chappey C.;
RT "Genetic analysis of human immunodeficiency virus type 1 envelope V3
RT region isolates from mothers and infants after perinatal
RT transmission.";
RL J. Virol. 69:1001-1012(1995).
DR EMBL; U16595; AAA64161.1; -.
DR GO; GO:0019031; C:Viral envelope; IEA.
KW Envelope protein.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1794 MW; 747C6A62800EF4A1 CRC64;

Query Match 29.6%; Score 29; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSNDYA 10
DB 4 EVIIRSDNFS 13

RESULT 3
Q9UC27 PRELIMINARY; PRT; 13 AA.
AC Q9UC27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 94 kDa epididymal cytokeatin-like protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95226590; PubMed=7536047;
RA Boue F., Duquenne C., Lassalle B., Lefevre A., Finaz C.;
RT "FLB1, a human protein of epididymal origin that is involved in the
RT sperm-oocyte recognition process.";
RL Biol. Reprod. 52:267-278(1995).
SQ SEQUENCE 13 AA; 1610 MW; 000A683B81B7A45B CRC64;

Query Match 28.6%; Score 28; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 NYATHY 13
DB 1 NYSTY 6

RESULT 4
NEJ2_FASHE STANDARD; PRT; 14 AA.
AC P80526;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Newly excysted juvenile protein 2 (Fragment).
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fascioloidae; Fasciolidae.
OX NCBI_TaxID=6192;
RN [1]
RP SEQUENCE.
RX MEDLINE=95366993; PubMed=7639732;
RA Tkalcovic J., Ashman K., Meusen E.;
RT "Fasciola hepatica: rapid identification of newly excysted juvenile
RT proteins.";
RL Biochem. Biophys. Res. Commun. 213:169-174(1995).
CC -!- DEVELOPMENTAL STAGE: Expressed at the newly excysted juvenile
stage.

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KW Direct protein sequencing.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1581 MW; 9E0F0090CC8C0DF1 CRC64;

Query Match 27.6%; Score 27; DB 1; Length 14;
Best Local Similarity 62.5%; Pred. No. 2.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 DNYATHYA 14
DB 3 DNGRTHWA 10

RESULT 5
Q7BVD9 PRELIMINARY; PRT; 15 AA.
AC Q7BVD9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Borrelia burgdorferi plasmid cp32-2, possible partition proteins,
DE complete cds. (Fragment).
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid cp32-2.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B31;
RX MEDLINE=98361033; PubMed=9695920;
RA Stevenson B., Casjens S., Rosa P.;
RT "Evidence of past recombination events among the genes encoding the
RT Erp antigens of Borrelia burgdorferi.";
RL Microbiology 144:1869-1879(1998).
DR EMBL; AF022479; AAC35441.1; -.
KW Plasmid.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1817 MW; 90E468E030E20078 CRC64;

Query Match 27.6%; Score 27; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 YATHYAESVK 18
DB 6 YRTYNIESIK 15

RESULT 6
Q7BVD5 PRELIMINARY; PRT; 17 AA.
AC Q7BVD5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Borrelia burgdorferi plasmid cp32-7, possible partition proteins,
DE complete cds. (Fragment).
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid cp32-7.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B31;
RX MEDLINE=98361033; PubMed=9695920;
RA Stevenson B., Casjens S., Rosa P.;
RT "Evidence of past recombination events among the genes encoding the
RT Erp antigens of Borrelia burgdorferi.";
RL Microbiology 144:1869-1879(1998).
DR EMBL; AF022483; AAC35457.1; -.
KW Plasmid.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2060 MW; 6B5830E468E030E2 CRC64;

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Query Match 27.6%; Score 27; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 YATHYAESVK 18
DB 6 YRTYNIESIK 15

RESULT 7
Q9L434 PRELIMINARY; PRT; 19 AA.
AC Q9L434;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein putative yciE (Fragment).
GN Namesputative yciE;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C52;
RX MEDLINE=21160188; PubMed=11260470;
RA Robbe-Saule V., Coynault C., Ibanez-Ruiz M., Hermant D., Norel F.;
RT "Identification of a non-haem catalase in Salmonella and its
regulation by RpoS (sigmas).";
RL Mol. Microbiol. 39:1533-1545(2001).
DR EMBL; AJ251362; CAB71038.1; -.
DR InterPro; IPR010287; DUF892.
DR Pfam; PF05974; DUF892; 1.
KW Hypothetical protein.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2448 MW; 05D3DB83C7CBE7E5 CRC64;

Query Match 27.6%; Score 27; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 NYATHY 13
DB 2 NYTEHY 7

RESULT 8
Q9KHJ4 PRELIMINARY; PRT; 13 AA.
AC Q9KHJ4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Proteolysis tag (Fragment).
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20345063; PubMed=10884408; DOI=10.1073/pnas.97.14.7778;
RA Keiler K.C., Shapiro L., Williams K.P.;
RT "tmRNAs that encode proteolysis-inducing tags are found in all known
bacterial genomes: A two-piece tmRNA functions in Caulobacter.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7778-7783(2000).
DR EMBL; AF255738; AAF87998.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1368 MW; CE5F60C57FCE1B1D CRC64;

Query Match 26.5%; Score 26; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 2.8e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 SDNYATHYA 14
DB 2 NDNFAEEFA 10

RESULT 9
Q85CA1 PRELIMINARY; PRT; 14 AA.
AC Q85CA1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN Name=COII;
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22707965; PubMed=12823452;
RA Biermann C.H., Kessing B.D., Palumbi S.R.;
RT "Phylogeny and development of marine model species: strongylocentrotid
sea urchins.";
RL Evol. Dev. 5:360-371(2003).
DR EMBL; AY221017; AAP21733.1; -.
DR EMBL; AY221018; AAP21736.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1820 MW; 2CB850A51E616CD3 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 3e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 DNYATHYAE 15
DB 5 ENWVTQYLE 13

RESULT 10
Q9UWH6 PRELIMINARY; PRT; 15 AA.
AC Q9UWH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Keto-valine-ferredoxin oxidoreductase alpha-subunit, VOR alpha
(Fragment).
OS Thermococcus litoralis.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OX NCBI_TaxID=2265;
RN [1]
RP SEQUENCE.
RX MEDLINE=96146528; PubMed=8550513;
RA Heider J., Mai X., Adams M.W.;
RT "Characterization of 2-ketoisovalerate ferredoxin oxidoreductase, a
new and reversible coenzyme A-dependent enzyme involved in peptide
fermentation by hyperthermophilic archaea.";
RL J. Bacteriol. 178:780-787(1996).
SQ SEQUENCE 15 AA; 1549 MW; 0C1766910B222944 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 3.3e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 RLKSDNYATHY 13
DB 3 RLKSDNYATHY 13

Db 3 KVVSGNYAAAY 13

RESULT 11

Q9TRT4 PRELIMINARY; PRT; 15 AA.
 AC Q9TRT4; MEDLINE=92144618; PubMed=1737046; DOI=10.1016/0167-4838(92)90279-M;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Pyruvate dehydrogenase (EC 1.2.4.1) (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92144618; PubMed=1737046; DOI=10.1016/0167-4838(92)90279-M;
 RA Koike K., Urata Y., Goto S.;
 RT "Proteinase-catalyzed activation of porcine heart muscle pyruvate
 RT dehydrogenase and identification of its cleavage site."
 RL Biochim. Biophys. Acta 1118:223-230(1992).
 DR GO; GO:0004739; F:pyruvate dehydrogenase (acetyl-transferring. . .; IEA.
 SQ SEQUENCE 15 AA; 1757 MW; 94D6BFFE4B126598 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 15;

Best Local Similarity 71.4%; Pred. No. 3.3e+03; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSD 7

|:| |||

Db 3 EVRSKSD 9

RESULT 12

Q9TRT6 PRELIMINARY; PRT; 15 AA.
 AC Q9TRT6; MEDLINE=92144618; PubMed=1737046; DOI=10.1016/0167-4838(92)90279-M;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Pyruvate dehydrogenase (EC 1.2.4.1) (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92144618; PubMed=1737046; DOI=10.1016/0167-4838(92)90279-M;
 RA Koike K., Urata Y., Goto S.;
 RT "Proteinase-catalyzed activation of porcine heart muscle pyruvate
 RT dehydrogenase and identification of its cleavage site."
 RL Biochim. Biophys. Acta 1118:223-230(1992).
 DR GO; GO:0004739; F:pyruvate dehydrogenase (acetyl-transferring. . .; IEA.
 SQ SEQUENCE 15 AA; 1787 MW; DB1265CDF7737E16 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 15;

Best Local Similarity 71.4%; Pred. No. 3.3e+03; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSD 7

|:| |||

Db 7 EVRSKSD 13

RESULT 13

Q84863 PRELIMINARY; PRT; 19 AA.
 AC Q84863; MEDLINE=92144618; PubMed=1737046; DOI=10.1016/0167-4838(92)90279-M;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).

OS unidentified human poliovirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 OC Enterovirus.
 OX NCBI_TaxID=40278;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87169734; PubMed=3031313;
 RA Kuge S., Saito I., Nomoto A.;
 RT "Primary structure of poliovirus defective-interfering particle
 RT genomes and possible generation mechanisms of the particles."
 RL J. Mol. Biol. 192:473-487(1986).
 DR EMBL; M30221; AAA66829.1; .
 KW Hypothetical protein.
 FT NON_TER 1
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 2106 MW; F774197992500AC8 CRC64;

Query Match 26.5%; Score 26; DB 2; Length 19;

Best Local Similarity 80.0%; Pred. No. 4.2e+03; Mismatches 0; Gaps 0;

QY 8 NYATH 12

||| ||

Db 9 NYTTH 13

RESULT 14

CXOXO THUOB STANDARD; PRT; 10 AA.
 AC P80982;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIIC (EC 1.9.3.1) (Fragment).
 OS Thunus obesus (Bigeye tuna).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 OX NCBI_TaxID=8241;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97454291; PubMed=9310366;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver."
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
 CC chains of cytochrome c oxidase, the terminal oxidase in
 CC mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.
 DR PIR; S77990; S77990.
 KW Direct protein sequencing; Inner membrane; Mitochondrion;
 KW Oxidoreductase.
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1059 MW; 126DE767687B1DCB CRC64;

Query Match 25.5%; Score 25; DB 1; Length 10;

Best Local Similarity 80.0%; Pred. No. 3.1e+03; Mismatches 0; Indels 0; Gaps 0;

QY 11 THYAE 15

:||||

Db 1 SHYAE 5

RESULT 15

Q9V2X3

```

ID Q9V2X3      PRELIMINARY;      PRT;      17 AA.
AC Q9V2X3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RNA polymerase subunit B'', (Fragment).
OS Methanobacterium thermoformicicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=145262;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88198019; PubMed=2834336;
RA Schallenberg J., Moes M., Truss M., Reiser W., Thomm M., Stetter K.O.,
RA Klein A.;
RT "Cloning and physical mapping of RNA polymerase genes from
RT Methanobacterium thermoautotrophicum and comparison of homologies and
RT gene orders with those of RNA polymerase genes from other methanogenic
RT archaeobacteria.";
RL J. Bacteriol. 170:2247-2253(1988).
DR EMBL; M20391; AAA72654.1; -.
FT NON TER
FT 17
SQ SEQUENCE 17 AA; 2137 MW; 0C03CD9E6D780560 CRC64;

Query Match      25.5%; Score 25; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 5.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 THYAES 16
Db 4 THYPEN 9

```

Search completed: April 18, 2005, 15:56:48
Job time : 180 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:39:15 ; Search time 168 Seconds
(without alignments)
43.741 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRLKSNDYATHYAESVKG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 691830

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	19	3 AAY32258	Aay32258 Light cha
2	91	92.9	19	4 AAB35297	Aab35297 Murine PS
3	89	90.8	19	8 ADR19267	Adr19267 Glycosyla
4	84	85.7	19	8 ADR19286	Adr19286 Glycosyla
5	83	84.7	19	8 ADR19285	Adr19285 Glycosyla
6	80	81.6	17	3 AAB30033	Aab30033 Scaffold
7	79	80.6	19	6 ABO10709	Abol10709 Murine J4
8	79	80.6	19	6 ABR44653	Abr44653 Murine J4
9	78	79.6	19	8 ADR19284	Adr19284 Glycosyla
10	76	77.6	19	8 ADQ92379	Adq92379 Human hul
11	76	77.6	19	8 ADQ80568	Adq80568 TNF-alpha
12	74	75.5	16	2 AAY40694	Aay40694 A3 deriva
13	74	75.5	19	8 ADH89399	Adh89399 Human tra
14	74	75.5	19	8 ADQ92375	Adq92375 Human hul
15	74	75.5	19	8 ADQ92377	Adq92377 Human hul
16	74	75.5	19	8 ADQ80564	Adq80564 TNF-alpha
17	74	75.5	19	8 ADQ80566	Adq80566 TNF-alpha
18	73	74.5	19	8 ADR19266	Adr19266 Glycosyla
19	70	71.4	19	3 AAB10002	Aab10002 H. pylori
20	69	70.4	19	8 ADQ92387	Adq92387 Human hul
21	69	70.4	19	8 ADQ92381	Adq92381 Human hul
22	69	70.4	19	8 ADQ80570	Adq80570 TNF-alpha
23	69	70.4	19	8 ADQ80576	Adq80576 TNF-alpha
24	68	69.4	19	2 AAR84529	Aar84529 CDRH2 of
25	68	69.4	19	8 ADM73987	Adm73987 Antigen/a

26	68	69.4	19	8 ADQ92383	Adq92383 Human hul
27	68	69.4	19	8 ADQ80572	Adq80572 TNF-alpha
28	65	66.3	19	5 AAO14988	Aao14988 Mouse mAb
29	65	66.3	19	5 ADF98248	Adf98248 Murine mAb
30	64	65.3	19	2 AAW94737	Aaw94737 Anti-Stop
31	64	65.3	19	8 ADL35119	Adl35119 CDR2 of m
32	57	58.2	15	7 ADI57829	Adi57829 Monoclonal
33	54	55.1	15	7 ADI57828	Adi57828 Monoclonal
34	52	53.1	15	7 ADI57830	Adi57830 Monoclonal
35	52	53.1	17	5 AAU82539	Aau82539 Lama CDR
36	52	53.1	19	8 ADE85719	Ade85719 Human Eph
37	51	52.0	13	7 ADI57890	Adi57890 Monoclonal
38	51	52.0	13	7 ADI57995	Adi57995 Anti-TNF-
39	50	51.0	15	7 ADI57827	Adi57827 Monoclonal
40	49	50.0	17	6 ADA90054	Ada90054 Anti-Abet
41	49	50.0	17	6 ADA90708	Ada90708 MS-Roche
42	49	50.0	17	6 ADA90083	Ada90083 Anti-Abet
43	49	50.0	17	6 ADA90835	Ada90835 MS-Roche
44	49	50.0	19	2 AAR74934	Aar74934 H-CDR-2 o
45	49	50.0	19	5 AAU70371	Aau70371 Human hea

ALIGNMENTS

RESULT 1

AAV32258

ID AAY32258 standard; peptide; 19 AA.

XX AC AAY32258;

XX DT 15-FEB-2000 (first entry)

XX DE Light chain CDR H2 of mouse anti-CD23 MAb C11.

XX KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;

XX KW monoclonal antibody; chimeric antibody; humanised antibody;

XX KW complementarity determining region; CDR; autoimmune disease;

XX KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;

XX KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

XX KW urticaria; nephrotic syndrome; glomerulonephritis;

XX KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;

XX KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinis;

XX KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;

XX KW therapy.

XX OS Mus musculus.

XX PN WO9958679-A1.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB001434.

XX PR 09-MAY-1998; 98GB-00009839.

XX PA (GLAX) GLAXO GROUP LTD.

XX PI Bonney JWP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX XX WPI; 2000-053101/04.

XX DR N-PSDB; AA234743.

XX XX Cell receptor specific antibodies useful for treating e.g. arthritis,

XX PT diabetes, multiple sclerosis and psoriasis.

XX PT Claim 1; Page 40; 81pp; English.

XX CC This sequence represents complementarity determining region 2 (CDR H2)

XX CC of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11

XX CC (see also AAY32263). The invention provides altered antibodies, such as

XX CC chimeric or humanised antibodies, which comprise sufficient of the amino

XX CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on
CC haematopoietic cells. The antibodies are used to block soluble CD23
CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's
CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,
CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,
CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute
CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,
CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes
CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They
CC are also useful for studying interactions between CD23 and various
CC ligands and determining the binding agents
XX
XX Sequence 19 AA;

Query Match 100.0%; Score 98; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHVAESVKG 19
| | | | | | | | | | | | | | | | | |
Db 1 EIRLKSNDNYATHVAESVKG 19

RESULT 2
AAB35297
ID AAB35297 standard; peptide; 19 AA.

AC AAB35297;

DT 08-MAY-2001 (first entry)

DE Murine PSCA antibody fragment #5.

KW Prostate stem cell antigen; PSCA; human; mouse; prostate cancer;
diagnosis; treatment; chromosome 8q24.2.

OS Mus sp.

XX WO200105427-A1.

XX 25-JAN-2001.

XX 20-JUL-2000; 2000WO-US019967.

XX 20-JUL-1999; 99US-00359326.

PR 03-MAY-2000; 2000US-00564329.

XX (REGC) UNIV CALIFORNIA.

PA (UROG-) UROGENESYS.

XX Reiter R, Witte O, Saffran DC, Jakobovits A;

XX WPI; 2001-159478/16.

XX Antibodies binding to prostate stem cell antigen inhibit the growth of
XX cancer cells and are used to detect and treat prostate, pancreatic or
XX bladder cancers.

XX Example 21; Fig 61; 229pp; English.

XX The present invention describes a method of treating cancer associated
XX with prostate stem cell antigen (PSCA) by administering an antibody which
XX selectively binds to PSCA and inhibits the growth of the cancer cells.
XX The PSCA gene is found on human chromosome 8q24.2. The invention provides
XX the human and murine PSCA protein and coding sequences, which can be used
XX not only in the treatment of, but also in detection and prognosis of
XX prostate cancer
XX

XX Sequence 19 AA;

Query Match 92.9%; Score 91; DB 4; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.6e-08;

Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKSNDNYATHVAESVKG 19
| | | | | | | | | | | | | | | | | |
Db 1 EIRLSENATHVAESVKG 19

RESULT 3

ADRI9267
ID ADRI9267 standard; peptide; 19 AA.

XX AC ADRI9267;

XX DT 21-OCT-2004 (first entry)

XX DE Glycosylated MUC1 tumour epitope recognition peptide, SEQ ID 4.

XX Recognition molecule; bind; glycosylated MUC1 tumour epitope; mucin 1;
XX tumour; metastatic; carcinoma; breast; colon; stomach; pancreas; ovary;
XX liver; kidney cell; intestinal; lung cancer; multiple myeloma.

XX OS Unidentified.

XX WO2004065423-A2.

XX PD 05-AUG-2004.

XX PF 23-JAN-2004; 2004WO-DE000132.

XX PR 23-JAN-2003; 2003DE-01003664.

XX PA (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.

XX PI Goletz S, Danielczyk A, Stahn R, Karsten U;

XX WPI; 2004-593433/57.

XX New recognition molecules that bind the glycosylated MUC1 tumor epitope,
XX useful for prevention, diagnosis, treatment and monitoring of tumors.
XX Claim 1; SEQ ID NO 4; 158pp; German.

XX The invention relates to novel recognition molecules comprising sequences
XX that bind specifically to a glycosylated MUC1 tumour epitope. The novel
XX recognition molecules comprise: sequences ADR19264 or ADR19265; sequences
XX ADR19266 or ADR19267 and sequences ADR19268 and ADR19269, and bind
XX specifically to the glycosylated mucin 1 (MUC1) tumour epitope. The
XX invention further comprises: a construct comprising the recognition
XX molecule fused, chemically coupled or non-covalently associated with
XX additional sequences and/or structures; an isolated nucleic acid that
XX encodes the recognition molecule or construct; expression cassette or
XX vector that contains the isolated nucleic acid, operatively linked to a
XX promoter; virus or host cell comprising at least one cassette or vector
XX of ADR19266; an organism containing at least one host cell of ADR19267; a
XX method for preparing the recognition molecule and construct; and a kit
XX containing the recognition molecule and/or construct. The recognition
XX molecules have cytostatic activity. The recognition molecules, constructs
XX containing them, the nucleic acid encoding them, and derived viruses,
XX cells and organisms, are used for prevention, diagnosis, treatment and
XX monitoring of tumours and/or metastases, specifically where MUC1
XX positive, particularly carcinoma of breast, colon, stomach, pancreas,
XX ovary, liver or kidney cells; (gastro)intestinal or lung cancers and
XX multiple myeloma. The recognition molecules show little or no binding to
XX MUC1 in either the serum or normal tissue, so provides simple, safe and
XX efficient detection of tumours, even at an early stage (carcinoma in
XX situ), and can differentiate between tumours and benign diseases. This
XX sequence represents one of the novel glycosylated MUC1 tumour epitope
XX recognition molecules of the invention.

XX Sequence 19 AA;

Query Match 90.8%; Score 89; DB 8; Length 19;
Best Local Similarity 89.5%; Pred. No. 1e-07;

Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
|||||:|||||
Db 1 EIRLKSNYYTHYAESVKG 19

RESULT 4

ADRI9286
ID ADR19286 standard; peptide; 19 AA.

AC ADR19286;

XX 21-OCT-2004 (first entry)

XX Glycosylated MUC1 tumour epitope recognition variant peptide, SEQ ID 23.

XX Recognition molecule; bind; glycosylated MUC1 tumour epitope; mucin 1;
KW tumour; metastatic; carcinoma; breast; colon; stomach; pancreas; ovary;
KW liver; kidney cell; intestinal; lung cancer; multiple myeloma; variant.

XX Synthetic; Unidentified.

XX WO2004065423-A2.

XX 05-AUG-2004.

XX 23-JAN-2004; 2004WO-DE000132.

XX 23-JAN-2003; 2003DE-01003664.

XX (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.

XX Goletz S, Danielczyk A, Stahn R, Karsten U;

XX WPI; 2004-593433/57.

XX New recognition molecules that bind the glycosylated MUC1 tumour epitope,
PT useful for prevention, diagnosis, treatment and monitoring of tumors.

XX Claim 9; SEQ ID NO 23; 158pp; German.

XX The invention relates to novel recognition molecules comprising sequences
CC that bind specifically to a glycosylated MUC1 tumour epitope. The novel
CC recognition molecules comprise: sequences ADR19264 or ADR19265; sequences
CC ADR19266 or ADR19267 and sequences ADR19268 and ADR19269, and bind
CC specifically to the glycosylated mucin 1 (MUC1) tumour epitope. The
CC invention further comprises: a construct comprising the recognition
CC molecule fused, chemically coupled or non-covalently associated with
CC additional sequences and/or structures; an isolated nucleic acid that
CC encodes the recognition molecule or construct; expression cassette or
CC vector that contains the isolated nucleic acid, operatively linked to a
CC promoter; virus or host cell comprising at least one cassette or vector
CC of ADR19266; an organism containing at least one host cell of ADR19267; a
CC method for preparing the recognition molecule and construct; and a kit
CC containing the recognition molecule and/or construct. The recognition
CC molecules have cytostatic activity. The recognition molecules, constructs
CC containing them, the nucleic acid encoding them, and derived viruses,
CC cells and organisms, are used for prevention, diagnosis, treatment and
CC monitoring of tumours and/or metastases, specifically where MUC1
CC positive, particularly carcinoma of breast, colon, stomach, pancreas,
CC ovary, liver or kidney cells; (gastro)intestinal or lung cancers and
CC multiple myeloma. The recognition molecules show little or no binding to
CC MUC1 in either the serum or normal tissue, so provides simple, safe and
CC efficient detection of tumours, even at an early stage (carcinoma in
CC situ), and can differentiate between tumours and benign diseases. This
CC sequence represents a variant glycosylated MUC1 tumour epitope
CC recognition peptide of the invention.

XX Sequence 19 AA;

Query Match 85.7%; Score 84; DB 8; Length 19;
Best Local Similarity 84.2%; Pred. No. 7.1e-07;

Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
|||||:|||||
Db 1 EIRLKSNYYTHYAESVKG 19

RESULT 5

ADRI9285
ID ADR19285 standard; peptide; 19 AA.

XX ADR19285;

XX 21-OCT-2004 (first entry)

XX Glycosylated MUC1 tumour epitope recognition variant peptide, SEQ ID 22.

XX Recognition molecule; bind; glycosylated MUC1 tumour epitope; mucin 1;
KW tumour; metastatic; carcinoma; breast; colon; stomach; pancreas; ovary;
KW liver; kidney cell; intestinal; lung cancer; multiple myeloma; variant.

XX Synthetic; Unidentified.

XX WO2004065423-A2.

XX 05-AUG-2004.

XX 23-JAN-2004; 2004WO-DE000132.

XX 23-JAN-2003; 2003DE-01003664.

XX (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.

XX Goletz S, Danielczyk A, Stahn R, Karsten U;

XX WPI; 2004-593433/57.

XX New recognition molecules that bind the glycosylated MUC1 tumour epitope,
PT useful for prevention, diagnosis, treatment and monitoring of tumors.

XX Claim 9; SEQ ID NO 22; 158pp; German.

XX The invention relates to novel recognition molecules comprising sequences
CC that bind specifically to a glycosylated MUC1 tumour epitope. The novel
CC recognition molecules comprise: sequences ADR19264 or ADR19265; sequences
CC ADR19266 or ADR19267 and sequences ADR19268 and ADR19269, and bind
CC specifically to the glycosylated mucin 1 (MUC1) tumour epitope. The
CC invention further comprises: a construct comprising the recognition
CC molecule fused, chemically coupled or non-covalently associated with
CC additional sequences and/or structures; an isolated nucleic acid that
CC encodes the recognition molecule or construct; expression cassette or
CC vector that contains the isolated nucleic acid, operatively linked to a
CC promoter; virus or host cell comprising at least one cassette or vector
CC of ADR19266; an organism containing at least one host cell of ADR19267; a
CC method for preparing the recognition molecule and construct; and a kit
CC containing the recognition molecule and/or construct. The recognition
CC molecules have cytostatic activity. The recognition molecules, constructs
CC containing them, the nucleic acid encoding them, and derived viruses,
CC cells and organisms, are used for prevention, diagnosis, treatment and
CC monitoring of tumours and/or metastases, specifically where MUC1
CC positive, particularly carcinoma of breast, colon, stomach, pancreas,
CC ovary, liver or kidney cells; (gastro)intestinal or lung cancers and
CC multiple myeloma. The recognition molecules show little or no binding to
CC MUC1 in either the serum or normal tissue, so provides simple, safe and
CC efficient detection of tumours, even at an early stage (carcinoma in
CC situ), and can differentiate between tumours and benign diseases. This
CC sequence represents a variant glycosylated MUC1 tumour epitope
CC recognition peptide of the invention.

XX Sequence 19 AA;

Query Match 84.7%; Score 83; DB 8; Length 19;
Best Local Similarity 84.2%; Pred. No. 1e-06;

Tue Apr 19 06:14:43 2005

us-09-674-716b-11.closed.rag

```
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 EIRLSDNYATHYAESVKG 19
Db 1 EIRLSKNKYTHYAESVKG 19

RESULT 6
AAB30033
ID AAB30033 standard; peptide; 17 AA.
AC AAB30033;
XX
XX 09-FEB-2001 (first entry)
XX
XX Scaffold protein SCA A3 peptide SEQ ID NO: 94.
XX
XX Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
KW diabetic retinopathy; atherosclerosis.
XX
XX Synthetic.
XX
XX WO200060070-A1.
XX
XX 12-OCT-2000.
XX
XX 01-APR-1999; 99WO-EP002283.
XX
XX 01-APR-1999; 99WO-EP002283.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX
XX WPI; 2000-665002/64.
XX
XX Scaffold composed of single-chain polypeptide having beta sandwich
PT architecture carrying new and randomized peptide sequences useful as
PT supporting framework and carrying antigen- or receptor binding fragments.
XX
XX Disclosure; Page 14; 68pp; English.
XX
XX The present invention is concerned with producing scaffold proteins based
CC upon the human CTLA-4 SCA domain. These scaffold proteins can be used as
CC a scaffold to bind antigen- or receptor-binding fragments. These can be
CC used in the treatment of diseases such as cancer, atherosclerosis,
CC thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy.
CC Sequences AAB29930-B29939 were used in the production of the proteins of
CC the invention
XX
XX Sequence 17 AA;
SQ
Query Match 81.6%; Score 80; DB 3; Length 17;
Best Local Similarity 88.2%; Pred. NO. 2.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 RLKSDNYATHYAESVKG 19
Db 1 RLNSDNFATHYAESVKG 17

RESULT 7
ABO10709
ID ABO10709 standard; peptide; 19 AA.
XX
XX ABO10709;
XX
XX 20-AUG-2003 (first entry)
XX
XX Murine J415 antibody heavy chain CDR2.
XX
XX Modified antibody; deimmunised antibody; anti-PMSEA antibody;
KW
```

```
KW prostate specific membrane antigen; immunogenic; CDR; murine;
KW complementarity determining region; J591; J415; J533; E99; mouse;
KW prostatic disorder; cancerous disorder; genitourinary inflammation;
KW prostatitis; benign enlargement; prostatic cancer; testicular cancer;
KW solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic;
KW antiinflammatory; cytostatic; framework region; variable heavy chain;
KW variable light chain; VH; VL; variable region.
XX
XX Mus musculus.
OS
XX WO200298897-A2.
XX
XX 12-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-US017068.
XX
XX 01-JUN-2001; 2001US-0295214P.
XX
XX 20-SEP-2001; 2001US-0323585P.
XX
XX 08-MAR-2002; 2002US-0362810P.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Bander N, Carr FJ, Hamilton A;
XX
XX WPI; 2003-156839/15.
XX
XX New modified anti-prostate specific membrane antigen (PSMA)
PT immunoglobulins, useful for treating or preventing a prostatic or
PT cancerous disorder, e.g. genitourinary inflammation, prostatitis, or
PT prostatic or testicular cancer.
XX
XX Disclosure; Fig 5; 254pp; English.
XX
XX The present invention relates to modified (e.g. deimmunised) antibodies
CC to prostate specific membrane antigen (PSMA). The modified anti-PSMA
CC antibodies are less immunogenic compared to the unmodified anti-PSMA
CC antibodies. The modified antibodies comprise complementarity determining
CC regions (CDRs) from a non-human antibody (e.g. murine antibody J591,J415,
CC J533 or E99), and framework sequences that are less immunogenic in humans
CC (e.g. less antigenic than the murine frameworks in which a murine CDR
CC naturally occurs). The modified antibodies bind with PSMA, preferably
CC human PSMA, with high affinity and specificity. The anti-PSMA antibodies
CC are useful for treating or preventing a prostatic or cancerous disorder,
CC e.g. genitourinary inflammation, prostatitis, benign enlargement,
CC prostatic cancer or testicular cancer, or solid tumours, soft tissue
CC tumours or metastatic lesions, and its associated pain. The present
CC sequence represents a CDR from a murine antibody
XX
XX Sequence 19 AA;
SQ
Query Match 80.6%; Score 79; DB 6; Length 19;
Best Local Similarity 78.9%; Pred. NO. 4.9e-06;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 EIRLSDNYATHYAESVKG 19
Db 1 EIRSQSNFATHYAESVKG 19

RESULT 8
ABR44653
ID ABR44653 standard; peptide; 19 AA.
XX
XX ABR44653;
XX
XX 25-JUL-2003 (first entry)
XX
XX Murine J415 antibody VH CDR2 peptide SEQ ID NO:30.
XX
XX Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic;
KW prostate specific membrane antigen; antipsoriatic; antiarthritic;
KW dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;
KW epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;
```


DE Human h1 CDRH2 variant peptide, 153Xaa.

XX Tumour necrosis factor alpha; TNF-alpha; TNF-alpha mediated disease;

KW sepsis; autoimmune disease; rheumatoid arthritis; inflammatory disease;

KW neurodegenerative disease; malignancy; TNF-secreting tumour;

KW alcohol-induced hepatitis; psoriasis; psoriatic arthritis;

KW Wegener's granulomatosis; ankylosing spondylitis; heart failure;

KW reperfusion injury; chronic obstructive pulmonary disease;

KW pulmonary fibrosis; hepatitis C infection; Kawasaki's pathology;

KW Refsum's disease; ataxia; telangiectasia; Alzheimer's disease;

KW Down's syndrome; Parkinson's disease; leukaemia; myelodysplastic syndrome;

KW lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma; Burkitt's syndrome;

KW hypokinetic movement disorder; drug-induced movement disorder;

KW Crohn's disease; ulcerative colitis; amyotrophic lateral sclerosis;

KW multiple sclerosis; Grave's disease; diabetes mellitus; atherosclerosis;

KW Shy-drager syndrome; cachexia; infectious disease; antibody therapy;

KW human; heavy chain variable region; VH; CDR;

KW complementarity determining region; variant; mutein; mutant.

XX Homo sapiens.

OS

XX

XX Key Location/Qualifiers

FT Misc-difference 7

FT /note= "Encoded by NNN"

FT

FT

PN US2004131613-A1.

XX

XX 08-JUL-2004.

PD

XX

XX 08-JAN-2003; 2003US-00338627.

PF

XX

XX 08-JAN-2003; 2003US-00338627.

PR

XX

XX (WATK/) WATKINS J D.

PA (VASS/) VASSEROT A P.

PA (MARQ/) MARQUIS D.

PA (HUSE/) HUSE W D.

XX

XX Watkins JD, Vasserot AP, Marquis D, Huse WD;

PI

XX WPI; 2004-524894/50.

DR N-PSDB; ADQ92380.

DR

XX

XX New composition comprising a tumor necrosis factor alpha (TNF-alpha)

PT binding molecule, useful for treating a TNF-alpha mediated disease such

PT as sepsis, an autoimmune disease, rheumatoid arthritis, and

PT neurodegenerative diseases.

XX

XX Disclosure; SEQ ID NO 47; 60pp; English.

PS

XX

XX The present invention relates to tumour necrosis factor alpha (TNF-alpha)

CC binding polypeptides and their encoding polynucleotides. The invention is

CC useful for treating TNF-alpha mediated disease such as sepsis, an

CC autoimmune disease, rheumatoid arthritis, inflammatory diseases,

CC neurodegenerative diseases, malignant pathologies involving TNF-secreting

CC tumours, alcohol-induced hepatitis, psoriasis, psoriatic arthritis,

CC Wegener's granulomatosis, ankylosing spondylitis, heart failure,

CC reperfusion injury, chronic obstructive pulmonary disease, pulmonary

CC fibrosis, hepatitis C infection, Kawasaki's pathology, Refsum's disease,

CC ataxia, telangiectasia, Alzheimer's disease, Down's syndrome, Parkinson's

CC disease, leukaemias (acute, chronic myelocytic, chronic lymphocytic

CC and/or myelodysplastic syndrome), lymphomas (Hodgkin's, non-Hodgkin's and

CC Burkitt's syndrome), hypokinetic movement disorders, drug-induced

CC movement disorders, Crohn's disease, ulcerative colitis, amyotrophic

CC lateral sclerosis, multiple sclerosis, Grave's disease, diabetes

CC mellitus, atherosclerosis, Shy-drager syndrome, cachexia and infectious

CC diseases. The invention is also useful in antibody therapy. The present

CC sequence is human h1 complementarity determining region (CDR) of heavy

CC chain variable (VH) region (CDRH) variant peptide. This sequence is used

CC in the invention.

XX

XX Sequence 19 AA;

SQ

Query Match 77.6%; Score 76; DB 8; Length 19;

Best Local Similarity 84.2%; Pred. No. 1-5e-05;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIRLKSDNYATHVAESVKG 19

Db 1 EIRSKSXNSATHVAESVKG 19

|||||

RESULT 11

ADQ80568

ID ADQ80568 standard; peptide; 19 AA.

XX

AC ADQ80568;

XX

DT 23-SEP-2004 (first entry)

XX

DE TNF-alpha binding molecule heavy chain CDR #7.

XX

XX TNF-alpha binding; complementarity determining region; CDR; TNF-alpha;

KW immunoassay; CDRH-3; sepsis; autoimmune disease;

KW rheumatoid arthritis; allergy; multiple sclerosis;

KW systemic lupus erythematosus; scleroderma; diabetes mellitus; cachexia;

KW parasitic disease; infectious disease; ulcerative colitis; Crohn's disease;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;

KW disseminated intravascular coagulation; Parkinson's disease;

KW Alzheimer's disease; Down's syndrome; psoriasis; ankylosing spondylitis;

KW Wegener's granulomatosis; idiopathic pulmonary fibrosis; asthma;

KW graft-versus-host disease; leukemia.

XX

OS Synthetic.

XX

XX US2004131612-A1.

PN

XX

XX 08-JUL-2004.

PD

XX

XX 08-JAN-2003; 2003US-00338552.

PF

XX

XX 08-JAN-2003; 2003US-00338552.

PR

XX

XX (WATK/) WATKINS J D.

PA (VASS/) VASSEROT A P.

PA (MARQ/) MARQUIS D.

PA (HUSE/) HUSE W D.

XX

XX Watkins JD, Vasserot AP, Marquis D, Huse WD;

PI

XX WPI; 2004-516978/49.

DR N-PSDB; ADQ80569.

DR

XX

XX Composition useful for treating diseases such as leukemia, asthma,

PT rheumatoid arthritis, Alzheimer's disease, psoriasis or multiple

PT sclerosis, comprises TNF-alpha binding molecule.

XX

XX Disclosure; SEQ ID NO 47; 60pp; English.

PS

XX

XX The invention relates to a composition which comprises a TNF-alpha

CC binding molecule having sequence of complementarity determining region

CC (CDR) in light chain variable region (CDRL)-3 and sequence of CDR in

CC heavy chain variable region (CDRH)-3. The composition is useful in the

CC treatment of TNF-alpha mediated diseases. TNF-alpha binding molecule is

CC useful for treating sepsis, autoimmune disease, rheumatoid arthritis,

CC allergy, multiple sclerosis, systemic lupus erythematosus, scleroderma,

CC diabetes mellitus, cachexia, acute and chronic parasitic and/or

CC infectious diseases, sarcoidosis, inflammatory bowel disease, ulcerative

CC colitis, Crohn's disease, disseminated intravascular coagulation,

CC Parkinson's disease, Alzheimer's disease, Down's syndrome, psoriasis,

CC ankylosing spondylitis, Wegener's granulomatosis, idiopathic pulmonary

CC fibrosis, asthma, graft-versus-host disease, or leukemia. TNF-alpha

CC binding molecule is useful in diagnostic methods for detecting TNF-alpha

CC in patients known to be or suspected of having TNF-alpha-mediated

CC disease. TNF-alpha binding molecule is useful in immunoassays for

CC detecting or quantifying TNF-alpha in a sample. The present sequence

QY 1 EIRLKSNDYATHYAESVKG 19
 |||||
 Db 1 EIRSKSINSATHYAESVKG 19
 |||||

RESULT 14
 ID ADQ92375
 ADQ92375 standard; peptide; 19 AA.
 XX
 AC ADQ92375;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human hul CDRH2 peptide.
 XX
 KW Tumour necrosis factor alpha; TNF-alpha; TNF-alpha mediated disease;
 KW sepsis; autoimmune disease; rheumatoid arthritis; inflammatory disease;
 KW neurodegenerative disease; malignancy; TNF-secreting tumour;
 KW alcohol-induced hepatitis; psoriasis; psoriatic arthritis;
 KW Wegener's granulomatosis; ankylosing spondylitis; heart failure;
 KW reperfusion injury; chronic obstructive pulmonary disease;
 KW pulmonary fibrosis; hepatitis C infection; Kawasaki's disease;
 KW Refsum's disease; ataxia; telangiectasia; Alzheimer's disease;
 KW Down's syndrome; Parkinson's disease; leukaemia; myelodysplastic syndrome;
 KW lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma; Burkitt's syndrome;
 KW hypokinetic movement disorder; drug-induced movement disorder;
 KW Crohn's disease; ulcerative colitis; amyotrophic lateral sclerosis;
 KW multiple sclerosis; Grave's disease; diabetes mellitus; atherosclerosis;
 KW Shy-drager syndrome; cachexia; infectious disease; antibody therapy;
 KW human; heavy chain variable region; VH; CDR;
 KW complementarity determining region.
 XX
 OS Homo sapiens.
 XX
 FN US2004131613-A1.
 XX
 PD 08-JUL-2004.
 XX
 PF 08-JAN-2003; 2003US-00338627.
 XX
 PR 08-JAN-2003; 2003US-00338627.
 XX
 PA (WATK/) WATKINS J D.
 PA (VASS/) VASSEROT A P.
 PA (MARQ/) MARQUIS D.
 PA (HUSE/) HUSE W D.
 XX
 PI Watkins JD, Vasserot AP, Marquis D, Huse WD;
 DR WPI; 2004-524894/50.
 DR N-PSDB; ADQ92376.
 XX
 XX New composition comprising a tumor necrosis factor alpha (TNF-alpha)
 PT binding molecule, useful for treating a TNF-alpha mediated disease such
 PT as sepsis, an autoimmune disease, rheumatoid arthritis, and
 PT neurodegenerative diseases.
 XX
 PS Disclosure; SEQ ID NO 43; 60pp; English.
 XX
 CC The present invention relates to tumour necrosis factor alpha (TNF-alpha)
 CC binding polypeptides and their encoding polynucleotides. The invention is
 CC useful for treating TNF-alpha mediated disease such as sepsis, an
 CC autoimmune disease, rheumatoid arthritis, inflammatory diseases,
 CC neurodegenerative diseases, malignant pathologies involving TNF-secreting
 CC tumours, alcohol-induced hepatitis, psoriasis, psoriatic arthritis,
 CC Wegener's granulomatosis, ankylosing spondylitis, heart failure,
 CC reperfusion injury, chronic obstructive pulmonary disease, pulmonary
 CC fibrosis, hepatitis C infection, Kawasaki's disease, Refsum's disease,
 CC ataxia, telangiectasia, Alzheimer's disease, Down's syndrome, Parkinson's
 CC disease, leukaemias (acute, chronic myelocytic, chronic lymphocytic
 CC and/or myelodysplastic syndrome), lymphomas (Hodgkin's, non-Hodgkin's and
 CC Burkitt's syndrome), hypokinetic movement disorders, drug-induced
 CC movement disorders, Crohn's disease, ulcerative colitis, amyotrophic

CC lateral sclerosis, multiple sclerosis, Grave's disease, diabetes
 CC mellitus, atherosclerosis, Shy-drager syndrome, cachexia and infectious
 CC diseases. The invention is also useful in antibody therapy. The present
 CC sequence is human hul complementarity determining region (CDR) of heavy
 CC chain variable (VH) region (CDRH) peptide. This sequence is used in the
 CC invention.
 XX
 SQ Sequence 19 AA;
 Query Match 75.5%; Score 74; DB 8; Length 19;
 Best Local Similarity 84.2%; Pred. NO. 3.3e-05;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIRLKSNDYATHYAESVKG 19
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 Db 1 EIRSKSINSATHYAESVKG 19
 |||||

RESULT 15
 ID ADQ92377 standard; peptide; 19 AA.
 AC ADQ92377;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human hul CDRH2 variant peptide, I53M.
 XX
 KW Tumour necrosis factor alpha; TNF-alpha; TNF-alpha mediated disease;
 KW sepsis; autoimmune disease; rheumatoid arthritis; inflammatory disease;
 KW neurodegenerative disease; malignancy; TNF-secreting tumour;
 KW alcohol-induced hepatitis; psoriasis; psoriatic arthritis;
 KW Wegener's granulomatosis; ankylosing spondylitis; heart failure;
 KW reperfusion injury; chronic obstructive pulmonary disease;
 KW pulmonary fibrosis; hepatitis C infection; Kawasaki's disease;
 KW Refsum's disease; ataxia; telangiectasia; Alzheimer's disease;
 KW Down's syndrome; Parkinson's disease; leukaemia; myelodysplastic syndrome;
 KW lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma; Burkitt's syndrome;
 KW hypokinetic movement disorder; drug-induced movement disorder;
 KW Crohn's disease; ulcerative colitis; amyotrophic lateral sclerosis;
 KW multiple sclerosis; Grave's disease; diabetes mellitus; atherosclerosis;
 KW Shy-drager syndrome; cachexia; infectious disease; antibody therapy;
 KW human; heavy chain variable region; VH; CDR;
 KW complementarity determining region; variant; mutant.
 XX
 OS Homo sapiens.
 XX
 FN US2004131613-A1.
 XX
 PD 08-JUL-2004.
 XX
 PF 08-JAN-2003; 2003US-00338627.
 XX
 PR 08-JAN-2003; 2003US-00338627.
 XX
 PA (WATK/) WATKINS J D.
 PA (VASS/) VASSEROT A P.
 PA (MARQ/) MARQUIS D.
 PA (HUSE/) HUSE W D.
 XX
 PI Watkins JD, Vasserot AP, Marquis D, Huse WD;
 DR WPI; 2004-524894/50.
 DR N-PSDB; ADQ92378.
 XX
 XX New composition comprising a tumor necrosis factor alpha (TNF-alpha)
 PT binding molecule, useful for treating a TNF-alpha mediated disease such
 PT as sepsis, an autoimmune disease, rheumatoid arthritis, and
 PT neurodegenerative diseases.
 XX
 PS Disclosure; SEQ ID NO 45; 60pp; English.
 XX
 CC The present invention relates to tumour necrosis factor alpha (TNF-alpha)

CC binding polypeptides and their encoding polynucleotides. The invention is
 CC useful for treating TNF-alpha mediated disease such as sepsis, an
 CC autoimmune disease, rheumatoid arthritis, inflammatory diseases,
 CC neurodegenerative diseases, malignant pathologies involving TNF-secreting
 CC tumours, alcohol-induced hepatitis, psoriasis, psoriatic arthritis,
 CC Wegener's granulomatosis, ankylosing spondylitis, heart failure,
 CC reperfusion injury, chronic obstructive pulmonary disease, pulmonary
 CC fibrosis, hepatitis C infection, Kawasaki's disease, Refsum's disease,
 CC ataxia, telangiectasia, Alzheimer's disease, Down's syndrome, Parkinson's
 CC disease, leukaemias (acute, chronic myelocytic, chronic lymphocytic
 CC and/or myelodysplastic syndrome), lymphomas (Hodgkin's, non-Hodgkin's and
 CC Burkitt's syndrome), hypokinetic movement disorders, drug-induced
 CC movement disorders, Crohn's disease, ulcerative colitis, amyotrophic
 CC lateral sclerosis, multiple sclerosis, Grave's disease, diabetes
 CC mellitus, atherosclerosis, Shy-drager syndrome, cachexia and infectious
 CC diseases. The invention is also useful in antibody therapy. The present
 CC sequence is human hUL complementarity determining region (CDR) of heavy
 CC chain variable (VH) region (CDRH) variant peptide. This sequence is used
 CC in the invention.

XX

SQ Sequence 19 AA;

Query Match 75.5%; Score 74; DB 8; Length 19;
 Best Local Similarity 84.2%; Pred. No. 3.3e-05;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIRLKSNDNVATHYAESVKG 19
 |||||
 Db 1 EIRKSNWNSATHYAESVKG 19
 |||||

Search completed: April 18, 2005, 15:53:43
 Job time : 170 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 15:56:54 ; Search time 130 Seconds
(without alignments)
48.577 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 284765

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	92.9	19	16	US-10-769-308-32
2	91	92.9	19	17	US-10-769-074-32
3	82	83.7	17	17	US-10-879-994-68
4	79	80.6	19	14	US-10-160-506-30
5	79	80.6	19	16	US-10-449-379-30
6	79	80.6	19	16	US-10-688-015-30
7	76	77.6	19	16	US-10-338-552-47
8	76	77.6	19	16	US-10-338-627-47
9	74	75.5	19	15	US-10-384-060-43
10	74	75.5	19	16	US-10-338-552-43
11	74	75.5	19	16	US-10-338-552-45
12	74	75.5	19	16	US-10-338-627-43
13	74	75.5	19	16	US-10-338-627-45

14	71	72.4	19	10	US-09-791-551-87	Sequence 87, Appl
15	70	71.4	19	11	US-09-842-776A-14	Sequence 14, Appl
16	69	70.4	19	16	US-10-338-552-49	Sequence 49, Appl
17	69	70.4	19	16	US-10-338-552-55	Sequence 55, Appl
18	69	70.4	19	16	US-10-338-627-49	Sequence 49, Appl
19	69	70.4	19	16	US-10-338-627-55	Sequence 55, Appl
20	68	69.4	19	9	US-09-839-666-4	Sequence 4, Appl
21	68	69.4	19	14	US-10-234-579-4	Sequence 4, Appl
22	68	69.4	19	15	US-10-372-735-46	Sequence 46, Appl
23	68	69.4	19	16	US-10-338-552-51	Sequence 51, Appl
24	68	69.4	19	16	US-10-338-627-51	Sequence 51, Appl
25	66	67.3	19	10	US-09-947-839-78	Sequence 78, Appl
26	65	66.3	19	9	US-09-835-087-18	Sequence 18, Appl
27	64	65.3	19	14	US-10-230-880-125	Sequence 125, Appl
28	55	56.1	17	17	US-10-879-994-20	Sequence 20, Appl
29	53	54.1	17	17	US-10-879-994-71	Sequence 71, Appl
30	52	53.1	17	14	US-10-031-874A-105	Sequence 105, Appl
31	52	53.1	19	15	US-10-436-782-23	Sequence 23, Appl
32	49	50.0	19	10	US-09-563-222-51	Sequence 51, Appl
33	49	50.0	19	16	US-10-783-950-51	Sequence 51, Appl
34	48	49.0	17	9	US-09-192-854-60	Sequence 60, Appl
35	48	49.0	17	9	US-09-968-561A-98	Sequence 98, Appl
36	48	49.0	17	10	US-09-968-744A-98	Sequence 98, Appl
37	48	49.0	17	11	US-09-968-561A-98	Sequence 98, Appl
38	48	49.0	19	10	US-09-563-222-60	Sequence 60, Appl
39	48	49.0	19	16	US-10-783-950-60	Sequence 60, Appl
40	46	46.9	17	9	US-09-192-854-164	Sequence 164, Appl
41	46	46.9	17	9	US-09-968-561A-290	Sequence 290, Appl
42	46	46.9	17	10	US-09-968-744A-290	Sequence 290, Appl
43	46	46.9	17	11	US-09-968-561A-290	Sequence 290, Appl
44	46	46.9	17	16	US-10-327-598-481	Sequence 481, Appl
45	45.9	45.9	17	17	US-10-725-962-85	Sequence 85, Appl

ALIGNMENTS

RESULT 1

US-10-769-308-32
; Sequence 32, Application US/10769308
; Publication No. US20050003465A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Jakobovits, Aya
; APPLICANT: The Regents of the University of California
; APPLICANT: Agensys, Inc.
; TITLE OF INVENTION: PSCA: Prostate Stem Cell Antigen and Uses Thereof
; FILE REFERENCE: 02307K-141589US
; CURRENT APPLICATION NUMBER: US/10/769,308
; PRIOR FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 60/228,816
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: US 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: US 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: US 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 60/124,658
; PRIOR FILING DATE: 1999-03-16
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PSCA mab 2H9
; OTHER INFORMATION: CDR2
US-10-769-308-32

Query Match 92.9%; Score 91; DB 16; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.1e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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DB 1 EIRLRSNYATHYAESVKG 19

RESULT 2
US-10-769-074-32

; Sequence 32, Application US/10769074
; Publication No. US2005005909A1
; GENERAL INFORMATION:

; APPLICANT: Witte, Robert E.
; APPLICANT: Safran, Owen N.

; APPLICANT: Jakobovits, Aya
; APPLICANT: The Regents of the University of California

; APPLICANT: Agensys, Inc.

; TITLE OF INVENTION: PSCA: Prostate Stem Cell Antigen and Uses Thereof

; FILE REFERENCE: 02307K-141589US

; CURRENT APPLICATION NUMBER: US/10/769,074

; PRIOR FILING DATE: 2004-01-29

; PRIOR APPLICATION NUMBER: US/10/769,308

; PRIOR FILING DATE: 2004-01-29

; PRIOR APPLICATION NUMBER: US 08/814,279

; PRIOR FILING DATE: 1997-03-10

; PRIOR APPLICATION NUMBER: US 60/228,816

; PRIOR FILING DATE: 1997-03-10

; PRIOR APPLICATION NUMBER: US 60/071,141

; PRIOR FILING DATE: 1998-01-12

; PRIOR APPLICATION NUMBER: US 60/074,675

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 09/038,261

; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: US 09/203,939

; PRIOR FILING DATE: 1998-12-02

; PRIOR APPLICATION NUMBER: US 60/113,230

; PRIOR FILING DATE: 1998-12-21

; PRIOR APPLICATION NUMBER: US 09/251,835

; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: US 60/120,536

; PRIOR FILING DATE: 1999-02-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 32

; LENGTH: 19

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: PSCA mab 2H9

; OTHER INFORMATION: CDR2

US-10-769-074-32

Query Match 92.9%; Score 91; DB 17; Length 19;

Best Local Similarity 89.5%; Pred. No. 2.1e-07;

Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EIRLRSNYATHYAESVKG 19

RESULT 3

US-10-879-994-68

; Sequence 68, Application US/10879994

; Publication No. US20050032175A1

; GENERAL INFORMATION:

; APPLICANT: Stahl, Neil

; APPLICANT: Yancopoulos, George D.

; APPLICANT: Karow, Margaret

; APPLICANT: Smith, Eric

; TITLE OF INVENTION: HIGH AFFINITY FUSION PROTEINS AND THERAPEUTIC AND DIAGNOSTIC MET

; FILE REFERENCE: REG 203E2

; CURRENT APPLICATION NUMBER: US/10/879,994

; PRIOR FILING DATE: 2004-06-29

; PRIOR APPLICATION NUMBER: 10/610,452

; PRIOR FILING DATE: 2003-06-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 68

; LENGTH: 17

; TYPE: PRT

; ORGANISM: mus musculus

US-10-879-994-68

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Best Local Similarity 94.1%; Pred. No. 4.8e-06;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EIRLKSNNYATHYAESV 17

RESULT 4

US-10-160-506-30

; Sequence 30, Application US/10160506

; Publication No. US20030161832A1

; GENERAL INFORMATION:

; APPLICANT: Bender, Neil H.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING

; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR

; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN

; FILE REFERENCE: 10448-162001

; CURRENT APPLICATION NUMBER: US/10/160,506

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: 60/324,100

; PRIOR FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/362,612

; PRIOR FILING DATE: 2002-03-08

; NUMBER OF SEQ ID NOS: 128

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 30

; LENGTH: 19

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-160-506-30

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Db 1 EIRSQNNFYATHYAESVKG 19

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US-10-449-379-30

; Sequence 30, Application US/10449379

; Publication No. US20040120958A1


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; GENERAL INFORMATION:
; APPLICANT: Banger, Neil H.
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 10448-163002
; CURRENT APPLICATION NUMBER: US/10/449,379
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 10/160,505
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/323,585
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,810
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/295,214
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-449-379-30

```

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Query Match      80.6%; Score 79; DB 16; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.6e-05;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAEVKG 19
    ||| : ||| ||| |||
Db 1 EIRSQNNPATHYAEVKG 19

```

```

RESULT 6
US-10-688-015-30
; Sequence 30, Application US/10688015
; Publication No. US20040136998A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; TITLE OF INVENTION: INSULIN-RELATED DISORDERS USING BINDING AGENTS SPECIFIC FOR
; TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
; FILE REFERENCE: 10448-196001
; CURRENT APPLICATION NUMBER: US/10/688,015
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/422,396
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-688-015-30

```

```

Query Match      80.6%; Score 79; DB 16; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.6e-05;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIRLSDNYATHYAESVKG 19
    ||| : ||| ||| |||
Db 1 EIRSQNNFATHYAESVKG 19
    ||| : ||| ||| |||

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RESULT 7
US-10-338-552-47
; Sequence 47, Application US/10338552
; Publication No. US20040131612A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Marquis, David
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: TWP-alpha Binding

```

; FILE REFERENCE: AWE-06971
; CURRENT APPLICATION NUMBER: US/10/338,552
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; US-10-338-552-47

```

Query Match 77.6%; Score 76; DB 16; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.8e-05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy

1 EIRLKSDNYATHYAESVKG 19
||| ||| ||| ||| ||| |||

Dd

1 EIRSKSXNSATHYAESVKG 19

```

RESULT 8
US-10-338-627-47
; Sequence 47, Application US/10338627
; Publication No. US20040131613A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Marquis, David
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: TNF-alpha Binding Molecules
; FILE REFERENCE: AME-07497
; CURRENT APPLICATION NUMBER: US/10/338,627
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: Xaa can be any naturally occ
; US-10-338-627-47

```

Query Match 77.6%; Score 76; DB 16; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.8e-05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIRLKSDNYATHAESVKG 19
 ||| | | | | | |
Dd 1 EIRSKSXNSATHAESVKG 19

RESULT 9
US-10-384-060-43
; Sequence 43, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060

; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: P VH CDR2 sequence
US-10-384-060-43

Query Match 75.5%; Score 74; DB 15; Length 19;
Best Local Similarity 84.2%; Pred. No. 9.8e-05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19
Db 1 EIRKSINSATHYAESVKG 19

RESULT 10
US-10-338-552-43
; Sequence 43, Application US/10338552
; Publication No. US20040131612A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Marquis, David
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: TNF-alpha Binding Molecules
; FILE REFERENCE: AME-06971
; CURRENT APPLICATION NUMBER: US/10/338,552
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-338-552-43

Query Match 75.5%; Score 74; DB 16; Length 19;
Best Local Similarity 84.2%; Pred. No. 9.8e-05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19
Db 1 EIRKSINSATHYAESVKG 19

RESULT 11
US-10-338-552-45
; Sequence 45, Application US/10338552
; Publication No. US20040131612A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Marquis, David
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: TNF-alpha Binding Molecules
; FILE REFERENCE: AME-06971
; CURRENT APPLICATION NUMBER: US/10/338,552
; CURRENT FILING DATE: 2003-01-08

; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-338-552-45

Query Match 75.5%; Score 74; DB 16; Length 19;
Best Local Similarity 84.2%; Pred. No. 9.8e-05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19
Db 1 EIRKSMSATHYAESVKG 19

RESULT 12
US-10-338-627-43
; Sequence 43, Application US/10338627
; Publication No. US20040131613A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Marquis, David
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: TNF-alpha Binding Molecules
; FILE REFERENCE: AME-07497
; CURRENT APPLICATION NUMBER: US/10/338,627
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-338-627-43

Query Match 75.5%; Score 74; DB 16; Length 19;
Best Local Similarity 84.2%; Pred. No. 9.8e-05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19
Db 1 EIRKSINSATHYAESVKG 19

RESULT 13
US-10-338-627-45
; Sequence 45, Application US/10338627
; Publication No. US20040131613A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Marquis, David
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: TNF-alpha Binding Molecules
; FILE REFERENCE: AME-07497
; CURRENT APPLICATION NUMBER: US/10/338,627
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-338-627-45

Qy

1 EIRLSDNYATHAESVKG 19
||| || | | | | | | | |

Db

1 EIRSKMNSATHAESVKG 19

Qy 1 EIRKSDNYATHYAESVKG 19
||| |:|:|:|:|:|
Db 1 EIRSKAHNHATYYAESVKG 19

QY 2 IRLKSDNYATHYAESVK 18

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:48:43 ; Search time 40 Seconds
(without alignments)
35.458 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRKSDNYATHVAESVKG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 187692

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	69.4	19	2	US-08-737-085A-4
2	68	69.4	19	3	US-09-246-258-4
3	68	69.4	19	3	US-09-532-106-4
4	68	69.4	19	4	US-09-839-666-4
5	66	67.3	19	1	US-07-977-696C-78
6	66	67.3	19	1	US-08-129-930B-78
7	66	67.3	19	3	US-08-376-288A-78
8	49	50.0	19	1	US-08-318-970B-6
9	49	50.0	19	4	US-09-563-222C-51
10	48	49.0	17	4	US-09-192-854-60
11	48	49.0	19	4	US-09-563-222C-60
12	47	48.0	19	1	US-08-318-970B-5
13	46	46.9	17	4	US-09-192-854-164
14	45	45.9	17	4	US-09-424-840B-63
15	45	45.9	17	4	US-09-424-840B-74
16	45	45.9	19	2	US-08-765-783A-85
17	45	45.9	19	3	US-09-416-557-85
18	45	45.9	19	4	US-08-407-620A-2
19	44	44.9	17	1	US-08-264-093-22
20	43	43.9	17	4	US-09-192-854-37
21	43	43.9	17	4	US-09-424-840B-64
22	41	41.8	17	4	US-09-192-854-4
23	41	41.8	17	4	US-09-192-854-115
24	41	41.8	17	4	US-09-424-840B-72
25	41	41.8	17	4	US-09-424-840B-88
26	40	40.8	17	4	US-09-192-854-10
27	40	40.8	17	4	US-09-192-854-18

28	40	40.8	17	4	US-09-192-854-96	Sequence 96, Appl
29	40	40.8	17	4	US-09-424-840B-107	Sequence 107, Appl
30	39	39.8	14	2	US-08-452-724A-41	Sequence 41, Appl
31	39	39.8	14	4	US-08-453-623-41	Sequence 41, Appl
32	39	39.8	17	2	US-08-650-262-14	Sequence 14, Appl
33	39	39.8	17	4	US-09-192-854-29	Sequence 29, Appl
34	39	39.8	17	4	US-09-192-854-68	Sequence 68, Appl
35	39	39.8	17	4	US-09-192-854-93	Sequence 93, Appl
36	39	39.8	17	4	US-09-192-854-124	Sequence 124, Appl
37	39	39.8	17	4	US-09-192-854-139	Sequence 139, Appl
38	38	38.8	17	1	US-08-053-171-31	Sequence 31, Appl
39	38	38.8	17	4	US-09-424-840B-76	Sequence 76, Appl
40	37	37.8	16	4	US-09-155-106-2	Sequence 2, Appl
41	37	37.8	17	4	US-09-192-854-22	Sequence 22, Appl
42	37	37.8	17	4	US-09-192-854-64	Sequence 64, Appl
43	37	37.8	17	4	US-09-192-854-71	Sequence 71, Appl
44	37	37.8	17	4	US-09-192-854-86	Sequence 86, Appl
45	37	37.8	17	4	US-09-192-854-99	Sequence 99, Appl

ALIGNMENTS

RESULT 1
US-08-737-085A-4
; Sequence 4, Application US/08737085A
; Patent No. 5869232
; GENERAL INFORMATION:
; APPLICANT: SALLBERG, MATTI
; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
; TITLE OF INVENTION: EXCHANGER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DARBY & DARBY PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08737,085A
FILING DATE: 27-DEC-1996
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 3846/0C569
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7659
TELEFAX: 212-753-6237
TELEX: 236687

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-737-085A-4

Query Match 69.4%; Score 68; DB 2; Length 19;
Best Local Similarity 72.2%; Pred. No. 0.00018;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 IRLKSDNYATHVAESVKG 19

TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-839-666-4

Query Match 69.4%; Score 68; DB 4; Length 19;
Best Local Similarity 72.2%; Pred. No. 0.00018;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRLKSDNYATHYAESVKG 19
DB 2 VRKSPNYATYADSVKG 19

RESULT 5
US-07-977-696C-78
; Sequence 78, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
; TITLE OF INVENTION: and Therapeutic Methods.
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,696C
; FILING DATE: 11-16-92
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38227
; TELEPHONE: (510) 748-6868
; TELEFAX: (510) 748-6688
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-977-696C-78

Query Match 67.3%; Score 66; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 0.00038;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
DB 1 EIRKNNHATYIDESVKG 19

RESULT 6
US-08-129-930B-78
; Sequence 78, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRECC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-129-930B-78

Query Match 67.3%; Score 66; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 0.00038;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
DB 1 EIRKNNHATYIDESVKG 19

RESULT 7
US-08-976-288A-78
; Sequence 78, Application US/08976288A
; Patent No. 6315997
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski

STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,696
FILING DATE: No. 6315997ember 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6639938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-976-288A-78

Query Match 67.3%; Score 66; DB 3; Length 19;
Best Local Similarity 68.4%; Pred. No. 0.00038;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
||| |::|||:|||||
DB 1 EIRKANNHATYYDES VKG 19

RESULT 8
US-08-318-970B-6
; Sequence 6, Application US/08318970B
; Patent No. 5589573
; GENERAL INFORMATION:
; APPLICANT: Hideaki HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg

REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: S-2371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 549-2282
TELEFAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: H-CDR2-3
OTHER INFORMATION: hypervariable region
US-08-318-970B-6

Query Match 50.0%; Score 49; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 0.21;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IRLKSDNYATHYAESVKG 19
||| |::|||:|||||
DB 2 IIRKANNYTTTEYSASVKG 19

RESULT 9
US-09-563-222C-51
; Sequence 51, Application US/09563222C
; Patent No. 6696820
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 51
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-51

Query Match 50.0%; Score 49; DB 4; Length 19;
Best Local Similarity 60.0%; Pred. No. 0.21;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 KSDNYATHYAESVKG 19
||| |::|||:|||||
DB 5 KTDGGSTYYADSVKG 19

RESULT 10
US-09-192-854-60
; Sequence 60, Application US/09192854
; Patent No. 6696245
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: Patent In Ver. 2.0


```
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-60

Query Match          49.0%; Score 48; DB 4; Length 17;
Best Local Similarity 52.9%; Pred. No. 0.28;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAEVSKG 19
   | : |||: |||
Db 1 RIPARGTVHYADSVKG 17

RESULT 11
US-09-563-222C-60
; Sequence 60, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 60
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-60

Query Match          49.0%; Score 48; DB 4; Length 19;
Best Local Similarity 52.9%; Pred. No. 0.31;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAEVSKG 19
   | : |||: |||
Db 3 RNKANDYTEYSASVKG 19

RESULT 12
US-08-318-970B-5
; Sequence 5, Application US/08318970B
; Patent No. 5589573
; GENERAL INFORMATION:
; APPLICANT: Hideaki HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
```

```
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg
; REGISTRATION NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: H-CDR2-2
; OTHER INFORMATION: hypervariable region
US-08-318-970B-5

Query Match          48.0%; Score 47; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 0.45;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IRLKSDNYATHYAEVSKG 19
   || |:: | | | |
Db 2 IIRKANLYTTDYSVKG 19

RESULT 13
US-09-192-854-164
; Sequence 164, Application US/09192854
; Patent No. 6696245
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 164
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-164

Query Match          46.9%; Score 46; DB 4; Length 17;
Best Local Similarity 64.3%; Pred. No. 0.58;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 SDNYATHYAEVSKG 19
   | | | | | | |
Db 4 SSGYGTGYADSVKG 17

RESULT 14
US-09-424-840B-63
; Sequence 63, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
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; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-424-840B-63

```

```

Query Match      45.9%; Score 45; DB 4; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.84;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 THYAESVKG 19
      ||||:||||
Db      9 THYADSVKG 17

```

```

RESULT 15
US-09-424-840B-74
; Sequence 74, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-424-840B-74

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```

Query Match      45.9%; Score 45; DB 4; Length 17;
Best Local Similarity 88.9%; Pred. No. 0.84;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 THYAESVKG 19
      ||||:||||
Db      9 THYADSVKG 17

```

Search completed: April 18, 2005, 15:58:24
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:59:59 ; Search time 5.93023 Seconds
(without alignments)
48.674 Million cell updates/sec

Title: US-09-674-716B-13

Perfect score: 16
Sequence: 1 FID 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	18	2 S43834	DNA topoisomerase
2	16	100.0	21	2 D48518	PEB1 5'-region hyp
3	16	100.0	23	1 S20453	pyrroloquinoline q
4	16	100.0	25	2 F84066	hypothetical prote
5	16	100.0	30	2 A26188	lipocortin I - pig
6	16	100.0	30	2 A44682	nitrobenzene nitro
7	16	100.0	31	2 H82818	hypothetical prote
8	16	100.0	32	2 PQ0413	nonstructural prot
9	16	100.0	33	2 PQ0416	RNA-directed RNA p
10	16	100.0	33	2 A95119	hypothetical prote
11	16	100.0	33	2 H82096	hypothetical prote
12	16	100.0	33	2 S33646	hypothetical prote
13	16	100.0	35	2 PS0363	protein-tyrosine-p
14	16	100.0	35	2 PS0364	protein-tyrosine-p
15	16	100.0	36	2 D87544	hypothetical prote
16	16	100.0	37	2 C70186	hypothetical prote
17	16	100.0	37	2 G95919	probable transposa
18	16	100.0	38	2 S33402	Ig heavy chain V r
19	16	100.0	38	2 B19803	proline-rich phosph
20	16	100.0	39	2 D82085	hypothetical prote
21	16	100.0	39	2 A96026	hypothetical prote
22	16	100.0	40	2 A23098	labiridical toxin -
23	16	100.0	43	1 ZDBPT9	gene 55.4 protein
24	16	100.0	43	2 B97505	hypothetical prote
25	16	100.0	45	2 H83816	hypothetical prote
26	16	100.0	45	2 C34669	calmodulin-related
27	16	100.0	46	2 B82461	hypothetical prote
28	16	100.0	47	2 FC4133	hypothetical 47 pr
29	16	100.0	48	2 T07316	hypothetical prote

30 16 100.0 48 2 C95060 hypothetical prote
31 16 100.0 50 2 AB0367 hypothetical prote
32 16 100.0 51 2 S00576 hypothetical prote
33 16 100.0 52 2 S15922 hypothetical prote
34 16 100.0 52 2 C82621 hypothetical prote
35 16 100.0 52 2 AF0293 hypothetical prote
36 16 100.0 52 2 FN0481 cell division cycl
37 16 100.0 52 2 A71002 hypothetical prote
38 16 100.0 53 2 A82862 hypothetical prote
39 16 100.0 53 2 H98094 hypothetical prote
40 16 100.0 54 2 E95230 hypothetical prote
41 16 100.0 54 2 S46848 gene A52R protein
42 16 100.0 54 2 T04034 hypothetical prote
43 16 100.0 54 2 D84144 hypothetical prote
44 16 100.0 54 2 AH1362 Bacteriophage A118
45 16 100.0 54 2 S32360 SNAP receptor - bo

ALIGNMENTS

RESULT 1

S43834
DNA topoisomerase (EC 5.99.1.2) - Klebsiella sp. (ATCC 15380) (fragment)
C:Species: Klebsiella sp.
A:Variety: ATCC 15380
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 07-May-1999
C:Accession: S43834
R:Lynch, A.S.; Tyrrell, R.; Smerdon, S.J.; Briggs, G.S.; Wilkinson, A.J.
Biochem. J. 299, 129-136, 1994
A:Title: Characterization of the CysB protein of Klebsiella aerogenes: direct evidence
A:Reference number: S43834; MUID:94220019; PMID:8166630
A:Accession: S43834
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-18 <LYN>
A:Experimental source: ATCC 15380
C:Genetics:
A:Gene: topI
C:Function:
A:Description: catalyzes ATP-independent transient breakage of DNA phosphodiester bonds
rejoining; this reaction will lead to the conversion of one topological isomer of DNA to
C:Superfamily: bacterial type I DNA topoisomerase
C:Keywords: DNA binding; DNA replication; isomerase; zinc finger

Query Match 100.0%; Score 16; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 1 FID 3

DB 8 FID 10

RESULT 2

D48518
PEB1 5'-region hypothetical protein A - Campylobacter jejuni (fragment)
C:Species: Campylobacter jejuni
C:Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 09-Jul-2004
C:Accession: D48518
R:Pei, Z.; Blaser, M.J.
J. Biol. Chem. 268, 18717-18725, 1993
A:Title: PEB1, the major cell-binding factor of Campylobacter jejuni, is a homolog of t
A:Reference number: A48518; MUID:93366784; PMID:8360165
A:Accession: D48518
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-21 <PEI>
A:Cross-references: UNIPROT:Q9PP09; GB:U13662

Query Match 100.0%; Score 16; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

```

C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Feb-1997
C;Accession: A26188
R;De, B.K.; Misono, K.S.; Lukas, T.J.; Mroczkowski, B.; Cohen, S.
J. Biol. Chem. 261, 13784-13792, 1986
A;Title: A calcium-dependent 35-kilodalton substrate for epidermal growth factor receptor
A;Reference number: A26188; MUID:87008618; PMID:3020049
A;Accession: A26188
A;Molecule type: protein
A;Residues: 1-30 <DEB>
C;Superfamily: annexin I; annexin repeat homology
C;Keywords: phosphoprotein

Query Match      100.0%; Score 16; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
      |||
Db      1 FID 3
      |||

RESULT 6
A44682
nitrobenzene nitroreductase (EC 1.-.-.-) - Pseudomonas pseudoalcaligenes (fragment)
C;Species: Pseudomonas pseudoalcaligenes
C;Date: 28-Feb-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C;Accession: A44682
R;Somerville, C.C.
A;Submitted to the Protein Sequence Database, February 1995
A;Description: Purification and characterization of nitrobenzene nitroreductase from Pse
F;15-19/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted
F;15-19/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted

Query Match      100.0%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
      |||
Db      7 FID 9
      |||

RESULT 4
F84066
hypothetical protein BH3334 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: F84066
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84066
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-25 <STO>
A;Cross-references: UNIPROT:Q9K7M7; GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BA070
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3334

Query Match      100.0%; Score 16; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
      |||
Db     13 FID 15
      |||

RESULT 5
A26188
lipocortin I - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)

```

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A;Reference number: A59328
A;Content: annotation
C;Genetics:
A;Gene: XF0341

Query Match 100.0%; Score 16; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
DB 16 FID 18

RESULT 8

PQ0413
nonstructural protein NS1 - influenza A virus (strain A/Hebei/24/89 [H1N2]) (fragment)
C;Species: influenza A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PQ0413
R;Li, X.S.; Zhao, C.Y.; Gao, H.M.; Zhang, Y.Q.; Ishida, M.; Kanegae, Y.; Endo, A.; Nerom J. Gen. Virol. 73, 1329-1337, 1992
A;Title: Origin and evolutionary characteristics of antigenic reassortant influenza A (H A;Reference number: PQ0408; MUID:92300326; PMID:1607856
A;Accession: PQ0413
A;Molecule type: genomic RNA
A;Residues: 1-32 <Lia>
A;Cross-references: UNIPROT:Q7LZX4
C;Genetics:
A;Map position: segment 8
C;Superfamily: influenza virus nonstructural protein NS1
C;Keywords: nonstructural protein

Query Match 100.0%; Score 16; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
DB 10 FID 12

RESULT 9

PQ0416
RNA-directed RNA polymerase (EC 2.7.7.48) 3 - influenza A virus (strain A/Yamagata/120/8 N;Alternate names: P2 protein; PA protein
C;Species: influenza A virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PQ0416
R;Li, X.S.; Zhao, C.Y.; Gao, H.M.; Zhang, Y.Q.; Ishida, M.; Kanegae, Y.; Endo, A.; Nerom J. Gen. Virol. 73, 1329-1337, 1992
A;Title: Origin and evolutionary characteristics of antigenic reassortant influenza A (H A;Reference number: PQ0408; MUID:92300326; PMID:1607856
A;Accession: PQ0416
A;Molecule type: genomic RNA
A;Residues: 1-33 <Lia>
A;Cross-references: UNIPROT:Q7M023
C;Genetics:
A;Map position: segment 3
C;Superfamily: influenza virus RNA-directed RNA polymerase 3
C;Keywords: nucleotidyltransferase

Query Match 100.0%; Score 16; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
DB 11 FID 13

RESULT 10

A95119
hypothetical protein SP1031 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: A95119
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hel on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: A95119
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-33 <KUR>
A;Cross-references: UNIPROT:Q97R10; GB:AE005672; PIDN:AAK75146.1; PID:g14972505; GSPDB: A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1031

Query Match 100.0%; Score 16; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
DB 22 FID 24

RESULT 11

H82096
hypothetical protein VC2284 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: H82096
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bacs, S.; Qin, H.; Dragoi, I.; Sellers, l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: H82096
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-33 <HEI>
A;Cross-references: UNIPROT:Q9KP88; GB:AE004299; GB:AE003852; NID:g9656835; PIDN:AAF954 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2284
A;Map position: 1

Query Match 100.0%; Score 16; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
DB 19 FID 21

RESULT 12

S33646
hypothetical protein 2 - pin mould (Absidia glauca) plasmid PSSP15 (fragment)
C;Species: Absidia glauca
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S33646
R;Haenfler, J.; Woestemeyer, J.; Weigel, C.T. submitted to the EMBL Data Library, June 1992
A;Description: Complete nucleotide sequence of the pApD9 extrachromosomal DNA element o

Tue Apr 19 06:14:51 2005

us-09-674-716b-13.open.rpr

A:Reference number: S33645
A:Accession: S33646
A:Molecule type: DNA
A:Residues: 1-33 <RAE>
A:Cross-references: UNIPROT:Q00062; EMBL:M94861
C:Genetics:
A:Genome: plasmid

Query Match 100.0%; Score 16; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
DB 22 FID 24

RESULT 13

PS0363
protein-tyrosine-phosphatase (EC 3.1.3.48) (clone PTP5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 20-Mar-1998
C:Accession: PS0363
R:den Hertog, J.; Pals, C.E.G.M.; Jonk, L.J.C.; Kruijer, W.
Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992
A:Title: Differential expression of a novel murine non-receptor protein tyrosine phosphatase
A:Reference number: JH0609; MUID:92272714; PMID:1590786
A:Accession: PS0363

A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA

A:Residues: 1-35 <DEN>
A:Experimental source: embryonal carcinoma cell, P19 cell
C:Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repeat
-tyrosine-phosphatase homology
C:Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase

Query Match 100.0%; Score 16; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
DB 6 FID 8

RESULT 14

PS0364
protein-tyrosine-phosphatase (EC 3.1.3.48) (clone PTP31) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 20-Mar-1998
C:Accession: PS0364
R:den Hertog, J.; Pals, C.E.G.M.; Jonk, L.J.C.; Kruijer, W.
Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992
A:Title: Differential expression of a novel murine non-receptor protein tyrosine phosphatase
A:Reference number: JH0609; MUID:92272714; PMID:1590786
A:Accession: PS0364

A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA

A:Residues: 1-35 <DEN>
A:Experimental source: embryonal carcinoma cell, P19 cell
C:Superfamily: protein-tyrosine-phosphatase, receptor type mu; fibronectin type III repeat
-tyrosine-phosphatase homology
C:Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase

Query Match 100.0%; Score 16; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
DB 6 FID 8

RESULT 15

D87544
hypothetical protein CC2381 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: D87544
R:Nierman, W.C.; Feidblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: D87544

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-36 <STO>
A:Cross-references: UNIPROT:Q9A5R6; GB:AE005673; MID:gl3423914; PIDN:AAK24352.1; GSPDB:C

C:Genetics:

A:Gene: CC2381

Query Match 100.0%; Score 16; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
DB 28 FID 30

Search completed: April 18, 2005, 14:23:36
Job time : 7.93023 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:57:43 ; Search time 27.2791 Seconds
(without alignments)
56.316 Million cell updates/sec

Title: US-09-674-716B-13
Perfect score: 16
Sequence: 1 FID 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	15	2 Q9KIV5	Q9KIV5 anabaena sp
2	16	100.0	15	2 Q9R4K0	Q9R4K0 nocardia. n
3	16	100.0	16	1 FIBA RABIT	P14461 oryctolagus
4	16	100.0	16	2 Q7R7Y9	Q7R7Y9 plasmidium
5	16	100.0	18	1 TOPI KLEAE	P46155 klebsiella
6	16	100.0	20	2 Q85485	Q85485 avian leuko
7	16	100.0	21	2 Q7RBP5	Q7RBP5 plasmidium
8	16	100.0	23	1 PQQA ENTIT	P59726 enterobacte
9	16	100.0	23	1 PQQA KLEPN	P27503 klebsiella
10	16	100.0	23	2 Q7RDS0	Q7RDS0 plasmidium
11	16	100.0	24	2 Q9R2R0	Q9R2R0 streptococc
12	16	100.0	24	2 Q9Z630	Q9Z630 streptococc
13	16	100.0	24	2 Q8CGM9	Q8CGM9 mus musculu
14	16	100.0	25	2 Q9K7M7	Q9K7M7 bacillus ha
15	16	100.0	28	2 Q8K587	Q8K587 escherichia
16	16	100.0	29	2 Q6JTX2	Q6JTX2 isohypaibiu
17	16	100.0	29	2 Q7RLD1	Q7RLD1 plasmidium
18	16	100.0	29	2 Q7RTA7	Q7RTA7 plasmidium
19	16	100.0	29	2 Q6U204	Q6U204 helicobacte
20	16	100.0	29	2 Q6UNW4	Q6UNW4 vibrio chol
21	16	100.0	29	2 Q87L17	Q87L17 vibrio para
22	16	100.0	29	2 Q8CLJ9	Q8CLJ9 versinia pe
23	16	100.0	30	2 Q9NRC5	Q9NRC5 homo sapien
24	16	100.0	30	2 Q7RBY6	Q7RBY6 plasmidium
25	16	100.0	30	2 Q7RB68	Q7RB68 plasmidium
26	16	100.0	30	2 Q7MI28	Q7MI28 pseudomonas
27	16	100.0	30	2 Q81NQ6	Q81NQ6 bacillus an
28	16	100.0	31	2 Q7R863	Q7R863 plasmidium
29	16	100.0	31	2 Q6UK06	Q6UK06 vibrio chol
30	16	100.0	31	2 Q6WLW6	Q6WLW6 rhizobium s
31	16	100.0	31	2 Q8KGF6	Q8KGF6 chlorobium

32 16 100.0 31 2 Q8EIW8 Q8EIW8 shewanella
33 16 100.0 31 2 Q9PGG1 Q9PGG1 xylella fas
34 16 100.0 31 2 Q9S0E6 Q9S0E6 borrelia bu
35 16 100.0 32 1 RS19 YEREN Q56847 versinia en
36 16 100.0 32 2 Q501I0 Q501I0 mycobacteri
37 16 100.0 32 2 Q6V7H0 Q6V7H0 vibrio chol
38 16 100.0 32 2 Q87IK8 Q87IK8 vibrio para
39 16 100.0 32 2 Q7LZX4 Q7LZX4 influenza a
40 16 100.0 33 2 Q7RQV0 Q7RQV0 plasmidium
41 16 100.0 33 2 Q9S7Y3 Q9S7Y3 picea abies
42 16 100.0 33 2 Q6JSD0 Q6JSD0 haemophilus
43 16 100.0 33 2 Q6ZJF9 Q6ZJF9 burkholderi
44 16 100.0 33 2 Q97R10 Q97R10 streptococ
45 16 100.0 33 2 Q9KPS8 Q9KPS8 vibrio chol

ALIGNMENTS

RESULT 1

Q9KIV5 PRELIMINARY; PRT; 15 AA.
AC Q9KIV5;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE Putative deoxyribose-phosphate aldolase (Fragment).
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC7120;
RA Matveyev A.V., Young K.T., Elhai J.;
RT "DNA methyltransferases of the cyanobacterium Anabaena PCC 7120.";
RL Nucleic Acids Res. 29:1493-1506 (2001).
DR EMBL; AF220508; AAF75233.1; -.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1608 MW; 1B1307FDA6850099 CRC64;

Query Match 100.0%; Score 16; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
DB 13 FID 15

RESULT 2

Q9R4K0 PRELIMINARY; PRT; 15 AA.
AC Q9R4K0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Nitric oxide synthase (EC 4.14.23.-) (Fragment).
OS Nocardia.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae.
OX NCBI_TaxID=1817;
RN [1]
RP SEQUENCE.
RX MEDLINE=953394819; PubMed=7545152;
RA Chen Y., Rosazza J.P.;
RT "Purification and characterization of nitric oxide synthase (NOSNoc)
from a Nocardia species.";
RL J. Bacteriol. 177:5122-5128 (1995).
FT NON_TER 15
SQ SEQUENCE 15 AA; 1818 MW; 2BD5B859DE288B77 CRC64;

Query Match 100.0%; Score 16; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 13 FID 15

RESULT 3

FIBA RABBIT
ID FIBA RABBIT STANDARD; PRT; 16 AA.
AC P14461;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FGA;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]

SEQUENCE.

RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19.1789-1791(1965).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.
CC -!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains (alpha, beta and gamma), linked to each other by disulfide bonds.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.
KW Blood coagulation; Direct protein sequencing; Plasma.
FT PEPTIDE 1 16 Fibrinopeptide A.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1651 MW; DFB623279EA55EB6 CRC64;

Query Match 100.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 8 FID 10

RESULT 4

O7R7Y9 PRELIMINARY; PRT; 16 AA.
AC O7R7Y9;
DT 01-MAR-2004 (TREMELrel. 26, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=PY07435;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XN1;
RX PubMed=1236865; DOI=10.1038/nature01099;

RA Carlton J.M., Anguillo S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabai A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,

RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC EMBL; AABL01002729; EAA19883.1; -.
DR Hypothetical protein.
KW NON TER 16
SQ SEQUENCE 16 AA; 1946 MW; B13FDBDB22FD127 CRC64;

Query Match 100.0%; Score 16; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 6 FID 8

RESULT 5

TOPI KLEAE STANDARD; PRT; 18 AA.
ID TOPI KLEAE
AC P46155;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
DE (Untwisting enzyme) (Swivelase) (Fragment).
GN Name=topA;
OS Klebsiella aerogenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=28451;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 418 / ATCC 15380;
RX MEDLINE=94220019; PubMed=8166630;
RA Lynch A.S., Tyrrell R., Smerdon S.J., Briggs G.S., Wilkinson A.J.;
RT "Characterization of the CysB protein of Klebsiella aerogenes: direct evidence that N-acetylserine rather than O-acetylserine serves as the inducer of the cysteine regulon.";
RL Biochem. J. 299:129-136(1994).

CC -!- FUNCTION: The reaction catalyzed by topoisomerases leads to the conversion of one topological isomer of DNA to another.
CC -!- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded DNA, followed by passage and rejoining.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- MISCELLANEOUS: When a topoisomerase transiently breaks a DNA backbone bond, it simultaneously forms a protein-DNA link, in which a tyrosyl oxygen in the enzyme is joined to a DNA phosphorus at one end of the enzyme-severed DNA strand.
CC -!- SIMILARITY: Belongs to the prokaryotic type I/III topoisomerase family.

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CC EMBL; X78729; -; NOT_ANNOTATED_CDS.
CC HSSP; P06612; IYUA.

DR InterPro; IPR000380; DNA tpisomrase.
DR PROSITE; PS00396; TOPOISOMERASE_I_PROK; PARTIAL.
KW DNA-binding; Isomerase; Topoisomerase.
FT NON TER 1
SQ SEQUENCE 18 AA; 2043 MW; 8C1C81238FF0EPA4 CRC64;


```
Query Match      100.0%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 8 FID 10

RESULT 6
Q85485 ID Q85485 PRELIMINARY; PRT; 20 AA.
AC Q85485;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gag-erbB fusion protein (Fragment).
OS Avian leukosis virus.
OC Viruses; Retrovirdae; Retroviridae; Alpharetrovirus.
NCBI_TaxID=11864;
[1]
SEQUENCE FROM N.A.
STRAIN=RAV1;
RX MEDLINE=88230605; Pubmed=2897475;
RA Raines M.A., Mahle N.J., Moscovici C., Crittenden L., Kung H.-J.;
RT "Mechanism of c-erbB transduction: newly released transducing viruses
RT retain poly(A) tracts of erbB transcripts and encode C-terminally
RT intact erbB proteins.";
RL J. Virol. 62:2437-2443(1998).
DR EMBL; M19970; AAA42586.1; -.
DR InterPro; IPR009030; Grow_fac_recept.
FT NON TER 1 20
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2167 MW; 2A4EFD2E3A709011 CRC64;

Query Match      100.0%; Score 16; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 11 FID 13

RESULT 7
Q7RBPS ID Q7RBPS PRELIMINARY; PRT; 21 AA.
AC Q7RBPS;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY06095;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
[1]
SEQUENCE FROM N.A.
STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angioli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegh M., Shoalbi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).

-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABL01002024; EAA18247.1; -.
KW Hypothetical protein.
SQ SEQUENCE 21 AA; 2603 MW; 6633105FCS69A116 CRC64;

Query Match      100.0%; Score 16; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 5 FID 7

RESULT 8
PQQA_ENTIT ID PQQA_ENTIT STANDARD; PRT; 23 AA.
AC P59726;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Coenzyme PQQ synthesis protein A (Pyrroloquinoline quinone
DE biosynthesis protein A).
GN Name=pqqa;
OS Enterobacter intermedius.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
NCBI_TaxID=61648;
[1]
SEQUENCE FROM N.A.
RA Kim C.H., Han S.H., Kim K.Y., Cho B.H., Kim Y.H., Gu B.S., Kim Y.C.;
RT "Cloning and expression of pyrroloquinoline (PQQ) genes from a
RT phosphate-solubilizing bacterium Enterobacter intermedius.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Required for coenzyme pyrroloquinoline quinone (PQQ)
CC biosynthesis. Probably provides the glutamate and tyrosine
CC residues that are cross-linked and modified to form the coenzyme
CC (By similarity).
CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
CC -!- SIMILARITY: Belongs to the pqqa family.
-----
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-----
DR EMBL; AY216683; AAP34378.1; -.
DR HAMAP; MF00656; -.
KW PQQ; PQQ Biosynthesis.
FT CROSSELINK 15 19
FT FT
SQ SEQUENCE 23 AA; 2764 MW; ACCB321460871C5D CRC64;

Query Match      100.0%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 7 FID 9

RESULT 9
PQQA_KLEPN ID PQQA_KLEPN STANDARD; PRT; 23 AA.
AC P27503;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
```

05-JUL-2004 (Rel. 44, Last annotation update)
 Coenzyme PQQ synthesis protein A (pyrroloquinoline quinone biosynthesis protein A).
 Name=pqqa;
 Klebsiella pneumoniae.
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Klebsiella.
 NCBI_TaxID=573;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=NCTC 418;
 MEDLINE=92212293; PubMed=1313537;
 Meulenbergh J.J.M., Sellink E., Riegman N.H., Postma P.W.;
 "Nucleotide sequence and structure of the Klebsiella pneumoniae pqq operon.";
 Mol. Gen. Genet. 232:284-294(1992).
 [2]
 FUNCTION.
 STRAIN=NCTC 418;
 MEDLINE=95394815; PubMed=7665488;
 Velterop J.S., Sellink E., Meulenbergh J.J., David S., Bulder I., Postma P.W.;
 "Synthesis of pyrroloquinoline quinone in vivo and in vitro and detection of an intermediate in the biosynthetic pathway.";
 J. Bacteriol. 177:5088-5098(1995).
 -1- FUNCTION: Required for coenzyme pyrroloquinoline quinone (PQQ) biosynthesis. Probably provides the glutamate and tyrosine residues that are cross-linked and modified to form the coenzyme.
 -1- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
 -1- SIMILARITY: Belongs to the pqa family.

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 EMBL; X58778; CAA41579.1; -.
 PIR; S20453; S20453.
 HAMAP; MF 00656; -; 1.
 DR PQQ; PQQ Biosynthesis.
 FT CROSSLINK 15 19
 Pyrroloquinoline quinone (Glu-Tyr) (Probable).
 FT SEQUENCE 23 AA; 2764 MW; ACCB321460871C5D CRC64;
 Query Match 100.0%; Score 16; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FID 3
 Db 7 FID 9
 RESULT 10
 Q7RDSO PRELIMINARY; PRT; 23 AA.
 AC Q7RDSO;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=PY05351;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 SEQUENCE FROM N.A.
 STRAIN=17XNL;
 RX PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Persea M.,

RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J., Carucci D.J.;
 "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii.";
 Nature 419:512-519(2002).
 CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
 CC EMBL; AABL01001686; EAA17363.1; -.
 DR Hypothetical protein.
 KW SEQUENCE 23 AA; 2779 MW; 338868E33689DBC7 CRC64;
 Query Match 100.0%; Score 16; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FID 3
 Db 6 FID 8
 RESULT 11
 Q9R2R0 PRELIMINARY; PRT; 24 AA.
 ID Q9R2R0;
 AC Q9R2R0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Capsular polysaccharide B (Fragment).
 GN Name=cpsB;
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=D39;
 RX MEDLINE=99287847; PubMed=10348877;
 RA Morona J.K., Morona R., Paton J.C.;
 "Analysis of the 5' portion of the type 19A capsule locus identifies two classes of cpsC, cpsD, and cpsE genes in Streptococcus pneumoniae.";
 J. Bacteriol. 181:3599-3605(1999).
 RL EMBL; AF106134; AAD17979.1; -.
 DR EMBL; AF106132; AAD17975.1; -.
 DR EMBL; AF106133; AAD17977.1; -.
 FT NON_TER 1
 FT SEQUENCE 24 AA; 2820 MW; ED047715CF90483B CRC64;
 Query Match 100.0%; Score 16; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FID 3
 Db 11 FID 13
 RESULT 12
 Q9Z630 PRELIMINARY; PRT; 24 AA.
 ID Q9Z630;
 AC Q9Z630;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Capsular polysaccharide B (Fragment).

```

GN Name=cpsB;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9287847; PubMed=10348877;
RA Morona J.K., Morona R., Paton J.C.;
RT "Analysis of the 5' portion of the type 19A capsule locus identifies
RT two classes of cpsC, cpsD, and cpsE genes in Streptococcus
RT pneumoniae.";
RL J. Bacteriol. 181:3599-3605 (1999).
DR EMBL; AF106135; AAD17981.1; -.
FT NON_TER 1
SQ SEQUENCE 24 AA; 2834 MW; ED047715CF82D83B CRC64;

Query Match 100.0%; Score 16; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 11 FID 13

RESULT 13
Q8CGM9 PRELIMINARY; PRT; 24 AA.
AC Q8CGM9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Retinoblastoma-binding protein 1 (Fragment).
GN Name=Rbbp1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129X1/SVU;
RA Binda O., Branton P.E.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY163235; AAN84616.1; -.
FT NON_TER 1
FT NON_TER 24
SQ SEQUENCE 24 AA; 2685 MW; BF6991AC3D52BC4E CRC64;

Query Match 100.0%; Score 16; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
Db 20 FID 22

RESULT 14
Q9K7M7 PRELIMINARY; PRT; 25 AA.
AC Q9K7M7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE BH3334 protein.
GN OrderedLocusNames=BH3334;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125;

```

```

RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331 (2000).
DR EMBL; AF001518; BAB07053.1; -.
DR PIR; F84066; F84066.
KW Complete proteome.
SQ SEQUENCE 25 AA; 2986 MW; OC21EA93BE976875 CRC64;

```

```

Query Match 100.0%; Score 16; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 FID 3
Db 13 FID 15

```

RESULT 15

```

Q8KS87 PRELIMINARY; PRT; 28 AA.
AC Q8KS87;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative oxidoreductase Fe-S subunit (Fragment) (Fragment).
GN Name=b1589; Synonyms=z2577;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ECOR-9;
RX MEDLINE=22053230; PubMed=12057959;
RX DOI=10.1128/JB.184.13.3640-3648.2002;
RA Sandt C.H., Hopper J.E., Hill C.W.;
RT "Activation of prophage eib genes for immunoglobulin-binding proteins
RT by genes from the IbrAB genetic island of Escherichia coli ECOR-9.";
RL J. Bacteriol. 184:3640-3648 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CB6220;
RA Koch C., Hertwig S., Appel B.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF520223; AAM53254.1; -.
DR EMBL; AJ576011; CAE11225.1; -.
FT NON_TER 28
FT NON_TER 28
SQ SEQUENCE 28 AA; 3185 MW; A2F42416487ED57B CRC64;

```

```

Query Match 100.0%; Score 16; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 FID 3
Db 8 FID 10

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Search completed: April 18, 2005, 14:22:02

Job time : 32.2791 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 13:32:07 ; Search time 31.6047 Seconds
(without alignments)
36.712 Million cell updates/sec

Title: US-09-674-716B-13

Perfect score: 16

Sequence: 1 FID 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1980s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	3	3 AAY32259	Aay32259 Light cha
2	16	100.0	5	1 AAP94794	Aap94794 Periferat
3	16	100.0	5	2 AAW55773	Aaw55773 Immunizat
4	16	100.0	5	5 AAU86974	Aau86974 Estradiol
5	16	100.0	5	5 ABB84336	Abb84336 Human MBP
6	16	100.0	6	2 AAR29321	Aar29321 Endothell
7	16	100.0	6	2 AAR69115	Aar69115 Endothell
8	16	100.0	6	2 AAW31469	Aaw31469 Transcrip
9	16	100.0	7	3 AAB06774	Aab06774 Claudin-6
10	16	100.0	7	3 AAB06594	Aab06594 Claudin-3
11	16	100.0	7	3 AAB06656	Aab06656 Claudin-4
12	16	100.0	7	6 ABU96533	Abu96533 Human cyt
13	16	100.0	7	6 ABU96535	Abu96535 Human cyt
14	16	100.0	7	7 ADL17604	Adl17604 Human MAG
15	16	100.0	8	3 AAB06597	Aab06597 Claudin-3
16	16	100.0	8	3 AAB06777	Aab06777 Claudin-6
17	16	100.0	8	3 AAB06659	Aab06659 Claudin-4
18	16	100.0	8	4 AAU25282	Aau25282 Schizophr
19	16	100.0	8	4 AAU15626	Aau15626 Schizophr
20	16	100.0	8	5 ABG73046	Abg73046 Cryptococ
21	16	100.0	8	5 ABP46831	Abp46831 Human BLY
22	16	100.0	8	5 ABG65708	Abg65708 Plant ICK
23	16	100.0	8	5 ABG65705	Abg65705 Plant ICK
24	16	100.0	8	7 ADG97658	Adg97658 scfVr VHCD
25	16	100.0	8	7 ADL17538	Adl17538 Human MAG

26	16	100.0	8	8 ADH35824	Adh35824 Vitamin D
27	16	100.0	8	8 ADH35805	Adh35805 Kininogen
28	16	100.0	8	8 ADH35831	Adh35831 Vitamin D
29	16	100.0	8	8 ADO78893	Ado78893 Schizophr
30	16	100.0	8	8 ADR72194	Adr72194 PET analy
31	16	100.0	9	2 AAR48299	Aar48299 Vitamin E
32	16	100.0	9	2 AAW13609	Aaw13609 HLA-A2.1
33	16	100.0	9	3 AAB06662	Aab06662 Claudin-4
34	16	100.0	9	3 AAB06780	Aab06780 Claudin-6
35	16	100.0	9	3 AAB06600	Aab06600 Claudin-3
36	16	100.0	9	4 AAB75620	Aab75620 HLA class
37	16	100.0	9	4 AAB75667	Aab75667 HLA class
38	16	100.0	9	4 AAB67398	Aab67398 Modified
39	16	100.0	9	4 AAB67397	Aab67397 Modified
40	16	100.0	9	4 AAB67395	Aab67395 Tobacco m
41	16	100.0	9	5 AAM49930	Aam49930 Human D40
42	16	100.0	9	5 AAU95252	Aau95252 Human nov
43	16	100.0	9	5 AAU94879	Aau94879 Human nov
44	16	100.0	9	6 ABM66263	Abm66263 Propionib
45	16	100.0	9	6 ABJ60588	Abj60588 184PIB2-r

ALIGNMENTS

RESULT 1
AAY32259
ID AAY32259 standard; peptide; 3 AA.
XX
AC AAY32259;
XX
DT 15-FEB-2000 (first entry)
XX
DE Light chain CDR H3 of mouse anti-CD23 Mab C11.
XX
KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
therapy.
XX
OS Mus musculus.
XX
PN WO9558679-A1.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-GB001434.
XX
PR 09-MAY-1998; 98GB-00009839.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
XX
DR WPI; 2000-053101/04.
XX
DR N-PSDB; AA234744.
XX
PT Cell receptor specific antibodies useful for treating e.g. arthritis,
PT diabetes, multiple sclerosis and psoriasis.
XX
PS Claim 1; Page 40; 81pp; English.
XX
CC This sequence represents complementarity determining region 3 (CDR H3)
CC of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11
CC (see also AAY32263). The invention provides altered antibodies, such as
CC chimeric or humanised antibodies, which comprise sufficient of the amino
CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on
 CC haematopoietic cells. The antibodies are used to block soluble CD23
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They
 CC are also useful for studying interactions between CD23 and various
 CC ligands and determining the binding agents

XX Sequence 3 AA;

Query Match 100.0%; Score 16; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
 |||
 Db 1 FID 3

RESULT 2
 AAP94794
 ID AAP94794 standard; protein; 5 AA.

XX AAP94794;

AC 25-MAR-2003 (revised)
 DT 03-JUL-1990 (first entry)

XX Periferal nervous system myelin protein, proteolipid protein, a PNS CNS
 DE myelin component and acetyl choline receptor epitope associated motif.

XX Autoantigen; MBP; myelin basic protein; transplantation antigen;
 KW myasthenia gravis; myasthenics; Transplantation antigen.

XX Synthetic.

XX EP304279-A.

XX 22-FEB-1989.

XX 17-AUG-1988; 88EP-00307608.

XX 17-AUG-1987; 87US-00086694.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Steinman L, Zamvil S;

XX WPI; 1989-055696/08.

XX Oligopeptide and polypeptide compsns. - based on the amino acid sequence
 PT of an immunogen and used for modulating the immune system.

XX Disclosure; Page; 7pp; English.

XX Sequences will normally be part of 9 to 15 AA sequence, excluded as
 CC motifs for immunisation but useful in tolerisation. (Updated on 25-MAR-
 CC 2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 5 AA;

Query Match 100.0%; Score 16; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
 |||

Db 3 FID 5

RESULT 3

AAW55773

ID AAW55773 standard; peptide; 5 AA.

XX AAW55773;

AC 25-MAR-2003 (revised)

XX 08-JUL-1998 (first entry)

XX Immunisation motif associated with AChr 4.

XX Myelin basic protein; immunity; immune response; neurological; T-cell;
 KW human; immunogen; B-cell; transplantation antigen; immunomodulator.

XX Unidentified.

XX EP805162-Al.

XX PD 05-NOV-1997.

XX PF 17-AUG-1988; 97EP-00106788.

XX PR 17-AUG-1987; 87US-00086694.

XX PR 17-AUG-1988; 88EP-00307608.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Steinman L, Zamvil S;

XX WPI; 1998-034664/04.

XX Polypeptide comprising human myelin basic protein fragment - useful as
 PT immuno modulator.

XX Disclosure; Page 8; 8pp; English.

XX The present sequence represents an immunisation motif normally excluded,
 CC but which may be used with advantage for tolerisation by itself or in
 CC conjunction with other epitope sequences from the present invention. The
 CC present invention describes a polypeptide comprising a human myelin basic
 CC protein (hMBP) fragment including P89-101 of hMBP, excluding native hMBP.
 CC The term P89-101 is not defined but may be intended to mean amino acids
 CC 89-101 of hMBP. The polypeptide can be used for tolerising a mammalian
 CC host immune system comprising B and T cells to an immunogen of interest,
 CC wherein said immunogen is restricted by a transplantation antigen of said
 CC host. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-
 CC 2003 to correct PR field.)

XX Sequence 5 AA;

Query Match 100.0%; Score 16; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
 |||

Db 3 FID 5

RESULT 4

AAU86974

ID AAU86974 standard; peptide; 5 AA.

XX AAU86974;

XX 21-MAY-2002 (first entry)

XX Estradiol mimotope peptide #22.

XX Estradiol; mimotope; estrone-3-glucuronide; steroid detection;

KW immunoassay; phage display; immunogen.

XX Synthetic.

XX WO200212270-A1.

XX 14-FEB-2002.

XX 26-JUL-2001; 2001WO-EP008705.

XX 03-AUG-2000; 2000EP-00306613.

XX (UNIL) UNILEVER PLC.

XX (UNIL) UNILEVER NV.

XX (UNIL) HINDUSTAN LEVER LTD.

XX Badley RA, Berry MJ, Williams SC;

XX WPI; 2002-241729/29.

XX Peptide mimotope capable of binding specifically to antibody specific to estradiol, useful for assaying presence and/or amount of estradiol, especially estrone-3-glucuronide in sample.

XX Claim 3; Page 22; 57pp; English.

XX The invention relates to a purified peptide mimotope capable of binding specifically to an antibody specific to estradiol. Also included are a solid support having immobilised (releasably or non-releasably) peptide mimotopes, an immunoassay test device for the detection of estradiol in the sample, comprising the mimotopes and an antibody capable of binding specifically to the mimotopes to generate a detectable signal and an isolated nucleic acid encoding the peptide mimotopes. The mimotope is useful for assaying the presence and/or amount of estradiol preferably estrone-3-glucuronide in a sample which is urine or serum sample to be tested and is also utilised in an immunoassay test device, and further can be used as immunogens. The mimotope be used to construct new, or improve the performance of old, immunoassay test formats and devices. They can, for example, be utilised essentially to tune the signal in conventional displacement assays for the detection of estradiol. The mimotope can be bound directly to certain assay surfaces which are otherwise non-compatible with estradiol on such surfaces needing to be bound to the surface by complexing with another - often proteinaceous - molecule. The mimotope is capable of being bound to the antigen-binding site of an antibody in a selective fashion in the presence of excess quantities of other undesired materials, and tightly enough (i.e. with high enough affinity) that when used in an immunoassay, it provides a useful result). The present sequence is a peptide mimotopes of the invention

XX Sequence 5 AA;

Query Match 100.0%; Score 16; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 3 FID 5

RESULT 5

ABB84336
ID ABB84336 standard; peptide; 5 AA.

XX ABB84336;

XX 17-OCT-2002 (first entry)

XX Human MBP protein derived peptide SEQ ID 36.

XX MBP; myelin basic protein; human; tolerance; immune system;
KW multiple sclerosis; autoimmune response; autoimmune disease;

KW immunosuppressive; neuroprotective.

XX Homo sapiens.

XX US2002076412-A1.

XX 20-JUN-2002.

XX 07-JUN-1995; 95US-00484409.

XX 17-AUG-1987; 87US-00086694.

XX 12-JUL-1989; 89US-00379500.

XX 01-MAY-1990; 90US-00517245.

XX 01-MAY-1991; 91WO-US002991.

XX 30-APR-1992; 92US-00877444.

XX 21-MAY-1993; 93US-00066325.

XX 22-SEP-1993; 93US-00125407.

XX (STEI/) STEINMAN L.

XX (ZAMV/) ZAMVIL S.

XX Steinman L, Zamvil S;

XX WPI; 2002-598709/64.

XX Modulating or tolerizing the immune system, useful for treating multiple sclerosis, by administering a peptide derived from human myelin binding protein.

XX Disclosure; Page 15; 21pp; English.

XX This invention describes a novel method for modulating or tolerizing the immune system, and for treating multiple sclerosis comprising administering a peptide derived from hMBP (human myelin basic protein). The peptide induces an autoimmune response (T cell) to a self-antigen (or part of it), and binds to an MHC (major histocompatibility complex) antigen of a host susceptible to autoimmune diseases, i.e. competes with binding to MBP and inhibit proliferation of MBP-reactive cells. The peptide has immunosuppressive and neuroprotective activity. This sequence represents a peptide derived from the human MBP protein which can be used for tolerization

XX Sequence 5 AA;

Query Match 100.0%; Score 16; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 3 FID 5

RESULT 6

AAR29321

ID AAR29321 standard; peptide; 6 AA.

XX AAR29321;

XX 25-MAR-2003 (revised)

DT 13-APR-1993 (first entry)

XX Endothelin antagonist peptide.

XX Hypertension; myocardial infarction; congestive heart failure;
KW endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias;
KW acute renal failure; preclampsia; diabetes; metabolic; endocrinological;
KW neurological; disorders.

XX Synthetic.

XX Key Location/Qualifiers
FT Misc-difference 1

```

FT XX /note= "Ac-D-Phe"
XX PN WO2220706-A1.
XX PD 26-NOV-1992.
XX PF 24-APR-1992; 92WO-US003408.
XX PR 16-MAY-1991; 91US-00701274.
XX PR 18-DEC-1991; 91US-00809746.
XX PA (WARN ) WARNER LAMBERT CO.
XX PI Cody WL, Depue P, Doherty AM, Taylor MD;
XX PS WPI; 1992-415706/50.
XX DR
XX XX New peptide(s) used as endothelin antagonists - for treating
XX PT hypertension, metabolic and endocrine disorders, heart failure, diabetes,
XX PT asthma, neurological disorders, etc.
XX XX
XX PS Claim 5; Page 86; 116pp; English.
XX CC The peptide is an endothelin antagonist useful in controlling
XX CC hypertension, myocardial infarction, congestive heart failure, endotox-
XX CC shock, subarachnoid haemorrhage, asthma, arrhythmias, acute renal
XX CC failure, preclampsia, diabetes and metabolic, endocrinological and
XX CC neurological disorders. Administration is oral parenteral or by
XX CC inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/ day. It may be
XX CC prepared by conventional peptide synthesis. (Updated on 25-MAR-2003 to
XX CC correct PN field.)
XX XX
XX XX Sequence 6 AA;
XX XX
XX XX Query Match 100.0%; Score 16; DB 2; Length 6;
XX XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 FID 3
XX DB 1 FID 3
XX XX
XX XX RESULT 8
XX XX AAW31469
XX XX ID AAW31469 standard; protein; 6 AA.
XX XX AC AAW31469;
XX XX DT 04-AUG-1998 (first entry)
XX XX DE Transcriptional activator peptide fragment LS132.
XX XX KW Activating sequence; Gal4; transcriptional activator; RNA polymerase;
XX XX KW Protein-protein interaction; gene therapy; therapeutic; holoenzyme;
XX XX KW Gal11; DNA binding domain.
XX XX OS Synthetic.
XX XX PN WO9744447-A2.
XX XX PD 27-NOV-1997.
XX XX PF 02-MAY-1997; 97WO-US007338.
XX XX PR 03-MAY-1996; 96US-0017016P.
XX XX PR 01-MAY-1997; 97US-00017016.
XX XX PA (HARD ) HARVARD COLLEGE.
XX XX PI Ptashne M, Lu X, Wu Y;
XX XX DR WPI; 1998-018502/02.
XX XX DR N-PSDB; AAV02567.
XX XX PT New transcriptional activator containing DNA binding domain bound to
XX XX PT peptide - useful for controlling gene expression, especially in gene
XX XX PT therapy, and in protein-protein interaction assays, does not inhibit
XX XX PT other transcription activators.
XX XX PS Example 1; Page 26; 55pp; English.
XX XX AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW39053-W39076 are
XX XX CC fragments used in an assay to determine novel transcriptional activators.
XX PI Cody WL, Depue P, Doherty AM, He JX, Taylor MD;

```


CC The method involves the production of transcriptional activators
 CC comprising of a DNA-binding group and a 6-25 amino acid peptide that is
 CC covalently bonded to the DNA binding group and does not represent a
 CC fragment of a natural transcription activator. Protein-protein
 CC interactions are identified in the assay by fusing a DNA-binding domain
 CC to a library of DNA fragments and introducing this and a fusion of target
 CC protein and a polypeptide containing a region of Gal4 which interacts
 CC with Gal4p into a cell containing Gal4p and identifying members of the
 CC library that interact with the target from activation of transcription.
 CC Such constructs are used to activate transcription in a cell, e.g. for
 CC controlling gene activity, particularly in gene therapy (e.g. recognizing
 CC a site close to a selected therapeutic gene). Transcription can be
 CC activated without blocking other transcriptional activators. They
 CC probably act by interacting with a component of the RNA polymerase II
 CC holoenzyme, Gal11, the strongest known yeast activator, which provides a
 CC more sensitive assay allowing detection of even weak protein-protein
 CC interactions. Such activators do not create toxicity problems even when
 CC overexpressed
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 16; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
 |||
 Db 1 FID 3

RESULT 9
 AAB06774
 ID AAB06774 standard; peptide; 7 AA.

XX
 AC AAB06774;

XX 28-SEP-2000 (first entry)

XX Claudin-6/9 cyclic cell adhesion recognition sequence SEQ ID NO: 345.

XX Claudin-6 modulating agent; claudin-9 modulating agent;
 KW cell adhesion recognition sequence; CAR sequence; autoimmune disease;
 KW inflammatory disease; cancer; graft rejection; cyclic.

XX Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA001029.

XX 03-NOV-1998; 98US-00185908.

XX 30-MAR-1999; 99US-00282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI; 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
 PT vasopermeability, for delivering drugs to tumors and the nervous system
 PT and across the skin.

XX Claim 73; Page 103; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
 CC cell adhesion modulators. The claudin-6 and claudin-9 groups of proteins
 CC are cadherins, which are membrane glycoproteins involved in cell
 CC adhesion. In some situations, cell adhesion occurs at abnormal levels,
 CC and these peptides can be used to modulate these levels, and thus treat
 CC autoimmune diseases, inflammatory diseases and cancer, and aid wound

CC healing and implant adhesion. In addition, they can also be used to
 CC facilitate drug delivery to the desired target site. The present sequence
 CC has a cyclic conformation
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 16; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
 |||
 Db 5 FID 7

RESULT 10
 AAB06594
 ID AAB06594 standard; peptide; 7 AA.

XX
 AC AAB06594;

XX 28-SEP-2000 (first entry)

XX Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 227.

XX Claudin-3 modulating agent; cell adhesion recognition sequence;
 KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
 KW graft rejection; cyclic.

XX Mammalia.

XX WO200026360-A1.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-CA001029.

XX 03-NOV-1998; 98US-00185908.

XX 30-MAR-1999; 99US-00282029.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuck OW, Symonds JM, Gour BJ;

XX WPI; 2000-365610/31.

XX Antibody modulation of claudin-mediated cell adhesion for increasing
 PT vasopermeability, for delivering drugs to tumors and the nervous system
 PT and across the skin.

XX Claim 55; Page 99; 121pp; English.

XX The present invention relates to the use of peptides as claudin-mediated
 CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
 CC which are membrane glycoproteins involved in cell adhesion. In some
 CC situations, cell adhesion occurs at abnormal levels, and these peptides
 CC can be used to modulate these levels, and thus treat autoimmune diseases,
 CC inflammatory diseases and cancer, and aid wound healing and implant
 CC adhesion. In addition, they can also be used to facilitate drug delivery
 CC to the desired target site. The present sequence has a cyclic
 CC conformation

XX Sequence 7 AA;

Query Match 100.0%; Score 16; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
 |||
 Db 5 FID 7

[illegible]

XX New polymorphic variants of the gene encoding Cytochrome P450 polypeptide
PT 2C8 (CYP2C8), useful for diagnosing or treating a disease, e.g.
PT arachidonic acid metabolism, cancer or cardiovascular diseases.
XX
XX Disclosure; Page 58; 178pp; English.
XX
CC The invention describes a new polynucleotide comprises a polynucleotide:
CC (a) having any of 101 nucleic acid sequences with 18-19 bp fully defined
CC in the specification; (b) encoding any of seven polypeptides having 7
CC amino acids, or a polypeptide with 3 amino acids; (c) capable of
CC hybridising to a Cytochrome P450 polypeptide 2C8 (CYP2C8) gene; (d)
CC encoding a molecular CYP2C8 variant polypeptide or its fragment. The
CC polynucleotide, gene, vector, polypeptide or antibody is useful for
CC diagnosing or treating a disease, for preparing a diagnostic composition
CC for diagnosing a disease, or for preparing a pharmaceutical composition
CC for treating a disease. This disease includes arachidonic acid
CC metabolism, cancer or cardiovascular diseases. This is the amino acid
CC sequence of a human cytochrome P450 polypeptide 2C8 (CYP2C8) wild type
CC peptide
XX
XX Sequence 7 AA;

Query Match 100.0%; Score 16; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
DB 3 FID 5

RESULT 14
ADL17604
ID ADL17604 standard; peptide; 7 AA.
XX
AC ADL17604;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human MAG13 PDZ3 domain peptide SEQ ID NO:567.
DE
XX 95 kDa post-synaptic density protein/Discs large/ZO-1 domain;
KW PSD-95/Discs large/ZO-1 domain; PDZ domain; fusion protein;
KW phage coat protein; PDZ domain binding peptide; cytoskeletal; nontropic;
KW neuroprotective; antiparkinsonian; neuroleptic; antitumor;
KW immunosuppressive; pulmonary; muscular; gene therapy;
KW rickettsial disease; murine typhus; chronic myeloid leukaemia;
KW Alzheimer's disease; neurological disorder; Parkinson's disease;
KW schizophrenia; X-linked autoimmune enteropathy; tsutsugamushi disease;
KW fascioscapulohumeral muscular dystrophy; late onset demyelinating disease;
KW Usher syndrome type 1; USH1; nitric oxide-mediated tissue damage; tumour;
KW cystic fibrosis; human; MAG13.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO2003004604-A2.
XX
XX 16-JAN-2003.
XX
XX 03-JUL-2002; 2002WO-US020993.
XX
XX 06-JUL-2001; 2001US-0303634P.
XX
XX (GETH) GENENTECH INC.
XX
XX Held HA, Lasky LA, Laura RP, Sidhu SS, Wong WL, Wu Y;
XX WPI; 2003-267930/26.
XX
XX New polypeptide that interacts with a 95 kDa post-synaptic density
PT protein 95/Discs large/ZO-1 (PDZ) domain, useful for producing, selecting

PT and identifying PDZ domain binding peptides.
XX
PS Claim 26; SEQ ID NO 567; 228pp; English.
XX
XX The present invention describes an isolated polypeptide (I) that
CC interacts with a 95 kDa post-synaptic density protein (PSD-95)/Discs
CC large/ZO-1 (PDZ) domain. Also described: (1) a fusion protein (II)
CC comprising a portion of a phage coat protein bonded through its carboxyl-
CC terminus, optionally through a peptide linker, to a PDZ domain binding
CC peptide, where the peptide contains 3-20 amino acid residues; (2) a
CC library of (II), where the fusion proteins in the library comprise a
CC number of PDZ domain binding peptides; (3) an assay for a PDZ domain
CC binding compound; (4) a polypeptide that binds to the same epitope as
CC (1), or that competes for binding to a PDZ domain with (1); (5) a
CC polynucleotide (PN) encoding (I); (6) inhibiting a polypeptide-
CC polypeptide interaction, by contacting a mixture comprising a first and a
CC second polypeptide with an inhibitor of interaction between a PDZ domain
CC and its ligand, where the first polypeptide comprises the PDZ domain and
CC the second polypeptide comprises the ligand; (7) screening for a
CC substance that modulates interaction between a PDZ domain polypeptide and
CC a molecule known to bind to the PDZ domain of the polypeptide; and (8)
CC screening (M) for a substance that inhibits binding of a PDZ domain
CC polypeptide to a molecule known to bind to the PDZ domain of the
CC polypeptide. (I) has cytostatic, nontropic, neuroprotective,
CC antiparkinsonian, neuroleptic, antitumor, immunosuppressive, pulmonary
CC and muscular activities, and can be used in gene therapy. The library of
CC a fusion protein (II) is useful for producing a PDZ domain binding
CC peptide library, and for selecting PDZ domain binding peptides in
CC recombinant host cells. The library of (II) is also useful for
CC identifying a PDZ domain binding protein, by selecting PDZ domain binding
CC peptides using a new method. PN is useful for gene therapy, and in
CC diagnoses of diseases. (I) and PN are useful for treating a subject at
CC risk of a disorder or having a disorder associated with aberrant PDZP.
CC PDZD, PDZ interacting protein (PIP) or PDZ domain binding peptides (PDBP)
CC expression or activity such as rickettsial diseases, murine typhus,
CC chronic myeloid leukaemia, Alzheimer's disease, neurological disorders
CC such as Parkinson's disease and schizophrenia, X-linked autoimmune
CC enteropathy, tsutsugamushi disease, fascioscapulohumeral muscular
CC dystrophy, late onset demyelinating disease, Usher syndrome type 1
CC (USH1), nitric oxide-mediated tissue damage, tumours and cystic fibrosis.
CC (I) is useful to identify cognate protein ligands for the PDZ domains.
CC Structural analysis of the peptides are useful to understand PDZ domain
CC structure and function, and also to identify intracellular biological
CC functions for these motifs and the proteins that contain them. The
CC peptides are further useful as PDZ domain inhibitors and are also useful
CC as structural models in the design of small molecule inhibitors/agonists
CC of the binding interaction between a PDZ domain containing protein and
CC its cognate ligand. The present sequence represents a peptide which is
XX used in the exemplification of the present invention.
XX
XX Sequence 7 AA;

Query Match 100.0%; Score 16; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
DB 4 FID 6

RESULT 15
AAB06597
ID AAB06597 standard; peptide; 8 AA.
XX
XX AAB06597;
XX
XX 28-SEP-2000 (first entry)
XX
XX Claudin-3 cyclic cell adhesion recognition sequence SEQ ID NO: 230.
DE
XX Claudin-3 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;

KW graft rejection; cyclic.
XX Mammalia.
OS WO200026360-A1.
XX
PN
XX
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA001029.
PF
XX
XX 03-NOV-1998; 98US-00185908.
PR
PR 30-MAR-1999; 99US-00282029.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX
XX Blaschuck OW, Symonds JM, Gour BJ;
PI
XX
XX WPI; 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin.
XX
XX Claim 55; Page 99; 121pp; English.
PS
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-3 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 16; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 6 FID 8

Search completed: April 18, 2005, 14:15:23
Job time : 33.6047 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:22:17 ; Search time 22.6744 Seconds
(without alignments)
43.975 Million cell updates/sec

Title: US-09-674-716B-13

Perfect score: 16

Sequence: 1 FID 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*

15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*

16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*

17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*

18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*

19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	5	8	US-08-484-409-36
2	16	100.0	5	11	US-09-920-306-25
3	16	100.0	6	11	US-09-943-944E-130
4	16	100.0	7	9	US-09-185-908-174
5	16	100.0	7	9	US-09-185-908-227
6	16	100.0	7	14	US-10-190-082-567
7	16	100.0	8	9	US-09-946-678-8
8	16	100.0	8	9	US-09-791-378-511
9	16	100.0	8	9	US-09-185-908-177
10	16	100.0	8	9	US-09-185-908-230
11	16	100.0	8	10	US-09-880-748-2842
12	16	100.0	8	11	US-09-791-377-511
13	16	100.0	8	14	US-10-190-082-501

Sequence 2842, Ap
Sequence 92, Appl
Sequence 108, App
Sequence 1352, Ap
Sequence 1352, Ap
Sequence 1352, Ap
Sequence 180, App
Sequence 233, App
Sequence 862, App
Sequence 1235, Ap
Sequence 121, App
Sequence 357, App
Sequence 241, App
Sequence 45, Appl
Sequence 644, App
Sequence 1464, Ap
Sequence 2015, Ap
Sequence 2017, Ap
Sequence 3882, Ap
Sequence 153, App
Sequence 356, App
Sequence 563, App
Sequence 583, App
Sequence 1361, Ap
Sequence 8, Appli
Sequence 693, App
Sequence 45, Appl
Sequence 462, App
Sequence 216, App
Sequence 5, Appli
Sequence 560, App
Sequence 560, App

14 100.0 8 15 US-10-293-418-2842
15 100.0 8 15 US-10-601-100-92
16 100.0 8 15 US-10-601-100-108
17 100.0 8 16 US-10-712-425-1352
18 100.0 8 17 US-10-773-032-1352
19 100.0 9 9 US-09-185-908-180
20 100.0 9 9 US-09-185-908-233
21 100.0 9 10 US-09-932-165-862
22 100.0 9 10 US-09-932-165-1235
23 100.0 9 15 US-10-363-791-121
24 100.0 9 17 US-10-801-990-357
25 100.0 9 17 US-10-820-467-241
26 100.0 9 17 US-09-757-417-45
27 100.0 10 10 US-09-572-404B-644
28 100.0 10 10 US-09-572-404B-1464
29 100.0 10 10 US-09-572-404B-2015
30 100.0 10 10 US-09-572-404B-2017
31 100.0 10 10 US-09-572-404B-3882
32 100.0 10 10 US-09-572-404B-3883
33 100.0 10 10 US-09-932-165-153
34 100.0 10 10 US-09-932-165-356
35 100.0 10 10 US-09-932-165-563
36 100.0 10 10 US-09-932-165-583
37 100.0 10 10 US-09-932-165-1361
38 100.0 10 10 US-09-573-822C-8
39 100.0 10 10 US-09-573-822C-693
40 100.0 10 14 US-10-042-945-45
41 100.0 10 16 US-10-327-598-462
42 100.0 10 17 US-10-833-951-216
43 100.0 11 9 US-09-817-310-5
44 100.0 11 14 US-10-097-065-560
45 100.0 11 15 US-10-372-876-560

ALIGNMENTS

RESULT 1
US-08-484-409-36
Sequence 36, Application US/08484409
Publication No. US20020076412A1
GENERAL INFORMATION:
APPLICANT: Steinman, Lawrence
APPLICANT: Zamil, Scott
TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,409
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 690068.409C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid

;
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-484-409-36

Query Match 100.0%; Score 16; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 3 FID 5

RESULT 2

US-09-920-306-25
; Sequence 25, Application US/09920306
; Publication No. US20040029808A1
; GENERAL INFORMATION:
; APPLICANT: Unilever PLC
; APPLICANT: Unilever NV
; TITLE OF INVENTION: Peptides Capable of Functioning as Mimotopes for
; TITLE OF INVENTION: Hormonal Analyses
; FILE REFERENCE: Peptide Mimotopes
; CURRENT APPLICATION NUMBER: US/09/920,306
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: EP00306613.1
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-920-306-25

Query Match 100.0%; Score 16; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 3 FID 5

RESULT 3

US-09-943-944E-130
; Sequence 130, Application US/09943944E
; Publication No. US20040014036A1
; GENERAL INFORMATION:
; APPLICANT: Ptashne, et al.,
; TITLE OF INVENTION: Transcriptional Activation System, Activators, and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 0342941-0065
; CURRENT APPLICATION NUMBER: US/09/943,944E
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 130
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Random peptide
; OTHER INFORMATION: sequences.
US-09-943-944E-130

Query Match 100.0%; Score 16; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 1 FID 3

RESULT 4

US-09-185-908-174
; Sequence 174, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; TITLE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 174
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R
; OTHER INFORMATION: sequences
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-174

Query Match 100.0%; Score 16; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 5 FID 7

RESULT 5

US-09-185-908-227
; Sequence 227, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; TITLE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 227
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-227

Query Match 100.0%; Score 16; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
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Db 5 FID 7

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RESULT 6
US-10-190-082-567
; Sequence 567, Application US/10190082
; Publication No. US20030148264A1
; GENERAL INFORMATION:
; APPLICANT: Laskey, Lawrence A.
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Held, Heike A.
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
; FILE REFERENCE: P1905R1
; CURRENT APPLICATION NUMBER: US/10/190,082
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 567
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-190-082-567

Query Match      100.0%; Score 16; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
        |||
Db      4 FID 6

RESULT 7
US-09-946-678-8
; Sequence 8, Application US/09946678
; Patent No. US20020106782A1
; GENERAL INFORMATION:
; APPLICANT: ITO, Kotaro
; APPLICANT: KOYAMA, Yasuji
; TITLE OF INVENTION: Protein Having Glutaminase Activity and Gene Encoding the Same
; FILE REFERENCE: 0283-0158P
; CURRENT APPLICATION NUMBER: US/09/946,678
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: JP 2000-270371
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Cryptococcus nodaensis
US-09-946-678-8

Query Match      100.0%; Score 16; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
        |||
Db      2 FID 4

RESULT 8
US-09-791-378-511
; Sequence 511, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999

; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 511
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-511

Query Match      100.0%; Score 16; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
        |||
Db      2 FID 4

RESULT 9
US-09-185-908-177
; Sequence 177, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; TITLE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 177
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R
; OTHER INFORMATION: sequences
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-177

Query Match      100.0%; Score 16; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
        |||
Db      6 FID 8

RESULT 10
US-09-185-908-230
; Sequence 230, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; TITLE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 230
; LENGTH: 8
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-230

Query Match      100.0%; Score 16; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
Db      6 FID 8

RESULT 11
US-09-880-748-2842
; Sequence 2842, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2842
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2842

Query Match      100.0%; Score 16; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
Db      5 FID 7

RESULT 12
US-09-791-377-511
; Sequence 511, Application US/09791377
; Publication No. US20040110938A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-060-999
; CURRENT APPLICATION NUMBER: US/09/791,377
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 511
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-09-791-377-511

```
Query Match      100.0%; Score 16; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 FID 3
Db      2 FID 4
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RESULT 13

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US-10-190-082-501
; Sequence 501, Application US/10190082
; Publication No. US20030148264A1
; GENERAL INFORMATION:
; APPLICANT: Lasky, Lawrence A.
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Held, Heike A.
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
; FILE REFERENCE: P1905R1
; CURRENT APPLICATION NUMBER: US/10/190,082
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 501
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-190-082-501
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Query Match      100.0%; Score 16; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 FID 3
Db      5 FID 7
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RESULT 14

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US-10-293-418-2842
; Sequence 2842, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-03-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2842
; LENGTH: 8
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-293-418-2842

Query Match 100.0%; Score 16; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
|||
Db 5 FID 7

RESULT 15

US-10-601-100-92
; Sequence 92, Application US/10601100
; Publication No. US20040072261A1
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of
; TITLE OF INVENTION: Neurological Diseases
; FILE REFERENCE: 11362.0038.NPUS01
; CURRENT APPLICATION NUMBER: US/10/601,100
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02447121.1
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/396,437
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-601-100-92

Query Match 100.0%; Score 16; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
|||
Db 2 FID 4

Search completed: April 18, 2005, 14:54:44
Job time : 23.6744 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 14:01:43 ; Search time 8.16279 Seconds
(without alignments)
27.435 Million cell updates/sec

Title: US-09-674-716B-13

Perfect score: 16

Sequence: 1 FID 3

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	7	1	US-08-197-792-25
2	16	100.0	7	1	US-08-459-850-25
3	16	100.0	7	1	US-08-459-214-25
4	16	100.0	7	4	US-09-282-029A-174
5	16	100.0	7	4	US-09-282-029A-227
6	16	100.0	7	4	US-09-282-029A-345
7	16	100.0	7	4	US-09-185-908-174
8	16	100.0	7	4	US-09-185-908-227
9	16	100.0	7	4	US-09-434-355A-174
10	16	100.0	7	4	US-09-434-355A-227
11	16	100.0	7	4	US-09-434-355A-345
12	16	100.0	7	4	US-09-042-071-52
13	16	100.0	8	4	US-09-946-678-8
14	16	100.0	8	4	US-09-282-029A-177
15	16	100.0	8	4	US-09-282-029A-230
16	16	100.0	8	4	US-09-282-029A-348
17	16	100.0	8	4	US-09-185-908-177
18	16	100.0	8	4	US-09-185-908-230
19	16	100.0	8	4	US-09-434-355A-177
20	16	100.0	8	4	US-09-434-355A-230
21	16	100.0	8	4	US-09-434-355A-348
22	16	100.0	9	4	US-09-359-304B-2
23	16	100.0	9	4	US-09-359-304B-5
24	16	100.0	9	4	US-09-359-304B-7
25	16	100.0	9	4	US-09-000-217-2
26	16	100.0	9	4	US-09-341-982-67
27	16	100.0	9	4	US-09-282-029A-180

28	16	100.0	9	4	US-09-282-029A-233	Sequence 233, App
29	16	100.0	9	4	US-09-282-029A-351	Sequence 351, App
30	16	100.0	9	4	US-09-185-908-180	Sequence 180, App
31	16	100.0	9	4	US-09-185-908-233	Sequence 233, App
32	16	100.0	9	4	US-09-434-355A-180	Sequence 180, App
33	16	100.0	9	4	US-09-434-355A-233	Sequence 233, App
34	16	100.0	9	4	US-09-434-355A-351	Sequence 351, App
35	16	100.0	10	1	US-08-277-007-1	Sequence 1, Appli
36	16	100.0	10	1	US-08-485-181-1	Sequence 1, Appli
37	16	100.0	10	2	US-08-964-338-1	Sequence 1, Appli
38	16	100.0	10	3	US-08-975-917-1	Sequence 1, Appli
39	16	100.0	11	4	US-09-817-310-5	Sequence 5, Appli
40	16	100.0	11	4	US-09-937-215-5	Sequence 5, Appli
41	16	100.0	11	4	US-10-355-724A-5	Sequence 5, Appli
42	16	100.0	11	5	PCT-US92-01433A-6	Sequence 6, Appli
43	16	100.0	12	1	US-08-434-255-15	Sequence 15, Appl
44	16	100.0	12	1	US-08-459-967-15	Sequence 15, Appl
45	16	100.0	12	1	US-08-460-327-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-08-197-792-25

; Sequence 25, Application US/08197792

; Patent No. 5525488

; GENERAL INFORMATION:

; APPLICANT: Anthony J. Mason

; APPLICANT: Peter H. Seeburg

; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or Beta Chains of Inhibin and

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/197,792

; FILING DATE: 16-FEB-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/958414

; FILING DATE: 08-OCT-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/744207

; FILING DATE: 12-AUG-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/215466

; FILING DATE: 05-JUL-1988

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 06/906729

; FILING DATE: 31-DEC-1986

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 06/827710

; FILING DATE: 07-FEB-1986

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 06/783910

; FILING DATE: 03-OCT-1985

; ATTORNEY/AGENT INFORMATION:

; NAME: Hasak, Janet E.

; REGISTRATION NUMBER: 28,616

; REFERENCE/DOCKET NUMBER: 297P2D4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1896

; TELEFAX: 415/952-9881

TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-197-792-25

Query Match 100.0%; Score 16; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 4 FID 6

RESULT 2
US-08-459-850-25
; Sequence 25, Application US/08459850
; Patent No. 5665568
; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seeburg
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
; TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
; TITLE OF INVENTION: Using such Nucleic Acid
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,850
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/197792
; FILING DATE: 17-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/958414
; FILING DATE: 08-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744207
; FILING DATE: 12-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/215466
; FILING DATE: 05-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/906729
; FILING DATE: 31-DEC-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/827710
; FILING DATE: 07-FEB-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/783910
; FILING DATE: 03-OCT-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 297P2D5
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-459-850-25

Query Match 100.0%; Score 16; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 4 FID 6

RESULT 3
US-08-459-214-25
; Sequence 25, Application US/08459214
; Patent No. 5716810
; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seeburg
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
; TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
; TITLE OF INVENTION: Using such Nucleic Acid
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,214
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/197792
; FILING DATE: 17-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/958414
; FILING DATE: 08-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744207
; FILING DATE: 12-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/215466
; FILING DATE: 05-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/906729
; FILING DATE: 31-DEC-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/827710
; FILING DATE: 07-FEB-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/783910
; FILING DATE: 03-OCT-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 297P2D6
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-459-214-25

Query Match 100.0%; Score 16; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 4 FID 6

RESULT 4

US-09-282-029A-174
; Sequence 174, Application US/09282029A
; Patent No. 6723700
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409C1
; CURRENT APPLICATION NUMBER: US/09/282,029A
; CURRENT FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 480
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 174
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-282-029A-174

Query Match 100.0%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 5 FID 7

RESULT 5

US-09-282-029A-227
; Sequence 227, Application US/09282029A
; Patent No. 6723700
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409C1
; CURRENT APPLICATION NUMBER: US/09/282,029A
; CURRENT FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 480
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 227
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide

US-09-282-029A-227

Query Match 100.0%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 5 FID 7

RESULT 6

US-09-282-029A-345
; Sequence 345, Application US/09282029A
; Patent No. 6723700
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409C1
; CURRENT APPLICATION NUMBER: US/09/282,029A
; CURRENT FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 480
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 345
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: claudin-6 cell adhesion recognition sequence
US-09-282-029A-345

Query Match 100.0%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
|||
Db 5 FID 7

RESULT 7

US-09-185-908-174
; Sequence 174, Application US/09185908A
; Patent No. 6756356
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 174
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-174

Query Match 100.0%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 FID 3
Db      5 FID 7

RESULT 8
US-09-185-908-227
; Sequence 227, Application US/09185908A
; Patent No. 6756356
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 227
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-227

Query Match      100.0%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
Db      5 FID 7

RESULT 9
US-09-434-355A-174
; Sequence 174, Application US/09434355A
; Patent No. 6830894
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: James Mathew Symonds
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409C2
; CURRENT APPLICATION NUMBER: US/09/434,355A
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 531
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 174
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R
; OTHER INFORMATION: sequences
; OTHER INFORMATION: Cyclic Peptide
US-09-434-355A-174

Query Match      100.0%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
Db      5 FID 7
```

```
RESULT 10
US-09-434-355A-227
; Sequence 227, Application US/09434355A
; Patent No. 6830894
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: James Mathew Symonds
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409C2
; CURRENT APPLICATION NUMBER: US/09/434,355A
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 531
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 227
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences
; OTHER INFORMATION: Cyclic Peptide
US-09-434-355A-227

Query Match      100.0%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
Db      5 FID 7

RESULT 11
US-09-434-355A-345
; Sequence 345, Application US/09434355A
; Patent No. 6830894
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: James Mathew Symonds
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE OF INVENTION: FUNCTIONS
; FILE REFERENCE: 100086.409C2
; CURRENT APPLICATION NUMBER: US/09/434,355A
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 531
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 345
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: claudin-6 cell adhesion recognition sequence
US-09-434-355A-345

Query Match      100.0%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FID 3
Db      5 FID 7

RESULT 12
US-09-042-071-52
; Sequence 52, Application US/09042071
; Patent No. 6294372
; GENERAL INFORMATION:
```

APPLICANT: Burian, Jan
APPLICANT: Kay, William W.
TITLE OF INVENTION: REPLICATION GENES AND GENE PRODUCTS FROM
TITLE OF INVENTION: SMALL CRYPTIC PLASMIDS AND METHODS FOR CONSTRUCTING
TITLE OF INVENTION: CONTROLLED-REPLICATION PLASMID VECTORS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,071
FILING DATE: 13-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McWaters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 660081.407
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-042-071-52

Query Match 100.0%; Score 16; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 2 FID 4

RESULT 13
US-09-946-678-8
Sequence 8, Application US/099466678
Patent No. 6541236
GENERAL INFORMATION:
APPLICANT: ITO, Kotaro
APPLICANT: UMITSUKI, Genryou
APPLICANT: KOYAMA, Yasuji
TITLE OF INVENTION: Protein Having Glutaminase Activity and Gene Encoding the Same
FILE REFERENCE: 0283-0158p
CURRENT APPLICATION NUMBER: US/09/946,678
CURRENT FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: JP 2000-270371
PRIOR FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Cryptococcus nodaensis
US-09-946-678-8

Query Match 100.0%; Score 16; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3

Db 2 FID 4
RESULT 14
US-09-282-029A-177
Sequence 177, Application US/09282029A
Patent No. 6723700
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
TITLE OF INVENTION: FUNCTIONS
FILE REFERENCE: 100086.409C1
CURRENT APPLICATION NUMBER: US/09/282,029A
CURRENT FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 480
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 177
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Product of
OTHER INFORMATION: synthesis based on human, mouse and monkey CPE-R
FEATURE:
OTHER INFORMATION: Cyclic Peptide
US-09-282-029A-177

Query Match 100.0%; Score 16; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 6 FID 8

RESULT 15
US-09-282-029A-230
Sequence 230, Application US/09282029A
Patent No. 6723700
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
TITLE OF INVENTION: FUNCTIONS
FILE REFERENCE: 100086.409C1
CURRENT APPLICATION NUMBER: US/09/282,029A
CURRENT FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 480
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 230
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Product of
OTHER INFORMATION: synthesis based on human and rat RVP-1 sequences
FEATURE:
OTHER INFORMATION: Cyclic Peptide
US-09-282-029A-230

Query Match 100.0%; Score 16; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FID 3
Db 6 FID 8

Search completed: April 18, 2005, 14:25:39
Job time : 8.16279 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 16:06:45 ; Search time 43 Seconds
(without alignments)
6.713 Million cell updates/sec

Title: US-09-674-716B-13
Perfect score: 16
Sequence: 1 FID 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 23

Minimum DB seq length: 0
Maximum DB seq length: 3

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	37.5	3	S68328	blood cell protein
2	3	18.8	3	A22565	R-phycoerythrin al
3	3	18.8	3	PQ0010	angiotensin-conver
4	3	18.8	3	A43391	TRH-like tripeptid
5	2	12.5	3	T13892	cytochrome-c oxida
6	2	12.5	3	A33802	thyrotropin-releas
7	1	6.2	3	S13894	histidinol dehydro
8	1	6.2	3	F37196	bradykinin-potenti
9	1	6.2	3	I50412	gene p20K protein
10	1	6.2	3	PT0578	T-cell receptor be
11	1	6.2	3	I78890	tyrosine protein k
12	1	6.2	3	B23751	spinal cord peptid
13	0	0.0	3	RHSHT	thyroliberin - she
14	0	0.0	3	A92971	thyroliberin - eas
15	0	0.0	3	RHTDFO	thyroliberin - Bom
16	0	0.0	3	E37196	bradykinin-potenti
17	0	0.0	3	PT0636	T-cell receptor be
18	0	0.0	3	PT0571	T-cell receptor be
19	0	0.0	3	PT0622	growth-modulating
20	0	0.0	3	GKHU	thyroliberin - pig
21	0	0.0	3	RHPGT	bursin - chicken
22	0	0.0	3	A60898	spinal cord peptid
23	0	0.0	3	A23751	

ALIGNMENTS

RESULT 1

S68328

blood cell protein A - Molgula manhattensis (fragment)

C:Species: Molgula manhattensis

C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C:Accession: S68328

R:Taylor, S.W.; Ross, M.M.; Waite, J.H.

Arch. Biochem. Biophys. 324, 228-240, 1995

A:Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from t:

A:Reference number: S68325; MUID:96132650; PMID:8554314

A:Accession: S68328

A:Molecule type: protein

A:Residues: 1-3 <TAY>

Query Match 37.5%; Score 6; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 2 F 2

RESULT 2

A22565

R-phycoerythrin alpha-1 chain - red alga (Gastrocionium coulteri) (fragment)

C:Species: Gastrocionium coulteri

C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C:Accession: A22565

R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A:Reference number: A22565; MUID:85182601; PMID:3886644

A:Accession: A22565

A:Molecule type: protein

A:Residues: 1-3 <KLO>

Query Match 18.8%; Score 3; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 2 Y 2

RESULT 3

PQ0010

angiotensin-converting enzyme inhibitor (FLP-3) - common fig

N:Alternate names: ficus latex peptide 3

C:Species: Ficus carica (common fig)

C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C:Accession: PQ0010

R:Maruyama, S.; Miyoshi, S.; Tanaka, H.

Agric. Biol. Chem. 53, 2763-2767, 1989

A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.

A:Reference number: PQ0008

A:Accession: PQ0010

A:Molecule type: protein

A:Residues: 1-3 <MAR>

A:Experimental source: latex

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 18.8%; Score 3; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 I 2
Db 2 V 2

RESULT 4

A43391

TRH-like tripeptide - alfalfa
 C;Species: Medicago sativa (alfalfa)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: A43391
 R;Lackey, D.B.
 J. Biol. Chem. 267, 17508-17511, 1992
 A;Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroglutaminyl-L-histidyl-L-phenylalanine
 A;Reference number: A43391; PMID:1517203
 A;Accession: A43391
 A;Molecule type: protein
 A;Residues: 1-3 <LAC>
 C;Keywords: amidated carboxyl end; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 18.8%; Score 3; DB 3; Length 3;
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 Db 2 Y 2

RESULT 5
 T13892
 cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (fragment)
 C;Species: Lampetra fluviatilis (river lamprey)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: T13892
 R;Delarbre, C.; Barriol, V.; Tillier, S.; Janvier, P.; Gachelin, G.
 Mol. Biol. Evol. 14, 807-813, 1997
 A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI
 A;Reference number: Z17775; PMID:97398704; PMID:9254918
 A;Accession: T13892
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-3
 A;Cross-references: EMBL:Y09528; NID:92340016; PIDN:CMA70721.1; PID:G4379123
 C;Genetics:
 A;Genome: mitochondrion
 A;Note: COI
 C;Keywords: mitochondrion; oxidoreductase

Query Match 12.5%; Score 2; DB 3; Length 3;
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 I 2
 Db 3 L 3

RESULT 6
 A33802
 thyrotropin-releasing hormone-like peptide - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
 C;Accession: A33802
 R;Cockle, S.M.; Aitken, A.; Beg, F.; Smyth, D.G.
 J. Biol. Chem. 264, 7788-7791, 1989
 A;Title: A novel peptide, pyroglutamylglutamate, in the rabbit prostate compound
 A;Reference number: A33802; PMID:89255196; PMID:2498305
 A;Accession: A33802
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-3 <COC>
 C;Keywords: amidated carboxyl end; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 12.5%; Score 2; DB 3; Length 3;
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 D 3
 Db 2 E 2

RESULT 7
 S13894
 histidinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)
 C;Species: Brassica oleracea (wild cabbage)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: S13894
 R;Nagai, A.; Scheidegger, A.
 Arch. Biochem. Biophys. 284, 127-132, 1991
 A;Title: Purification and characterization of histidinol dehydrogenase from cabbage.
 A;Reference number: S13894; PMID:91112783; PMID:1989490
 A;Accession: S13894
 A;Molecule type: protein
 A;Residues: 1-3 <NAG>
 A;Experimental source: var. capitata
 C;Keywords: dimer; NAD; oxidoreductase

Query Match 6.2%; Score 1; DB 3; Length 3;
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 I 2
 Db 2 M 2

RESULT 8
 F37196
 bradykinin-potentiating peptide 6 - island jararaca
 C;Species: Bothrops insularis (island jararaca)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: F37196
 R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
 J. Protein Chem. 9, 221-227, 1990
 A;Title: Primary structure and biological activity of bradykinin potentiating peptides
 A;Reference number: A37196; PMID:90351557; PMID:2386615
 A;Accession: F37196
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-3 <CIN>
 C;Keywords: pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 6.2%; Score 1; DB 3; Length 3;
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 Db 3 W 3

RESULT 9
 I50412
 gene p20K protein - chicken (fragment)
 C;Species: Gallus gallus (chicken)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: I50412
 R;Mao, P.L.; Beauchemin, M.; Bedard, P.A.
 J. Biol. Chem. 268, 8131-8139, 1993
 A;Title: Quiescence-dependent activation of the p20K promoter in growth-arrested chicken
 A;Reference number: A46643; PMID:93216790; PMID:8463325
 A;Accession: I50412
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-3 <MAO>
 A;Cross-references: GB:I02537; NID:9212616; PID:9212617

C;Genetics:
A;Gene: p20K

Query Match 6.2%; Score 1; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 I 2
: 1 M 1
Db

RESULT 10

PT0578
T-cell receptor beta chain V-D-J region (141-1BD) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0578
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0578
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 6.2%; Score 1; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 I 2
: 3 M 3
Db

RESULT 11

I78890
tyrosine protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: I78890
R;Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.
Oncogene 9, 3437-3448, 1994
A;Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine protein kinase.
A;Reference number: I58407; MUID:95060800; PMID:7970703
A;Accession: I78890
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3 <RES>
A;Cross-references: GB:I33339; NID:G609536; PIDN:AAA64432.1; PID:G609538
C;Genetics:
A;Gene: p52ntk

Query Match 6.2%; Score 1; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 I 2
: 1 M 1
Db

RESULT 12

B23751
spinal cord peptide SCP-5 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
C;Accession: B23751
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.
Arch. Biochem. Biophys. 240, 178-183, 1985

A;Reference number: A23751; MUID:85250425; PMID:4015098
A;Accession: B23751
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-3 <HS1>

Query Match 6.2%; Score 1; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 I 2
: 1 M 1
Db

RESULT 13

RHSH7
thyroliberin - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
C;Accession: A93750; A01415
R;Desiderio Jr., D.M.; Burgess, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.
Org. Mass Spectrom. 5, 221-228, 1971
A;Title: The elucidation of the primary structure of the hypothalamic thyroïd stimulatory hormone.
A;Reference number: A93750
A;Accession: A93750
A;Molecule type: protein
A;Residues: 1-3 <DES>
A;Cross-references: UNIPROT:P01151
R;Burgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.
Nature 226, 321-325, 1970
A;Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.
A;Reference number: A93161; MUID:70163386; PMID:4985794
A;Contents: annotation
A;Note: physicochemical characteristics and biological activities of the natural and synthetic peptides.
C;Superfamily: thyroliberin
C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 D 3
1 Q 1
Db

RESULT 14

A92971
thyroliberin - eastern newt (tentative sequence)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
C;Accession: A92971; A01415
R;Grimm-Jorgensen, Y.; McKelvy, J.F.
J. Neurochem. 23, 471-478, 1974
A;Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain.
A;Reference number: A92971; MUID:75035605; PMID:4214528
A;Accession: A92971
A;Molecule type: protein
A;Residues: 1-3 <GRI>
A;Cross-references: UNIPROT:P01151
A;Note: a peptide with the chromatographic and electrophoretic characteristics of thyrotropin releasing factor.
C;Superfamily: thyroliberin
C;Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Tue Apr 19 06:14:49 2005

QY 3 D 3
Db 1 Q 1

RESULT 15

RHTDIO

thyroliberin - Bombina orientalis

C:Species: Bombina orientalis

C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004

C/Accession: A90919; A01415

R:Yasuhara, T.; Nakajima, T.

Chem. Pharm. Bull. 23, 3301-3303, 1975

A>Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.

A/Reference number: A90919; PMID:76138399; PMID:815011

A/Accession: A90919

A/Molecule type: protein

A/Residues: 1-3 <YAS>

A/Cross-references: UNIPROT:P01151

C/Superfamily: thyroliberin

C/Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid

F;1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred. No. 2.8e+05;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 D 3
Db 1 Q 1

Search completed: April 18, 2005, 16:16:15
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:58:29 ; Search time 174 Seconds
(without alignments)
8.829 Million cell updates/sec

Title: US-09-674-716B-13
Perfect score: 16
Sequence: 1 FID 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0
Maximum DB seq length: 3

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6	37.5	3	1 LUXE VIBFI	P24272 vibrio fisc
2	1	6.2	2	1 GWA SEPOF	P83570 sepio offic
3	0	0.0	3	1 GRWM HUMAN	P01157 homo sapien
4	0	0.0	3	1 THYL_BOMOR	P62970 bombina ori
5	0	0.0	3	1 THYL_NOTVI	P62971 notophthalm
6	0	0.0	3	1 THYL_PIG	P62968 sus scrofa
7	0	0.0	3	1 THYL_SHEEP	P62969 ovis aries

ALIGNMENTS

RESULT 1
LUXE VIBFI
ID LUXE VIBFI STANDARD; PRT; 3 AA.
AC P24272; 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-protein synthetase) (Fragment).
GN Name=luxe;
OS Vibrio fischeri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91072226; PubMed=2254256;
RA Swartman E., Kapoor S., Graham A.F., Meighen E.A.;
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination

RT site for the lux operon.";
RL J. Bacteriol. 172:6797-6802(1990).
CC -!- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It is a component of the fatty acid reductase complex responsible for converting tetradecanoic acid to the aldehyde which serves as substrate in the luciferase-catalyzed reaction.
CC -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate + an acyl-protein thiolester.
CC -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
CC -!- SIMILARITY: Belongs to the luxE family.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC
CC
DR EMBL; M62812; -; NOT ANNOTATED_CDS.
KW Ligase; Luminescence.
FT NON_TER 1
SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;

Query Match 37.5%; Score 6; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 D 3
DB 3 D 3

RESULT 2

GWA SEPOF
ID GWA SEPOF STANDARD; PRT; 2 AA.
AC P83570;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neuropeptide Gwa.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OX Decapodiformes; Sepioidae; Sepiidae; Sepia.
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Optic lobe;
RX MEDLINE=98100358; PubMed=9437704; DOI=10.1016/S0196-9781(97)00241-6;
RA Henry J., Favrel P., Boucaud-Camou E.;
RT "Isolation and identification of a novel Ala-Pro-Gly-Tyr-amide-related peptide inhibiting the motility of the mature oviduct in the cuttlefish, Sepia officinalis.";
RL Peptides 18:1469-1474(1997).
CC -!- FUNCTION: Regulatory neuropeptide with myotropic activity targeting the distal oviduct. Inhibits the motility of the oviduct by decreasing tonus, frequency and amplitude of contractions.
CC -!- SUBCELLULAR LOCATION: Secreted
CC -!- MASS SPECTROMETRY: MW=239.9; METHOD=MALDI; RANGE=1-2; NOTE=Ref.1.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 2
SQ SEQUENCE 2 AA; 261 MW; 7378100000000000 CRC64;

Query Match 6.2%; Score 1; DB 1; Length 2;
Best Local Similarity 0.0%; Pred. No. 1.6e+06;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 2 W 2

RESULT 3

GRWM_HUMAN ID GRWM_HUMAN STANDARD; PRT; 3 AA.

AC P01157;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Growth-modulating peptide.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=77162369; PubMed=858356;

RA Schlesinger D.H., Pickart L., Thaler M.M.;

RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";

RL Experientia 33:324-325(1977).

CC -1- MISCELLANEOUS: This serum tripeptide has been found to stimulate

CC growth of some cell types and to inhibit other types in vitro.

DR GO; GO:0001558; P:regulation of cell growth; NAS.

KW Direct protein sequencing.

SQ SEQUENCE 3 AA; 340 MW; 6331B810000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;

Best Local Similarity 0.0%; Pred.No. 1.6e+06; 0; Gaps 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0;

QY 3 D 3

Db 1 G 1

RESULT 4

THYL_BOMOR ID THYL_BOMOR STANDARD; PRT; 3 AA.

AC P62970; P01151;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin releasing factor) (TSH-releasing factor) (Protirelin).

OS Bombina orientalis (Oriental fire-bellied toad).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.

OX NCBI_TaxID=8346;

RN [1]

RP SEQUENCE.

RX TISSUE=Skin;

RZ MEDLINE=76138399; PubMed=815011;

RA Yasuhara T., Nakajima T.;

RT "Occurrence of Pyr-His-Pro-NH2 in the frog skin.";

RL Chem. Pharm. Bull. 23:3301-3303(1975).

CC -1- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH in the anterior pituitary gland and as a neurotransmitter/neuromodulator in the central and peripheral nervous systems (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted.

DR PIR; A90919; RHDT0.

KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 Pyrrolidone carboxylic acid.

FT MOD RES 3 3 Proline amide.

SQ SEQUENCE 3 AA; 380 MW; 7761F6B0000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;

Best Local Similarity 0.0%; Pred.No. 1.6e+06; 0; Gaps 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0;

QY 3 D 3

Db 1 Q 1

RESULT 5

THYL_NOTVI ID THYL_NOTVI STANDARD; PRT; 3 AA.

AC P62971; P01151;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin releasing factor) (TSH-releasing factor) (Protirelin).

OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Notophthalmus.

OX NCBI_TaxID=8316;

RN [1]

RP SEQUENCE.

RX TISSUE=Brain;

RZ MEDLINE=75035605; PubMed=4214528;

RA Grimm-Joergensen Y., McKeiv J.F.;

RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain in vitro. Isolation and characterization of thyrotropin releasing factor.";

RL J. Neurochem. 23:471-478(1974).

CC -1- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH in the anterior pituitary gland and as a neurotransmitter/neuromodulator in the central and peripheral nervous systems.

CC -1- SUBCELLULAR LOCATION: Secreted.

DR PIR; A92971; A92971.

KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 Pyrrolidone carboxylic acid.

FT MOD RES 3 3 Proline amide.

SQ SEQUENCE 3 AA; 380 MW; 7761F6B0000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;

Best Local Similarity 0.0%; Pred.No. 1.6e+06; 0; Gaps 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0;

QY 3 D 3

Db 1 Q 1

THYL_NOTVI ID THYL_NOTVI STANDARD; PRT; 3 AA.

AC P62971; P01151;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin releasing factor) (TSH-releasing factor) (Protirelin).

OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Notophthalmus.

OX NCBI_TaxID=8316;

RN [1]

RP SEQUENCE.

RX TISSUE=Brain;

RZ MEDLINE=75035605; PubMed=4214528;

RA Grimm-Joergensen Y., McKeiv J.F.;

RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain in vitro. Isolation and characterization of thyrotropin releasing factor.";

RL J. Neurochem. 23:471-478(1974).

CC -1- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH in the anterior pituitary gland and as a neurotransmitter/neuromodulator in the central and peripheral nervous systems.

CC -1- SUBCELLULAR LOCATION: Secreted.

DR PIR; A92971; A92971.

KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 Pyrrolidone carboxylic acid.

FT MOD RES 3 3 Proline amide.

SQ SEQUENCE 3 AA; 380 MW; 7761F6B0000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;

Best Local Similarity 0.0%; Pred.No. 1.6e+06; 0; Gaps 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0;

QY 3 D 3

Db 1 Q 1

RESULT 6

THYL_PIG ID THYL_PIG STANDARD; PRT; 3 AA.

AC P62968; P01151;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin releasing factor) (TSH-releasing factor) (Protirelin).

GN Name=TRH;

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE.

RX TISSUE=Hypothalamus;

RZ MEDLINE=70136150; PubMed=4984938;

RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;

RT "Structure of porcine thyrotropin releasing hormone.";

RL Biochemistry 9:1103-1106(1970).

RN [2]

RP SYNTHESIS.

RX MEDLINE=70039904; PubMed=4982117;

RA Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;

RT "The identity of chemical and hormonal properties of the thyrotropin releasing hormone and pyroglutamyl-histidyl-proline amide.";

RL Biochem. Biophys. Res. Commun. 37:705-710(1969).

CC -1- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH in the anterior pituitary gland and as a neurotransmitter/neuromodulator in the central and peripheral nervous systems.

CC -1- SUBCELLULAR LOCATION: Secreted.

KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD_RES 3 3 Proline amide.
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;
 Best Local Similarity 0.0%; Pred. No. 1.6e+06;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 D 3
 Db 1 Q 1

RESULT 7
 THYL SHEEP
 ID THYL SHEEP STANDARD; PRT; 3 AA.
 AC P62969; F01151;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin
 releasing factor) (TSH-releasing factor) (Protirelin).
 GN Name=TRH;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hypothalamus;
 RA Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,
 RA Ward D.N.;
 RT "The elucidation of the primary structure of the hypothalamic thyroid
 stimulating hormone releasing factor of ovine origin by means of mass
 spectrometry.";
 RL Org. Mass Spectrom. 5:221-228 (1971).
 RN [2]
 RP SYNTHESIS.
 RX MEDLINE=70163386; PubMed=4985794;
 RA Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
 RA Guillemin R.;
 RT "Characterization of ovine hypothalamic hypophysiotropic TSH-releasing
 factor.";
 RL Nature 226:321-325 (1970).
 CC -1- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
 in the anterior pituitary gland and as a neurotransmitter/
 neuromodulator in the central and peripheral nervous systems.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 DR PIR: A93750; RHSHT.
 KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD_RES 3 3 Proline amide.
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;
 Best Local Similarity 0.0%; Pred. No. 1.6e+06;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 D 3
 Db 1 Q 1

Search completed: April 18, 2005, 16:15:24
 Job time : 174 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 15:57:44 ; Search time 167 Seconds
(without alignments)
6.948 Million cell updates/sec

Title: US-09-674-716B-13

Perfect score: 16

Sequence: 1 FID 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1330

Minimum DB seq length: 0

Maximum DB seq length: 3

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseqp16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	3	3	AAY32259 Light cha
2	11	68.8	3	2	AAR64556 RF-1 pept
3	11	68.8	3	8	ADF77860 Therapeut
4	10	62.5	3	2	AAW25193 IDA-pepti
5	10	62.5	3	6	ABR55054 MWP subet
6	9	56.2	3	2	AAY50605 Resin bou
7	9	56.2	3	2	AAY50604 Resin bou
8	9	56.2	3	5	ABG77789 Targettin
9	8	50.0	2	5	ABG63747 Human alb
10	8	50.0	2	7	ADC36684 Mutated v
11	8	50.0	2	8	ADL77012 Albumin f
12	8	50.0	3	2	AAR48960 NL4-3 tru
13	8	50.0	3	2	AAR82907 Non-RGD,
14	8	50.0	3	2	AAW25187 LDV-pepti
15	8	50.0	3	3	AAY49399 Morphine
16	8	50.0	3	3	AAB01568 Cell bind
17	8	50.0	3	4	AAB91692 Opioid pe
18	8	50.0	3	4	AAB91984 Fibronect
19	8	50.0	3	5	ABG93534 Human P-g
20	8	50.0	3	5	AAM48034 MDL pepti
21	8	50.0	3	5	ABG77875 Targettin
22	8	50.0	3	7	ADC36673 Mutated v
23	8	50.0	3	7	ADC36683 Mutated v
24	7	43.8	3	4	AAB91211 Neuropept
25	7	43.8	3	6	ABR44229 Linker pe

26	6	37.5	2	1	AAP10185 Sequence
27	6	37.5	2	2	ADH29634 Swinepox
28	6	37.5	2	2	ADH29618 Swinepox
29	6	37.5	2	2	ADH29628 Swinepox
30	6	37.5	2	3	AAB37936 Trypsin m
31	6	37.5	2	3	AAB27796 Human sec
32	6	37.5	2	4	AAB91687 Opioid pe
33	6	37.5	2	4	AAB91888 Apoptosis
34	6	37.5	2	4	AAB91688 Opioid pe
35	6	37.5	2	4	AAB91578 Opioid pe
36	6	37.5	2	4	AAB91037 Thyrotrop
37	6	37.5	2	4	AAB91857 Antimicro
38	6	37.5	2	5	ABG93488 Human P-g
39	6	37.5	2	5	ABG93585 Human P-g
40	6	37.5	2	5	ABG64373 Human alb
41	6	37.5	2	6	ABP99588 Human sec
42	6	37.5	2	6	ABU70941 Human adi
43	6	37.5	2	6	ABU06555 Maize Sta
44	6	37.5	2	8	ADL77640 Albumin f
45	6	37.5	3	1	AAP20375 Analgesic

ALIGNMENTS

RESULT 1
AAY32259
ID AAY32259 standard; peptide; 3 AA.
XX
AC AAY32259;
XX
DT 15-FEB-2000 (first entry)
XX
DE Light chain CDR H3 of mouse anti-CD23 Mab C11.
XX
KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insultitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
therapy.
XX
OS Mus musculus.
XX
PN WO958679-A1.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-GB001434.
XX
PR 09-MAY-1998; 98GB-00009839.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
XX
DR WPI; 2000-053101/04.
XX
DR N-PSDB; AA234744.
XX
PT Cell receptor specific antibodies useful for treating e.g. arthritis,
PT diabetes, multiple sclerosis and psoriasis.
XX
PS Claim 1; Page 40; 81pp; English.
XX
CC This sequence represents complementarity determining region 3 (CDR H3)
CC of the heavy chain of murine anti-CD23 (FCERII) monoclonal antibody C11
CC (see also AAY32263). The invention provides altered antibodies, such as
CC chimeric or humanised antibodies, which comprise sufficient of the amino
CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on
 CC haematopoietic cells. The antibodies are used to block soluble CD23
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They
 CC are also useful for studying interactions between CD23 and various
 CC ligands and determining the binding agents

XX
 XX Sequence 3 AA;

Query Match 100.0%; Score 16; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3
 |||
 Db 1 FID 3

RESULT 2
 AAR64556
 ID AAR64556 standard; peptide; 3 AA.

XX
 AC AAR64556;

XX 25-MAR-2003 (revised)

DT 01-SEP-1995 (first entry)

XX RF-1 peptide 1 from respiratory syncytial virus.

XX antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;
 KW human immunodeficiency virus; transmembrane protein; GP41; alpha helix;
 KW leucine zipper; DP-185; respiratory syncytial virus; RSV.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1
 /note= "optionally has an amino, acetyl, 9-
 FT fluorenylmethoxy-carbonyl, hydrophobic or macromolecular
 FT carrier gp. attached"

FT Modified-site 3
 /note= "optionally has a carboxyl, amido, hydrophobic or
 FT macromolecular carrier gp. attached"

XX WO9428920-A1.

XX 22-DEC-1994.

XX 07-JUN-1994; 94WO-US005739.

XX 07-JUN-1993; 93US-00073028.

XX (UYDU-) UNIV DUKE.

XX Bolognesi DP, Matthews TJ, Wild CT, Barney SO, Lambert DM;
 PI Petteway SR;

XX WPI; 1995-036105/05.

XX Computer search generated synthetic peptides - are inhibitors of HIV
 PT transmission.

XX Claim 14; Page 137; 182pp; English.

XX AAR64556-589 are peptide derivatives of a 37 mer RF-1 peptide derived
 CC from respiratory syncytial virus (RSV) (AAR64590) which have been
 CC truncated at the carboxy terminus. The peptides are DP-178 like peptides.

CC DP-178 corresponds to amino acids 638 to 673 of the HIV-1 isolate LAI
 CC transmembrane protein gp41. It forms a putative alpha helix at the C-
 CC terminal end of the gp41 ectodomain, and complexes with DP-107
 CC (corresponds to amino acids 558-595) which contains a leucine zipper
 CC motif. The peptides complex via non-covalent protein-protein
 CC interactions. The peptide derivatives were identified by a computer
 CC assisted peptide sequence search. The antiviral activity of this peptide
 CC is not stated in the specification. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 3 AA;

Query Match 68.8%; Score 11; DB 2; Length 3;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FID 3
 |||
 Db 1 FID 3

RESULT 3
 ADF77860
 ID ADF77860 standard; peptide; 3 AA.

XX
 AC ADF77860;

XX 11-MAR-2004 (first entry)

DE Therapeutic peptide of the invention #SEQ ID 13.

XX Antinflammatory; hypotensive; sarcoidosis;

KW vasoactive intestinal peptide; VIP;

KW pituitary adenylate cyclase-activating polypeptide; PACAP; lung;

KW secondary pulmonary hypertension; blood pressure.

XX Homo sapiens.

XX WO2003103702-A1.

XX 18-DEC-2003.

XX 05-JUN-2003; 2003WO-CH000357.

XX 10-JUN-2002; 2002EP-00012767.

XX (MOND-) MONDOBIOTECH LAB ANSTALT.

XX Bevec D;

XX WPI; 2004-081972/08./

XX Use of peptides having highly conserved amino acid sequence of vasoactive
 PT intestinal peptides in the manufacture of medicament for the treatment of
 PT disease correlated with sarcoidosis.

XX Claim 2; SEQ ID NO 13; 31pp; English.

XX The invention relates to the manufacture of a medicament for the
 CC treatment of a disease or disorder correlated with sarcoidosis. The
 CC medicament of the invention contains a peptide that is a vasoactive
 CC intestinal peptide (VIP) or a pituitary adenylate cyclase-activating
 CC polypeptide (PACAP). Peptides of the invention are useful for the
 CC treatment of a disease or disorder correlated with sarcoidosis in the
 CC human lung, and also secondary pulmonary hypertension. The peptides,
 CC having highly conserved sequence of amino acids exhibit an improved
 CC therapeutic efficacy than the prior art. The peptides reduce the
 CC pulmonary arterial pressure, the diastolic blood pressure and the
 CC systolic blood pressure. The current sequence represents a peptide of the
 CC invention.

XX Sequence 3 AA;

Query Match 68.8%; Score 11; DB 8; Length 3;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FID 3
 Db 1 FTD 3

RESULT 4
 AAW25193
 ID AAW25193 standard; peptide; 3 AA.
 XX
 AC AAW25193;
 XX
 DT 05-JAN-1998 (first entry)
 XX
 DE IDA-peptide capable of binding cell adhesion molecules.
 XX
 KW IDA; isoleucine; aspartic acid; alanine; cell adhesion molecule; binding;
 KW bladder irrigation; tumour removal; endoscopic operation;
 KW transurethral resection; cancer; neoplasia.
 XX
 OS Synthetic.
 XX
 PN DE19529909-A1.
 XX
 PD 20-FEB-1997.
 XX
 PF 15-AUG-1995; 95DE-01029909.
 XX
 PR 15-AUG-1995; 95DE-01029909.
 XX
 PA (PREP) PRESENTIUS AG.
 XX
 PI Boehle A;
 XX
 DR WPI; 1997-133793/13.
 XX
 PT Endoscopic irrigation solns. - contg. peptide(s) that bind to cell
 PT adhesion molecules.
 XX
 PS Claim 7; Page 8; 8pp; German.
 XX
 CC AAW25193-W25195 are peptides containing an IDA sequence or equivalent.
 CC The peptides are capable of binding to cell adhesion molecules and are
 CC used in aqueous irrigation solutions for use during and after endoscopic
 CC operations. Preferred irrigation solutions are electrolyte-free and
 CC contain 1 microg/ml to 100 mg/ml of one or more oligopeptides containing
 CC the amino acid sequences: RGD, LDV, IDA, DGEA, GPRP, VTL, YIGSR, KQAGDV
 CC and/or REDV (given in one letter amino acid code). The solutions are
 CC especially used for irrigating the bladder during and after tumour
 CC removal by transurethral resection. The peptides protect against
 CC recurrence of tumours
 XX
 SQ Sequence 3 AA;

Query Match 62.5%; Score 10; DB 2; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3
 Db 1 ID 2

RESULT 5
 ABR55054
 ID ABR55054 standard; peptide; 3 AA.
 XX
 AC ABR55054;
 XX
 DT 02-JUL-2003 (first entry)

Query Match 62.5%; Score 10; DB 2; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3
 Db 1 ID 2

RESULT 6
 AAY50605
 ID AAY50605 standard; peptide; 3 AA.
 XX
 AC AAY50605;
 XX
 DT 09-FEB-2000 (first entry)
 XX
 DE Resin bound cyclic peptide 38.
 XX
 KW Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;
 KW hypotensive; PTH receptor; treatment; hyper-calcaemia; hypo-calcaemia;
 KW osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;
 KW Cushing's syndrome; renal failure; hypertension; bone fracture repair.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Arg(PMC)"
 FT Misc-difference 3 /note= "This C-terminal amino acid is in the form of an
 FT

XX MMP substrate cleavage related peptide SEQ ID NO:56.
 DE Matrix metalloproteinase; MMP-2; MMP-9; MT1-MMP; substrate; cytostatic;
 XX peptidomimetic; antiinflammatory; neuroprotective; gene therapy;
 KW tumour angiogenesis; inflammatory disease; neurodegenerative disease.
 XX
 OS Synthetic.
 XX
 PN WO2003025125-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 13-SEP-2002; 2002WO-US029060.
 XX
 PR 14-SEP-2001; 2001US-00953592.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 PI Smith JW, Chen EI, Kridel SJ;
 XX WPI; 2003-354595/33.
 DR
 XX
 PT New isolated matrix metalloproteinase-2 (MMP-2), MMP-9, MT1-MMP selective
 PT substrate polypeptide, useful for diagnosing and treating tumor
 PT angiogenesis, inflammatory or neurodegenerative diseases.
 XX
 PS Disclosure; Page 67; 146pp; English.
 XX
 CC The present invention describes an isolated matrix metalloproteinase-2
 CC (MMP-2), MMP-9 or MT1-MMP selective substrate polypeptide (I), or its
 CC functional peptidomimetic. Also described is a method for preferentially
 CC directing a moiety to a site of MMP-2, MMP-9 or MT1-MMP activity by
 CC administering (I) to the subject. (I) have cytostatic, antiinflammatory
 CC and neuroprotective activities, and can be used in gene therapy. The
 CC polypeptides and methods from the present invention can be used for
 CC diagnosing and treating tumour angiogenesis, inflammatory or
 CC neurodegenerative diseases. ABR54999 to ABR55122 and ACC49718 to ACC49722
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 3 AA;

Query Match 62.5%; Score 10; DB 6; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3
 Db 1 ID 2

RESULT 6
 AAY50605
 ID AAY50605 standard; peptide; 3 AA.
 XX
 AC AAY50605;
 XX
 DT 09-FEB-2000 (first entry)
 XX
 DE Resin bound cyclic peptide 38.
 XX
 KW Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;
 KW hypotensive; PTH receptor; treatment; hyper-calcaemia; hypo-calcaemia;
 KW osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;
 KW Cushing's syndrome; renal failure; hypertension; bone fracture repair.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Arg(PMC)"
 FT Misc-difference 3 /note= "This C-terminal amino acid is in the form of an
 FT

```

FT Misc-difference 3 ester with benzyl alcohol"
FT FT /note= "Asp(Oallyl)"
FT FT
XX PN WO9952933-A1.
XX PD 21-OCT-1999.
XX PF 15-APR-1999; 99WO-US008435.
XX PR 15-APR-1998; 98US-0081897P.
XX PA (RHON ) RHONE-POULENC RORER PHARM INC.
XX PI Sledeski AW, Mancel JJ;
XX PI WPI; 1999-633822/54.
XX DR Convergent synthesis of peptides for treating e.g. bone disorders.
XX PT Disclosure; Page 79; 85pp; English.
XX PS This invention describes a novel method for the preparation of peptides
XX CC (II) that contain both cyclic and linear peptide fragments comprises
XX CC sequential reaction of a resin-bound linear fragment with the cyclic
XX CC fragment in N-protected form and optionally other linear fragments. The
XX CC products of the invention have osteopathic and hypotensive activity. (II)
XX CC bind to hPTH receptors and act as agonists or antagonists of hPTH. The
XX CC method is particularly used to prepare cyclic peptide analogs of
XX CC parathyroid hormone (PTH) or PTH-related peptides which are useful for
XX CC treating diseases that respond to treatment with agents that bind to PTH
XX CC receptors (with or without activation of adenylyl cyclase activity), e.g.
XX CC hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-
XX CC parathyroidism, Cushing's syndrome, renal failure and hypertension, also
XX CC for promoting repair of bone fractures. Separate synthesis of the cyclic
XX CC fragment allows convergent synthesis of resin-bound (II), with better
XX CC yields and higher throughput. The difficulties associated with
XX CC preparation of the bridged fragment are confined to a small peptide which
XX CC can be purified before reaction with the resin-bound component. AAY50568-
XX CC Y50614 represent the peptide fragments described in the method of the
XX CC invention
XX SQ Sequence 3 AA;

Query Match 56.2%; Score 9; DB 2; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3
Db 2 VD 3

RESULT 7
AAY50604
ID AAY50604 standard; peptide; 3 AA.
XX AC AAY50604;
XX XX
XX DT 09-FEB-2000 (first entry)
XX XX Resin bound cyclic peptide 37.
XX DE
XX KW Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;
XX KW hypotensive; PTH receptor; treatment; hyper-calcemia; hypo-calcemia;
XX KW osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;
XX KW Cushing's syndrome; renal failure; hypertension; bone fracture repair.
XX XX
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
FT Misc-difference 1 /note= "FMOC-Arg (PMC)"
FT FT

```

```

FT Misc-difference 3 /note= "This C-terminal amino acid is in the form of an
FT FT ester with benzyl alcohol"
FT FT
XX PN WO9952933-A1.
XX PD 21-OCT-1999.
XX PF 15-APR-1999; 99WO-US008435.
XX PR 15-APR-1998; 98US-0081897P.
XX PA (RHON ) RHONE-POULENC RORER PHARM INC.
XX PI Sledeski AW, Mancel JJ;
XX PI WPI; 1999-633822/54.
XX DR Convergent synthesis of peptides for treating e.g. bone disorders.
XX PT Disclosure; Page 78; 85pp; English.
XX PS This invention describes a novel method for the preparation of peptides
XX CC (II) that contain both cyclic and linear peptide fragments comprises
XX CC sequential reaction of a resin-bound linear fragment with the cyclic
XX CC fragment in N-protected form and optionally other linear fragments. The
XX CC products of the invention have osteopathic and hypotensive activity. (II)
XX CC bind to hPTH receptors and act as agonists or antagonists of hPTH. The
XX CC method is particularly used to prepare cyclic peptide analogs of
XX CC parathyroid hormone (PTH) or PTH-related peptides which are useful for
XX CC treating diseases that respond to treatment with agents that bind to PTH
XX CC receptors (with or without activation of adenylyl cyclase activity), e.g.
XX CC hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-
XX CC parathyroidism, Cushing's syndrome, renal failure and hypertension, also
XX CC for promoting repair of bone fractures. Separate synthesis of the cyclic
XX CC fragment allows convergent synthesis of resin-bound (II), with better
XX CC yields and higher throughput. The difficulties associated with
XX CC preparation of the bridged fragment are confined to a small peptide which
XX CC can be purified before reaction with the resin-bound component. AAY50568-
XX CC Y50614 represent the peptide fragments described in the method of the
XX CC invention
XX SQ Sequence 3 AA;

Query Match 56.2%; Score 9; DB 2; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3
Db 2 VD 3

RESULT 8
ABG77789
ID ABG77789 standard; peptide; 3 AA.
XX AC ABG77789;
XX XX
XX DT 05-NOV-2002 (first entry)
XX XX
XX DE Targetting peptide selective for human organ, tissue or cell type #322.
XX KW Human; cytostatic; antiinflammatory; antidiabetic; cardiovascular;
XX KW immunomodulator; antibacterial; antiviral; gene therapy; cancer;
XX KW arthritis; diabetes; inflammatory disease; atherosclerosis;
XX KW autoimmune disease; bacterial infection; viral infection;
XX KW cardiovascular disease; degenerative disease.
XX XX
XX XX Homo sapiens.
XX XX

```

PN WO200220723-A2.
 XX 14-MAR-2002.
 XX 07-SEP-2001; 2001WO-US028044.
 XX 08-SEP-2000; 2000US-0231266P.
 PR 17-JAN-2001; 2001US-00765101.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Arap W, Pasqualini R;
 PI WPI; 2002-599247/64.
 DR
 XX New targeting peptides identified by phage display, useful for treating a
 PT disease state, e.g. cancer, diabetes, inflammatory disease,
 PT atherosclerosis, autoimmune disease, bacterial or viral infection or
 PT cardiovascular disease.
 XX
 XX Claim 16; Page 79; 269pp; English.
 XX
 XX The invention describes an isolated peptide of 100 amino acids or less in
 CC size. The peptide is useful for treating a disease state, e.g. cancer,
 CC arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune
 CC disease, bacterial infection, viral infection, cardiovascular disease or
 CC degenerative disease. This sequence represents a human targeting peptide
 CC selective for human organs, tissues or cell types
 XX
 XX Sequence 3 AA;
 SQ

Query Match 56.2%; Score 9; DB 5; Length 3;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ID 3
 Db :
 2 VD 3

RESULT 9
 ABG63747
 ID ABG63747 standard; protein; 2 AA.
 XX AC ABG63747;
 XX
 DT 27-AUG-2002 (first entry)
 DE Human albumin fusion protein #422.
 XX
 XX Albumin fusion protein; therapeutic protein X; human albumin; HA;
 KW human serum albumin; HSA; cancer; reproductive disorder;
 KW digestive disorder; immune disorder; endocrine disorder;
 KW haematopoietic disorder; neural disorder; connective disorder;
 KW cytostatic; antifertility; antineoplastic; antitumor;
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; neurotropic;
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
 KW osteopathic; antiarthritic.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX WO200177137-A1.
 PN
 XX 18-OCT-2001.
 PD
 XX 12-APR-2001; 2001WO-US011988.
 XX
 XX 12-APR-2000; 2000US-0229358P.
 PR 25-APR-2000; 2000US-0199384P.
 PR 21-DEC-2000; 2000US-0256931P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA

XX Rosen CA, Haseltine WA;
 XX WPI; 2002-010886/01.
 XX
 PT New fusion protein for treating disease e.g. diabetes comprises an
 PT albumin fused to a therapeutic protein.
 XX
 XX Claim 1; Page 820; 2102pp; English.
 XX
 CC The present invention relates to albumin fusion proteins comprising a
 CC therapeutic protein X and human albumin (HA, also known as human serum
 CC albumin, HSA). The proteins are useful for treating a disease or disorder
 CC that may be modulated by therapeutic protein X. The albumin extends the
 CC shelf-life of protein X, and may increase its biological in vitro/in vivo
 CC activity. The protein is useful for treating and diagnosing disorders
 CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
 CC disease, ulcerative colitis), immune disorders (e.g. acquired
 CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
 CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,
 CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
 CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
 CC ABG63326-ABG65518 represent albumin fusion proteins of the invention
 XX
 XX Sequence 2 AA;
 SQ

Query Match 50.0%; Score 8; DB 5; Length 2;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FI 2
 Db :
 1 FL 2

RESULT 10
 ADC36684
 ID ADC36684 standard; peptide; 2 AA.
 XX AC ADC36684;
 XX
 DT 18-DEC-2003 (first entry)
 DE Mutated version JA-16 epitope peptide #20.
 XX
 KW Growth Differentiation Factor-8; GDF-8; Antidiabetic; Osteopathic;
 KW Immunomodulator; Anorectic; Neuroprotective; Inotropic;
 KW muscular disorder; neuromuscular disorder; osteoporosis.
 XX
 XX Homo sapiens.
 OS
 XX WO2003027248-A2.
 PN
 XX 03-APR-2003.
 PD
 PF 26-SEP-2002; 2002WO-US030452.
 XX
 PR 26-SEP-2001; 2001US-0324528P.
 XX
 XX (AMHP) WYETH.
 PA (DUNH/) DUNHAM W J.
 XX
 XX Aghajanian J, Wolfman NM, Veldman GM, Davies MV, Whittemore L;
 PI O'hara D, Bridges KG, Khurana TS, Bouxsein M;
 XX WPI; 2003-421158/39.
 DR
 XX New isolated anti-GDF-8 antibody, useful for treating, diagnosing and
 .PT preventing disorders associated with the GDF-8 protein, such as a type 2
 PT diabetes, muscular dystrophy, muscle atrophy, cachexia, obesity and/or
 PT osteoporosis.
 XX
 PS Disclosure; SEQ ID NO 85; 150pp; English.

XX The present invention relates to an isolated antibody that specifically
 CC binds to a Growth Differentiation Factor-8 (GDF-8) protein and reduces
 CC one or more biological activities associated with the GDF-8 protein. The
 CC methods and compositions of the present invention are useful for the
 CC treatment of disorders associated with the GDF-8 protein, such as a
 CC muscular disorder, neuromuscular disorder, adipose tissue disorder, type
 CC 2 diabetes or bone degenerative disorder, muscular dystrophy, muscle
 CC atrophy, congestive obstructive pulmonary disease, muscle wasting
 CC syndrome, sarcopenia, cachexia, obesity and/or osteoporosis. They can
 CC also be used for the diagnosis and prevention of the same disorders. The
 CC present sequence is a protein of the invention.
 XX Sequence 2 AA;
 SQ Query Match 50.0%; Score 8; DB 7; Length 2;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ID 3
 Db 1 LD 2
 RESULT 11
 ADL77012
 ID ADL77012 standard; peptide; 2 AA.
 XX AC ADL77012;
 XX DT 20-MAY-2004 (first entry)
 XX DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 494.
 XX KW albumin fusion protein; cytostatic; antianaemic; antiarthritic;
 KW antiaesthetic; anti-HIV; immunosuppressive; antiinflammatory;
 KW antiparasitic; antibacterial; osteopathic; dermatological; antitumor;
 KW immunomodulator; antiarrhythmic; cardiant; nontropic; antilipaeamic;
 KW nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer;
 KW antidiabetic; anabolic; hypertensive; vulnerable; gene therapy; cancer;
 KW reproductive system disorder; therapeutic protein.
 XX OS Unidentified.
 XX EN US2004010134-A1.
 XX PD 15-JAN-2004.
 XX PF 12-APR-2001; 2001US-00833245.
 XX PR 12-APR-2000; 2000US-0229358P.
 XX PR 25-APR-2000; 2000US-0199384P.
 XX PR 21-DEC-2000; 2000US-0256931P.
 XX PA (ROSE/) ROSEN C A.
 XX PA (HASE/) HASELTINE W A.
 XX PI Rosen CA, Haseltine WA;
 XX WI WPI; 2004-090519/09.
 XX PT New albumin fusion proteins, useful for diagnosing, treating, preventing
 PT or ameliorating diseases or disorders e.g. cancer, anemia, arthritis,
 PT asthma, inflammatory bowel disease or Alzheimer's disease.
 XX PS Disclosure; SEQ ID NO 494; 279pp; English.
 XX CC The invention relates to a novel albumin fusion protein. The invention
 CC further relates to: a composition comprising the albumin fusion protein
 CC and a pharmaceutical carrier; a kit comprising the composition of the
 CC albumin fusion protein formula; a method of treating a disease or
 CC disorder in a patient comprising the step of administering the albumin
 CC fusion protein; a method of treating a patient with a disease or disorder

CC that is modulated by Therapeutic protein: X, or its fragment or variant;
 CC a method of extending the shelf life of Therapeutic protein: X, or its
 CC fragment or variant; a nucleic acid molecule comprising a polynucleotide
 CC sequence encoding the albumin fusion protein; a vector comprising the
 CC nucleic acid molecule of the albumin fusion protein; and a host cell
 CC comprising the nucleic acid molecule of the albumin fusion protein. The
 CC albumin fusion protein and its compositions have the following
 CC activities: cytostatic, antianaemic, antiarthritic, antiaesthetic, anti-
 CC HIV, immunosuppressive, antiinflammatory, antiparasitic, antibacterial,
 CC osteopathic, dermatological, antitumor, immunomodulator, antiarrhythmic,
 CC cardiant, nontropic, antilipaeamic, nephrotropic, uropathic,
 CC neuroprotective, antiparkinsonian, tranquilizer, antidiabetic, anabolic,
 CC hypertensive, and vulnerary. The albumin fusion protein nucleic acid may
 CC be used in gene therapy to treat disorders. The albumin fusion protein is
 CC useful for diagnosing, treating, preventing or ameliorating diseases or
 CC disorders comprising indication: Y. The diseases or disorders include:
 CC cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer), acute
 CC immune or haematopoietic diseases (e.g. anaemia, Hodgkin's disease, AIDS,
 CC lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS,
 CC autoimmune disease, inflammatory bowel disease, psoriasis or Lyme
 CC disease), reproductive system disorders (e.g. prostaticitis, inguinal
 CC hernia, varicocele, penile carcinoma, ovarian adenocarcinoma or Sertoli-
 CC Leydig tumours), musculoskeletal diseases (e.g. giant cell tumours,
 CC Paget's disease, systemic lupus erythematosus, gout, muscular dystrophy
 CC or cachexia), cardiovascular disease (e.g. rhabdomyomas, heart disease,
 CC arrhythmia, cardiac arrest, heat valve disease, hypernatraemia or
 CC hyponatraemia), mixed foetal diseases (e.g. foetal alcohol syndrome,
 CC Down's syndrome, Patau syndrome, Turner's syndrome, Apert syndrome or Tay-
 CC Sachs disease), excretory diseases (e.g. urinary incontinence, urinary
 CC tract infections or renal disorders), neural or sensory disease (e.g.
 CC Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis,
 CC cerebellar ataxia, attention deficit disorder, autism or obsessive
 CC compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or
 CC occupational lung disease), endocrine diseases (e.g. diabetes, Addison's
 CC disease or glomerulonephritis), digestive diseases (e.g. portal
 CC hypertension, irritable bowel disease, gastric atrophy or pancreatitis)
 CC or connective tissue or epithelial diseases (e.g. Crohn's disease,
 CC scleroderma, wound healing or epidermolysis bullosa). This sequence
 CC represents a therapeutic protein X relating to the albumin fusion protein
 CC of the invention. The sequence listing data for this specification was
 CC downloaded from the USPTO website.
 XX Sequence 2 AA;
 SQ Query Match 50.0%; Score 8; DB 8; Length 2;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FI 2
 Db 1 FL 2

RESULT 12
 AAR48960
 ID AAR48960 standard; protein; 3 AA.
 XX AC AAR48960;
 XX DT 25-MAR-2003 (revised)
 XX DT 12-SEP-1994 (first entry)

NL4-3 truncated GAG C-terminal peptide.

XX HIV-1; HXB2; antisense; sequence inversion; antisense virus; infection;
 KW naturally occurring virus; NOV; translation; replication; infectivity;
 KW hepatitis B; HIV-2; SIV; flip-over PCR.

XX Synthetic.
 OS WO9403596-A1.
 PN 17-FEB-1994.
 XX

XX 30-JUL-1993; 93WO-US007179.
 XX 30-JUL-1992; 92US-00921104.
 XX (UYHA-) UNIV HAWAII.
 XX Hu W, Wang J;
 XX WPI; 1994-065685/08.
 XX N-PSDB; AAQ57688.
 XX New antisense viruses and anti:sense-ribozyme viruses - used for treating
 XX or preventing viral infections, partic. HIV-1, HIV-2 or SIV infection.
 XX Disclosure; Page 108; 167pp; English.
 XX This sequence is encoded by a PCR fragment of NL4-3 and represents the C-
 XX terminal peptide fragment of the truncated GAG protein. The DNA encoding
 XX this fragment was ligated into ClaI/SalI digested pX and the
 XX corresponding plasmid was used to produce the antisense virus of the
 XX invention. Antisense or truncated RNAs expressed by these viruses bind to
 XX the mRNAs expressed by the naturally occurring viruses (NOVs) and prevent
 XX the mRNAs from being translated into proteins, thereby preventing the NOV
 XX from replicating. The antisense viruses maintain the infectivity of the
 XX NOVs, allowing antisense RNAs to reach the mRNAs of the natural viruses.
 XX Antisense viruses such as these may be used for treating or preventing a
 XX viral infection, particularly HIV-1, HIV-2 or SIV infection or hepatitis
 XX B infection. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 3 AA;
 Query Match 50.0%; Score 8; DB 2; Length 3;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ID 3
 Db 1 LD 2

RESULT 13
 AAR82907
 ID AAR82907 standard; peptide; 3 AA.
 AC AAR82907;
 XX 20-DEC-1995 (first entry)
 DT Non-RGD, non-YISGR cancer metastasis inhibitory peptide #1.
 DE Cancer metastasis; adhesive peptide; core sequence; dextran; cancer;
 DE water soluble polysaccharide; metastasis; wound; immunogenicity.
 XX Synthetic.
 OS JP07089999-A.
 PN 04-APR-1995.
 PD 17-SEP-1993; 93JP-00254779.
 PF 17-SEP-1993; 93JP-00254779.
 PR 17-SEP-1993; 93JP-00254779.
 XX (JAPG) NIPPON ZEON KK.
 XX WPI; 1995-167254/22.
 XX Cancer metastasis inhibitive peptide derive. - useful for inhibition of
 XX cancer metastasis, healing of wounds and regulation of immunogenicity.
 XX Disclosure; Page 3; 6pp; Japanese.

CC The peptides AAR70472-90 and AAR82907-24 are peptide derivatives which
 CC inhibit cancer metastasis. They are composed of an adhesive peptide with
 CC a core sequence selected from: RGD (AAR70472-85), YIGSR (AAR70486-90) or
 CC other sequence (AAR82907-24), linked to a water soluble polysaccharide,
 CC preferably a water soluble dextran, at the C-terminus. The peptides are
 CC useful in inhibiting cancer metastasis, healing wounds and the regulation
 CC of immunogenicity
 XX
 XX Sequence 3 AA;
 Query Match 50.0%; Score 8; DB 2; Length 3;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ID 3
 Db 1 LD 2

RESULT 14
 AAW25187
 ID AAW25187 standard; peptide; 3 AA.
 XX AAW25187;
 AC AAW25187;
 XX 05-JAN-1998 (first entry)
 DT LDV-peptide capable of binding cell adhesion molecules.
 DE LDV; leucine; aspartic acid; valine; cell adhesion molecule; binding;
 KW bladder irrigation; tumour removal; endoscopic operation;
 KW transurethral resection; cancer; neoplasia.
 XX Synthetic.
 OS DE19529909-Al.
 PN 20-FEB-1997.
 PD 15-AUG-1995; 95DE-01029909.
 PF 15-AUG-1995; 95DE-01029909.
 PR (PREP) PRESENTIUS AG.
 XX Boehle A;
 PI WPI; 1997-133793/13.
 DR Endoscopic irrigation solns. - contg. peptide(s) that bind to cell
 PT adhesion molecules.
 PT Claim 6; Page 8; 8pp; German.
 XX AAW25187-W25192 are peptides containing an LDV sequence or equivalent.
 CC The peptides are capable of binding to cell adhesion molecules and are
 CC used in aqueous irrigation solutions for use during and after endoscopic
 CC operations. Preferred irrigation solutions are electrolyte-free and
 CC contain 1 microg/ml to 100 mg/ml of one or more oligopeptides containing
 CC the amino acid sequences: RGD, LDV, IDA, DGEA, GPRP, VTL, YIGSR, KQAGDV
 CC and/or REDV (given in one letter amino acid code). The solutions are
 CC especially used for irrigating the bladder during and after tumour
 CC removal by transurethral resection. The peptides protect against
 CC recurrence of tumours
 XX
 XX Sequence 3 AA;
 Query Match 50.0%; Score 8; DB 2; Length 3;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ID 3
 Db 1 LD 2

```

Db      1 LD 2

RESULT 15
AAY49399
ID      AAY49399 standard; peptide; 3 AA.
XX
XX      AAY49399;
AC
XX
XX      DT 13-MAR-2000 (first entry)
XX
XX      Morphine modulating neuropeptide as diagnostic marker.
DE
XX
XX      Diagnostic marker; human disorder; opiate; autism spectral disorder;
KW      autism pervasive developmental disorder; Aspergers syndrome;
KW      attention deficient disorder; attention hyperactivity disorder;
KW      multiple sclerosis; Parkinson's disease; Alzheimer's dementia; morphine;
KW      neuropeptide.
XX
XX      Synthetic.
OS      Homo sapiens.
XX
XX      EP969015-A2.
PN
XX
XX      05-JAN-2000.
PD
XX
XX      15-JUN-1999; 99EP-00304636.
PF
XX
XX      15-JUN-1998; 98US-0089237P.
PR
XX      15-JUN-1998; 98US-0089238P.
PR
XX      24-MAY-1999; 99US-00317702.
XX
XX      (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
PA
XX
XX      Shanahan MR, Venturini AJ, Daiss JL, Friedman AE;
XX      WPI; 2000-074781/07.
XX
XX      Diagnosing human disorders e.g. autism spectral disorders, multiple
PT      sclerosis, Parkinson's disease and Alzheimer's dementia.
XX
XX      Claim 8; Page 7; 44pp; English.
XX
XX      The invention provides diagnostic markers for a human disorder
CC      comprising either opiate-like peptides or opiate-derived peptides. The
CC      novel peptides are used as diagnostic marker, in ex-vivo methods of
CC      diagnosing human disorders e.g. autism spectral disorders including
CC      autism pervasive developmental disorder, Aspergers syndrome, attention
CC      deficient disorder and attention hyperactivity disorder, and multiple
CC      sclerosis, Parkinson's disease and Alzheimer's dementia. Sequences
CC      AAY49371-413 represent peptide diagnostic markers for the human disorders
CC      specified above
XX
XX      Sequence 3 AA;
SQ

Query Match      50.0%; Score 8; DB 3; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FI 2
        | :
        1 FL 2
Db

Search completed: April 18, 2005, 16:12:25
Job time : 169 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 16:15:33 ; Search time 130 Seconds
(without alignments)

7.670 Million cell updates/sec

Title: US-09-674-716B-13

Perfect score: 16

Sequence: 1 FID 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1055

Minimum DB seq length: 0

Maximum DB seq length: 3

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	81.2	3	17	US-10-823-888-1
2	11	68.8	3	15	US-10-416-822-13
3	10	62.5	3	15	US-10-243-613-56
4	9	56.2	3	9	US-09-853-918-6
5	9	56.2	3	11	US-09-920-306-6
6	9	56.2	3	11	US-09-920-306-64
7	9	56.2	3	15	US-10-363-208-27
8	9	50.0	2	11	US-09-833-245-494
9	8	50.0	2	14	US-10-253-532-85
10	8	50.0	2	9	US-09-922-261-7
11	8	50.0	3	9	US-09-982-172-54
12	8	50.0	3	14	US-10-253-532-74
13	8	50.0	3	14	US-10-253-532-84

14	8	50.0	3	15	US-10-408-166-372	Sequence 372, Appl
15	8	50.0	3	16	US-10-297-147A-6	Sequence 6, Appl
16	8	50.0	3	17	US-10-418-032-258	Sequence 258, Appl
17	7	43.8	2	14	US-10-187-339-6	Sequence 6, Appl
18	7	43.8	2	11	US-09-920-306-58	Sequence 58, Appl
19	6	37.5	2	9	US-09-867-847-33	Sequence 33, Appl
20	6	37.5	2	9	US-09-867-847-34	Sequence 34, Appl
21	6	37.5	2	9	US-09-867-847-35	Sequence 35, Appl
22	6	37.5	2	9	US-09-867-847-36	Sequence 36, Appl
23	6	37.5	2	9	US-09-867-847-37	Sequence 37, Appl
24	6	37.5	2	9	US-09-867-847-38	Sequence 38, Appl
25	6	37.5	2	9	US-09-867-847-39	Sequence 39, Appl
26	6	37.5	2	9	US-09-867-847-40	Sequence 40, Appl
27	6	37.5	2	9	US-09-867-847-41	Sequence 41, Appl
28	6	37.5	2	9	US-09-867-847-42	Sequence 42, Appl
29	6	37.5	2	9	US-09-867-847-43	Sequence 43, Appl
30	6	37.5	2	9	US-09-867-847-44	Sequence 44, Appl
31	6	37.5	2	9	US-09-982-172-8	Sequence 8, Appl
32	6	37.5	2	9	US-09-982-172-105	Sequence 105, Appl
33	6	37.5	2	11	US-09-833-245-1122	Sequence 1122, Appl
34	6	37.5	2	11	US-09-920-306-5	Sequence 5, Appl
35	6	37.5	2	14	US-10-206-699-296	Sequence 296, Appl
36	6	37.5	2	15	US-10-137-867-262	Sequence 262, Appl
37	6	37.5	2	15	US-10-371-472-3	Sequence 3, Appl
38	6	37.5	2	15	US-10-371-472-6	Sequence 6, Appl
39	6	37.5	2	15	US-10-371-472-13	Sequence 13, Appl
40	6	37.5	2	15	US-10-371-472-17	Sequence 17, Appl
41	6	37.5	2	15	US-10-371-472-20	Sequence 20, Appl
42	6	37.5	2	15	US-10-371-472-34	Sequence 34, Appl
43	6	37.5	2	15	US-10-371-472-37	Sequence 37, Appl
44	6	37.5	2	15	US-10-371-472-40	Sequence 40, Appl
45	6	37.5	2	16	US-10-109-048-461	Sequence 461, Appl

ALIGNMENTS

RESULT 1

US-10-823-888-1
; Sequence 1, Application US/10823888
; Publication No. US20050032138A1
; GENERAL INFORMATION:
; APPLICANT: Lathrop, Julia T.
; APPLICANT: Hammond, David J.
; APPLICANT: Cervenakova, Larisa
; APPLICANT: Gheorghiu, Liliana
; APPLICANT: Yakovleva, Oksana
; TITLE OF INVENTION: Method for Identifying Ligands Specific for Structural Isoforms
; FILE REFERENCE: 51821-0121 (51821-299534)
; CURRENT APPLICATION NUMBER: US/10/823,888
; PRIOR FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US 60/462,658
; PRIOR FILING DATE: 2003-04-14
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; TYPE: PRT
; LENGTH: 3
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-823-888-1

Query Match 81.2%; Score 13; DB 17; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FID 3

DB 1 YID 3

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RESULT 2
US-10-416-822-13
; Sequence 13, Application US/10416822
; Publication No. US20040063631A1
; GENERAL INFORMATION:
; APPLICANT: Mondobiotec SA
; TITLE OF INVENTION: Use of biologically active peptides for the treatment of pulmonary
; FILE REFERENCE: arteriolar hypertension and related diseases
; CURRENT APPLICATION NUMBER: US/10/416,822
; CURRENT FILING DATE: 2003-05-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-416-822-13
Query Match      68.8%; Score 11; DB 15; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FID 3
Db      1 FID 3

RESULT 3
US-10-243-613-56
; Sequence 56, Application US/10243613
; Publication No. US20040053823A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Jeffrey W.
; APPLICANT: Chen, Emily I.
; APPLICANT: Kridel, Steven J.
; TITLE OF INVENTION: Selective Substrates for Matrix
; FILE REFERENCE: P-LJ 5432
; CURRENT APPLICATION NUMBER: US/10/243,613
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/953,592
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-243-613-56
Query Match      62.5%; Score 10; DB 15; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ID 3
Db      1 ID 2

RESULT 4
US-09-853-918-6
; Sequence 6, Application US/09853918
; Patent No. US20020068346A1
; GENERAL INFORMATION:
; APPLICANT: Krystek, Stanley R.
; APPLICANT: Sheriff, Steven
; APPLICANT: Witmer, Mark R.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Yan, Ning
; APPLICANT: Mouravieff, Julie E.

```

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; APPLICANT: Einspahr, Howard M.
; APPLICANT: Kish, Kevin
; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
; FILE REFERENCE: POLYPEPTIDES AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/853,918
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,448
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-918-6
Query Match      56.2%; Score 9; DB 9; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ID 3
Db      2 VD 3

RESULT 5
US-09-920-306-6
; Sequence 6, Application US/09920306
; Publication No. US20040029808A1
; GENERAL INFORMATION:
; APPLICANT: Unilever PLC
; APPLICANT: Unilever NV
; TITLE OF INVENTION: Peptides Capable of Functioning as Mimotopes for
; FILE REFERENCE: Peptide Mimotopes
; CURRENT APPLICATION NUMBER: US/09/920,306
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: EP00306613.1
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-920-306-6
Query Match      56.2%; Score 9; DB 11; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 FID 3
Db      1 FED 3

RESULT 6
US-09-920-306-64
; Sequence 64, Application US/09920306
; Publication No. US20040029808A1
; GENERAL INFORMATION:
; APPLICANT: Unilever PLC
; APPLICANT: Unilever NV
; TITLE OF INVENTION: Peptides Capable of Functioning as Mimotopes for
; FILE REFERENCE: Hormonal Analyses
; CURRENT APPLICATION NUMBER: US/09/920,306
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: EP00306613.1

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; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-920-306-64

Query Match 56.2%; Score 9; DB 11; Length 3;
Best Local Similarity 33.3%; Pred. No. 1.3e+06;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FID 3
|
Db 1 YFD 3

RESULT 7
US-10-363-208-27
; Sequence 27, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774 P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(3)
; OTHER INFORMATION: synthetic construct
US-10-363-208-27

Query Match 56.2%; Score 9; DB 15; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FID 3
|
Db 1 FHD 3

RESULT 8
US-09-833-245-494
; Sequence 494, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 494
; LENGTH: 2
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-833-245-494

Query Match 50.0%; Score 8; DB 11; Length 2;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FI 2
|
Db 1 FL 2

RESULT 9
US-10-253-532-85
; Sequence 85, Application US/10253532
; Publication No. US20030138422A1
; GENERAL INFORMATION:
; APPLICANT: Agnajanian, Jane
; APPLICANT: Wolfman, Neil
; APPLICANT: Veldman, Geetruida
; APPLICANT: Davies, Monique
; APPLICANT: Whittemore, Lisa Anne
; APPLICANT: O'Hara, Denise
; APPLICANT: Bridges, Kristie
; APPLICANT: Khurana, Tejiv
; TITLE OF INVENTION: Antibody Inhibitors of GDF-8 and Uses Therefor
; FILE REFERENCE: 08702.00012-00000
; CURRENT APPLICATION NUMBER: US/10/253,532
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 60/324,528
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-532-85

Query Match 50.0%; Score 8; DB 14; Length 2;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3
|
Db 1 LD 2

RESULT 10
US-09-922-261-7
; Sequence 7, Application US/09922261
; Patent No. US2002011471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-922-261-7

Query Match      50.0%; Score 8; DB 9; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 ID 3
      :|
Db      2 LD 3

RESULT 11
US-09-982-172-54
; Sequence 54, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING EACH
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 54
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-54

Query Match      50.0%; Score 8; DB 9; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FI 2
      :|
Db      1 FL 2

RESULT 12
US-10-253-532-74
; Sequence 74, Application US/10253532
; Publication No. US20030138422A1
; GENERAL INFORMATION:
; APPLICANT: Aghajanian, Jane
; APPLICANT: Wolfman, Neil
; APPLICANT: Veldman, Geetruida
; APPLICANT: Davies, Monique
; APPLICANT: Whittemore, Lisa Anne
; APPLICANT: O'Hara, Denise
; APPLICANT: Bridges, Kristie
; APPLICANT: Khurana, Tejiv
; TITLE OF INVENTION: Antibody Inhibitors of GDF-8 and Uses Therefor
; FILE REFERENCE: 08702.00012-00000
; CURRENT APPLICATION NUMBER: US/10/253,532
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 60/324,528
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 74
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-532-74

Query Match      50.0%; Score 8; DB 14; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 ID 3
      :|
Db      2 LD 3

RESULT 13
US-10-253-532-84
; Sequence 84, Application US/10253532
; Publication No. US20030138422A1
; GENERAL INFORMATION:
; APPLICANT: Aghajanian, Jane
; APPLICANT: Wolfman, Neil
; APPLICANT: Veldman, Geetruida
; APPLICANT: Davies, Monique
; APPLICANT: Whittemore, Lisa Anne
; APPLICANT: O'Hara, Denise
; APPLICANT: Bridges, Kristie
; APPLICANT: Khurana, Tejiv
; TITLE OF INVENTION: Antibody Inhibitors of GDF-8 and Uses Therefor
; FILE REFERENCE: 08702.00012-00000
; CURRENT APPLICATION NUMBER: US/10/253,532
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 60/324,528
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 84
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-532-84

Query Match      50.0%; Score 8; DB 14; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 ID 3
      :|
Db      1 LD 2

RESULT 14
US-10-408-166-372
; Sequence 372, Application US/10408166
; Publication No. US20040018516A1
; GENERAL INFORMATION:
; APPLICANT: Francischetti, Ivo M. B.
; APPLICANT: Valenzuela, Jesus G.
; APPLICANT: Ribeiro, Jose M.C.
; TITLE OF INVENTION: Ixodes SCAPULARIS TISSUE FACTOR PATHWAY
; TITLE OF INVENTION: INHIBITOR
; FILE REFERENCE: NIH99.001C1
; CURRENT APPLICATION NUMBER: US/10/408,166
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: PCT/US01/42472
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/240,575
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 475
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Ixodes scapularis
US-10-408-166-372

Query Match      50.0%; Score 8; DB 15; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 ID 3
      :|
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Db 2 LD 3

RESULT 15
US-10-297-147A-6
; Sequence 6, Application US/10297147A
; Publication No. US20040110285A1
; GENERAL INFORMATION:
; APPLICANT: Mnemoscience GMBH
; TITLE OF INVENTION: SHAPE MEMORY THERMOPLASTICS AND POLYMER NETWORKS FOR TISSUE ENGINEERING
; FILE REFERENCE: MNE 102
; CURRENT APPLICATION NUMBER: US/10/297,147A
; CURRENT FILING DATE: 2001-03-31
; PRIOR APPLICATION NUMBER: US 60/208,285
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-297-147A-6

Query Match 50.0%; Score 8; DB 16; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.3e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3
; |
Db 1 LD 2

Search completed: April 18, 2005, 16:28:00
Job time : 131 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 16:07:21 ; Search time 42 Seconds
(without alignments)
5.332 Million cell updates/sec

Title: US-09-674-716B-13
Perfect score: 16
Sequence: 1 FID 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1169

Minimum DB seq length: 0
Maximum DB seq length: 3

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	62.5	3	3	US-09-086-421-2
2	9	56.2	2	3	US-09-284-709A-30
3	9	56.2	2	4	US-09-442-989-33
4	9	56.2	2	4	US-09-442-989-34
5	9	56.2	3	1	US-08-127-904-7
6	9	56.2	3	2	US-09-061-337-3
7	9	56.2	3	2	US-09-122-129-3
8	9	56.2	3	3	US-09-340-991-3
9	9	56.2	3	3	US-08-974-609-3
10	9	56.2	3	3	US-09-264-709A-26
11	9	56.2	3	4	US-09-549-098-3
12	9	56.2	3	4	US-09-442-989-35
13	9	56.2	3	4	US-09-442-989-36
14	9	56.2	3	5	PCT-US94-10475-7
15	8	50.0	3	1	US-08-081-539-117
16	8	50.0	3	1	US-08-466-647-117
17	8	50.0	3	1	US-08-411-389-20
18	8	50.0	3	1	US-08-634-060-36
19	8	50.0	3	1	US-08-338-282-11
20	8	50.0	3	2	US-08-934-222-12
21	8	50.0	3	2	US-08-933-402-12
22	8	50.0	3	2	US-09-207-621-12
23	8	50.0	3	2	US-08-532-818-12
24	8	50.0	3	3	US-09-231-797-12
25	8	50.0	3	3	US-09-086-421-1
26	8	50.0	3	3	US-08-934-224-12
27	8	50.0	3	3	US-08-933-843-12

28	8	50.0	3	3	US-08-934-223-12	Sequence 12, Appl
29	8	50.0	3	3	US-09-413-492-12	Sequence 12, Appl
30	8	50.0	3	3	US-09-461-697-7	Sequence 7, Appli
31	7	43.8	2	4	US-09-434-837-6	Sequence 6, Appli
32	7	43.8	3	1	US-08-118-135A-1	Sequence 1, Appli
33	7	43.8	3	1	US-08-118-135A-8	Sequence 8, Appli
34	7	43.8	3	1	US-08-118-135A-9	Sequence 9, Appli
35	7	43.8	3	1	US-08-446-908-14	Sequence 14, Appl
36	7	43.8	3	1	US-08-231-205A-14	Sequence 14, Appl
37	7	43.8	3	1	US-08-153-848-17	Sequence 17, Appl
38	7	43.8	3	2	US-08-642-045B-25	Sequence 25, Appl
39	7	43.8	3	2	US-08-871-163-14	Sequence 14, Appl
40	7	43.8	3	3	US-09-299-843A-17	Sequence 17, Appl
41	7	43.8	3	3	US-09-088-337B-17	Sequence 17, Appl
42	7	43.8	3	4	US-09-212-663-12	Sequence 12, Appl
43	7	43.8	3	5	PCT-US93-11153-17	Sequence 17, Appl
44	6	37.5	2	1	US-07-820-154A-15	Sequence 15, Appl
45	6	37.5	2	1	US-07-820-154A-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-09-086-421-2
; Sequence 2, Application US/09086421A
; Patent No. 6093696
; GENERAL INFORMATION:
; APPLICANT: Head, John C
; APPLICANT: Archibald, Sarah C
; APPLICANT: Warreilow, Graham J
; TITLE OF INVENTION: Tyrosine Derivatives
; FILE REFERENCE: CELLO058
; CURRENT APPLICATION NUMBER: US/09/086, 421A
; CURRENT FILING DATE: 1998-05-29
; EARLIER FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6093696el Sequence
US-09-086-421-2

Query Match 62.5%; Score 10; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ID 3
Db 1 ID 2

RESULT 2
US-09-264-709A-30
; Sequence 30, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
; APPLICANT: Roberts, Eugene
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
; FILE OF INVENTION: Improve the Quality of Life
; FILE REFERENCE: 2124-310
; CURRENT APPLICATION NUMBER: US/09/264, 709A
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 08/797, 782
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 2

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: memory-modulating peptide
US-09-264-709A-30

Query Match          56.2%; Score 9; DB 3; Length 2;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FI 2
Db      1 FV 2

RESULT 3
US-09-442-989-33
; Sequence 33, Application US/09442989
; Patent No. 6569993
; GENERAL INFORMATION:
; APPLICANT: Sledeski, Adam W.
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC
; FILE REFERENCE: A3113B-US
; CURRENT APPLICATION NUMBER: US/09/442,989
; CURRENT FILING DATE: 1999-11-18
; EARLIER APPLICATION NUMBER: 60/081,897
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 33
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: PEPTIDE
; LOCATION: (2)
; OTHER INFORMATION: Asp (Oallyl)
; FEATURE:
; OTHER INFORMATION: BOC-Val
; NAME/KEY: PEPTIDE
; LOCATION: (2)
; OTHER INFORMATION: "This C-terminal amino acid is in the form of an
; OTHER INFORMATION: ester with benzyl alcohol."
US-09-442-989-33

Query Match          56.2%; Score 9; DB 4; Length 2;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 ID 3
Db      1 VD 2

RESULT 4
US-09-442-989-34
; Sequence 34, Application US/09442989
; Patent No. 6569993
; GENERAL INFORMATION:
; APPLICANT: Sledeski, Adam W.
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC
; FILE REFERENCE: A3113B-US
; CURRENT APPLICATION NUMBER: US/09/442,989
; CURRENT FILING DATE: 1999-11-18
; EARLIER APPLICATION NUMBER: 60/081,897
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 34
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: PEPTIDE
; LOCATION: (1)
; OTHER INFORMATION: "The N-terminus is in the form of a hydrochloride
; OTHER INFORMATION: salt."
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (2)
; OTHER INFORMATION: Asp (Oallyl)
; FEATURE:
; OTHER INFORMATION: Asp (Oallyl)
; NAME/KEY: PEPTIDE
; LOCATION: (2)
; OTHER INFORMATION: "This C-terminal acid is in the form of an ester
; OTHER INFORMATION: with benzyl alcohol."
US-09-442-989-34

Query Match          56.2%; Score 9; DB 4; Length 2;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 ID 3
Db      1 VD 2

RESULT 5
US-08-127-904-7
; Sequence 7, Application US/08127904
; Patent No. 5470951
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For Antagonizing
; TITLE OF INVENTION: Amnestic Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving the
; TITLE OF INVENTION: Quality of Life in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4" diskette
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,904
; FILING DATE: 29 September 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: No. 5470951e
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: No. 5470951e
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; TELEX: No. 5470951e
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3
; TYPE: Amino Acid
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STRANDEDNESS:
TOPOLOGY: Unknown
US-08-127-904-7

Query Match 56.2%; Score 9; DB 1; Length 3;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FI 2
|:
Db 1 FV 2

RESULT 6
US-09-061-337-3
; Sequence 3, Application US/09061337
; Patent No. 5985540
; GENERAL INFORMATION:
; APPLICANT: Tan, Yuying
; APPLICANT: Lenz, Martin
; TITLE OF INVENTION: HIGH SPECIFICITY HOMOCYSTEINE ASSAYS FOR
; TITLE OF INVENTION: BIOLOGICAL SAMPLES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,337
; FILING DATE: 17-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/899,776
; FILING DATE: 24-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/918,214
; FILING DATE: 25-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/941,921
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Donahue, E. Victor
; REGISTRATION NUMBER: 35,492
; REFERENCE/DOCKET NUMBER: 31276-20013.21
; TELEPHONE: (202) 887-1546
; TELEFAX: (202) 822-0168
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-061-337-3

Query Match 56.2%; Score 9; DB 2; Length 3;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3
:|
Db 2 VD 3

RESULT 7
US-09-122-129-3
; Sequence 3, Application US/09122129
; Patent No. 5988191
; GENERAL INFORMATION:
; APPLICANT: Tan, Yuying
; APPLICANT: Lenz, Martin
; TITLE OF INVENTION: HIGH SPECIFICITY HOMOCYSTEINE ASSAYS FOR
; TITLE OF INVENTION: BIOLOGICAL SAMPLES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122,129
; FILING DATE: 24 July 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/899,776
; FILING DATE: 24-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/918,214
; FILING DATE: 25-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/941,921
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,609
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/061,337
; FILING DATE: 17-APRIL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Donahue, E. Victor
; REGISTRATION NUMBER: 35,492
; REFERENCE/DOCKET NUMBER: 312762001322
; TELEPHONE: (202) 887-1546
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-122-129-3

Query Match 56.2%; Score 9; DB 2; Length 3;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3
:|
Db 2 VD 3

RESULT 8
US-09-340-991-3
; Sequence 3, Application US/09340991
; Patent No. 6086467
; GENERAL INFORMATION:
; APPLICANT: Tan, Yuying
; APPLICANT: Lenz, Martin

```

; TITLE OF INVENTION: HIGH SPECIFICITY HOMOCYSTEINE ASSAYS FOR
; TITLE OF INVENTION: BIOLOGICAL SAMPLES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,991
; FILING DATE: 24 July 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/899,776
; FILING DATE: 24-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/918,214
; FILING DATE: 25-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/941,921
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,609
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/061,337
; FILING DATE: 17-APRIL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Donahue, E. Victor
; REGISTRATION NUMBER: 35,492
; REFERENCE/DOCKET NUMBER: 312762001322
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1546
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-340-991-3

Query Match 56.2%; Score 9; DB 3; Length 3;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3
Db 2 VD 3

RESULT 9
US-09-340-991-3
; Sequence 3, Application US/08974609
; Patent No. 6140102
; GENERAL INFORMATION:
; APPLICANT: Tan, Yuying
; APPLICANT: Lenz, Martin
; TITLE OF INVENTION: HIGH SPECIFICITY HOMOCYSTEINASES AND
; TITLE OF INVENTION: GENES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington

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; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,609
; FILING DATE: 24-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/941,921
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Donahue, E. Victor
; REGISTRATION NUMBER: 35,492
; REFERENCE/DOCKET NUMBER: 31276-20013.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-974-609-3

Query Match 56.2%; Score 9; DB 3; Length 3;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ID 3
Db 2 VD 3

RESULT 10
US-09-264-709A-26
; Sequence 26, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
; APPLICANT: Roberts, Eugene
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
; TITLE OF INVENTION: Improve the Quality of Life
; FILE REFERENCE: 2124-310
; CURRENT APPLICATION NUMBER: US/09/264,709A
; CURRENT FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 08/797,782
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 26
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:memory-modulating peptide
; US-09-264-709A-26

Query Match 56.2%; Score 9; DB 3; Length 3;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FI 2
Db 2 FV 3

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RESULT 11
US-09-549-098-3
; Sequence 3, Application US/09549098
; Patent No. 6468762
; GENERAL INFORMATION:
; APPLICANT: Tan, Yuying
; APPLICANT: Lenz, Martin
; TITLE OF INVENTION: HIGH SPECIFICITY HOMOCYSTEINE ASSAYS FOR
; TITLE OF INVENTION: BIOLOGICAL SAMPLES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/549,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/340,991
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/918,214
; FILING DATE: 25-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/941,921
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,609
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/061,337
; FILING DATE: 17-APRIL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Donahue, E. Victor
; REGISTRATION NUMBER: 35,492
; REFERENCE/DOCKET NUMBER: 312762001322
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1546
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-549-098-3

Query Match 56.2%; Score 9; DB 4; Length 3;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ID 3
;:
Db 2 VD 3

RESULT 12
US-09-442-989-35
; Sequence 35, Application US/09442989
; Patent No. 6569993
; GENERAL INFORMATION:
; APPLICANT: Sledeski, Adam W.
; APPLICANT: Mencil, James J.

; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: A3113B-US
; CURRENT APPLICATION NUMBER: US/09/442,989
; CURRENT FILING DATE: 1999-11-18
; EARLIER APPLICATION NUMBER: 60/081,897
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)
; OTHER INFORMATION: FMOC-Arg (PMC)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (3)
; OTHER INFORMATION: Asp(Oallyl)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (3)
; OTHER INFORMATION: "This C-terminal amino acid is in the form of an
; OTHER INFORMATION: ester with benzyl alcohol."
US-09-442-989-35

Query Match 56.2%; Score 9; DB 4; Length 3;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ID 3
;:
Db 2 VD 3

RESULT 13
US-09-442-989-36
; Sequence 36, Application US/09442989
; Patent No. 6569993
; GENERAL INFORMATION:
; APPLICANT: Sledeski, Adam W.
; APPLICANT: Mencil, James J.
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: A3113B-US
; CURRENT APPLICATION NUMBER: US/09/442,989
; CURRENT FILING DATE: 1999-11-18
; EARLIER APPLICATION NUMBER: 60/081,897
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)
; OTHER INFORMATION: Arg (PMC)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (3)
; OTHER INFORMATION: Asp(Oallyl)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (3)
; OTHER INFORMATION: "This C-terminal amino acid is in the form of an
; OTHER INFORMATION: ester with benzyl alcohol."
US-09-442-989-36

Query Match 56.2%; Score 9; DB 4; Length 3;

us-09-674-716b-13.closed.ra1

Tue Apr 19 06:14:48 2005

Best Local Similarity 50.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0; Mismatches 1; Conservative 0;

QY 2 ID 3
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Db 2 VD 3

RESULT 14
PCT-US94-10475-7
; Sequence 7, Application PC/TUS9410475
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For
; TITLE OF INVENTION: Antagonizing Amnestic
; TITLE OF INVENTION: Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving
; TITLE OF INVENTION: the Quality of Life
; TITLE OF INVENTION: in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4"
; MEDIUM TYPE: diskette
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10475
; FILING DATE: 16 September 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA: U. S. Application
; PRIOR APPLICATION DATA: Serial No.
; PRIOR APPLICATION DATA: 08/127,904; filed
; PRIOR APPLICATION DATA: 29 September 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: None
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 626-3564 or 783-6030
; TELEFAX: (202) 783-6031
; TELEX: None
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: Unknown
PCT-US94-10475-7

Query Match 56.2%; Score 9; DB 5; Length 3;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FI 2
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Db 1 FV 2

RESULT 15
US-08-081-539-117
; Sequence 117, Application US/08081539
; Patent No. 5501982
; GENERAL INFORMATION:
; APPLICANT: Braford-Goldberg, Sarah R.

APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Olin, Peter O.
TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
TITLE OF INVENTION: Chimeric Hybrid Polypeptides
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
ADDRESSEE: Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,539
FILING DATE: 19930621
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kanady, Mary J.
REGISTRATION NUMBER: 28623
REFERENCE/DOCKET NUMBER: 2724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-081-539-117

Query Match 50.0%; Score 8; DB 1; Length 3;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 2 LD 3

Search completed: April 18, 2005, 16:17:02
Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2005, 11:10:40 ; Search time 1545.75 seconds
(without alignments)
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Title: US-09-674-716B-17

Perfect score: 348

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Searched: 4708233 seqs, 24227607955 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: gb_uni.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	348	100.0	348	6	BD232451
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5	292	83.9	740	6	AX076853
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7	277.6	79.8	410	9	HSIGKLV46
8	276	79.3	353	9	HS272080
9	276	79.3	360	9	HSTOP003
10	276	79.3	360	9	HSTOP016
11	276	79.3	360	9	HSTOP019
12	276	79.3	360	9	HSTOP220
13	276	79.3	360	9	HSTOP305
14	276	79.3	360	9	HSTOP307
15	276	79.3	377	9	HSIGKLV45
16	276	79.3	407	9	HSIGKLV31
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22	274.4	78.9	360	9	HSTOP204	X93785 H.sapiens m
23	274.4	78.9	360	9	HSTOP214	X93789 H.sapiens m
24	274.4	78.9	360	9	HSTOP217	X93790 H.sapiens m
25	274.4	78.9	360	9	HSTOP237	X93793 H.sapiens m
26	274.4	78.9	360	9	HSTOP243	X93796 H.sapiens m
27	274.4	78.9	360	9	HSTOP247	X93797 H.sapiens m
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31	274.4	78.9	360	9	HSTOP303	X93803 H.sapiens m
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37	272.8	78.4	360	9	HSTOP001	X93769 H.sapiens m
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ALIGNMENTS

RESULT 1
BD232424 348 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Antibodies against CD23, derivatives thereof and therapeutic
utilization of the same.
ACCESSION BD232424.1 GI:33042194
VERSION JP 2002514421-A/8.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 348)
AUTHORS Bonnefoy,J.Y.M.P., Crowe,S.J., Ellis,J.H., Rapson,N.T. and Shearin,J.
TITLE Antibodies against CD23, derivatives thereof and therapeutic
utilization of the same
JOURNAL Patent: JP 2002514421-A 8 21-MAY-2002;
GLAXO GROUP LTD
COMMENT OS Artificial Sequence
PN JP 2002514421-A/8
PD 21-MAY-2002
PF 07-MAY-1999 JP 2000548470
PI 09-MAY-1998 GB 9809839.5
PI JEAN YVES MARCEL PAUL BONNEFOY,SCOTT JAMES CROWE,JONATHAN PI
HENRY ELLIS,
PI NICHOLAS TIMOTHY RAPSON,JEAN SHEARIN
PC C12N15/02,A61K39/395,C07K16/28,C12N15/00
CC Description of Artificial Sequence: Humanised anti-CD23 CC
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chain variable region
CC chain variable region
FH Key Location/Qualifiers
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Location/Qualifiers
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/organism="synthetic construct"
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FEATURES
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.3e-103;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS BD232451 348 bp DNA linear PAT 17-JUL-2003
DEFINITION Antibodies against CD23, derivatives thereof and therapeutic
utilization of the same.
ACCESSION BD232451.1 GI:33042221
VERSION JP 2002514421-A/35.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 348)
AUTHORS Bonnefoy,J.Y.M.P., Crowe,S.J., Ellis,J.H., Rapson,N.T. and Shearin,J.
TITLE Antibodies against CD23, derivatives thereof and therapeutic
utilization of the same
JOURNAL Patent: JP 2002514421-A 35 21-MAY-2002;
GLAXO GROUP LTD
COMMENT OS Artificial Sequence
PN JP 2002514421-A/35
PD 21-MAY-2002
PF 07-MAY-1999 JP 2000548470
PI 09-MAY-1998 GB 9809839.5
PI JEAN YVES MARCEL PAUL BONNEFOY, SCOTT JAMES CROWE, JONATHAN PI
HENRY ELLIS,
PI NICHOLAS TIMOTHY RAPSON, JEAN SHEARIN
PC C12N15/02,A61K39/395,C07K16/28,C12N15/00
CC Description of Artificial Sequence: Humanised anti-CD23 CC
antibody light
chain variable region
CC chain variable region
FH Key Location/Qualifiers
FT source 1..348
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Best Local Similarity 100.0%; Pred. No. 3.3e-103;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
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LOCUS AX010614 348 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 17 from Patent WO958679.
ACCESSION AX010614
VERSION AX010614.1 GI:9997425
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.
TITLE Antibodies to cd23, derivatives thereof, and their therapeutic uses
JOURNAL Patent: WO 958679-A 17 18-NOV-1999;
BONNEFOY JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON
NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY
(GB); SHEARIN JEAN (US)
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Query Match 100.0%; Score 348; DB 6; Length 348;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 TACCTGCAGAACGCGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGGCA 180

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QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGACACAGATTTTACACTGAAATC 240
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RESULT 4
AX010645/c
LOCUS AX010645 348 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 48 from Patent WO9958679.
ACCESSION AX010645
VERSION AX010645.1 GI:9997454
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.
TITLE Antibodies to cd23, derivatives thereof, and their therapeutic uses
JOURNAL Patent: WO 9958679-A 48 18-NOV-1999;
Bonnefoy JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON
NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY
(GB); SHEARIN JEAN (US)

FEATURES
source
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Humanised anti-CD23 antibody light chain variable region"

ORIGIN
Query Match 100.0%; Score 348; DB 6; Length 348;
Best Local Similarity 100.0%; Pred. No. 3.3e-103; Mismatches 0; Indels 0; Gaps 0;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTCGAGAGCGGCTCC 60
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Db 348 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTCGAGAGCGGCTCC 289
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Db 288 ATCTCTGTGCTCGAGTAAAGTCTCTGTATAAGATGGGAAGACATCTTGAATTGG 229
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QY 121 TACCTGCAGAACCGGCGAGTCTCCACAGCTCTCTGATCTATTGTGATGTCACCCCGGCA 180
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Db 228 TACCTGCAGAACCGGCGAGTCTCCACAGCTCTCTGATCTATTGTGATGTCACCCCGGCA 169
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QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGACACAGATTTTACACTGAAATC 240
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Db 168 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGACACAGATTTTACACTGAAATC 109
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QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
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Db 108 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 49
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QY 301 TTCACGTTCCGCGCAAGGACCAAGGTGGAGTCAAAAGCTACGGTGGCT 348
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Db 48 TTCACGTTCCGCGCAAGGACCAAGGTGGAGTCAAAAGCTACGGTGGCT 1
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RESULT 5
AX076853
LOCUS AX076853 740 bp DNA linear PAT 02-MAR-2001
DEFINITION Sequence 1 from Patent WO0107082.
ACCESSION AX076853

VERSION AX076853.1 GI:13121524
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Knick,V.C., Stimmel,J.B. and Thurmond,L.M.
TITLE Combination of an anti-ep-cam antibody with a chemotherapeutic agent
JOURNAL Patent: WO 0107082-A 1 01-FEB-2001;
GLAXO GROUP LIMITED (GB)
FEATURES
source
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Location/Qualifiers
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/mol_type="unassigned DNA"
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24..740
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NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSLTLSKADYKHKVAC
EVTHQGLSSPVTKSFNRGSC"

ORIGIN
Query Match 83.9%; Score 292; DB 6; Length 740;
Best Local Similarity 89.9%; Pred. No. 1e-84;
Matches 313; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTCGAGAGCGGCTCC 60
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Db 81 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTCGAGAGCGGCTCC 140
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QY 61 ATCTCTGTGCTCGAGTAAAGTCTCTGTATAAGATGGGAAGACATCTTGAATTGG 120
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Db 141 ATCTCTGTGCTCGAGTAAAGTCTCTGTATAAGATGGGAAGACATCTTGAATTGG 200
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QY 121 TACCTGCAGAACCGGCGAGTCTCCACAGCTCTCTGATCTATTGTGATGTCACCCCGGCA 180
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Db 201 TACCTGCAGAACCGGCGAGTCTCCACAGCTCTCTGATCTATCAGATGTCCAACCTTGC 260
| | | | |
QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGACACAGATTTTACACTGAAATC 240
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Db 261 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGACACAGATTTTACACTGAAATC 320
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QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
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Db 321 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCTCAAAATCTAGAGATTCT 380
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QY 301 TTCACGTTCCGCGCAAGGACCAAGGTGGAGTCAAAAGCTACGGTGGCT 348
| | | | |
Db 381 CGGACGTTCCGCGCAAGGACCAAGGTGGAGTCAAAAGCTACGGTGGCT 428
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RESULT 6
AX076855/c
LOCUS AX076855 740 bp DNA linear PAT 02-MAR-2001
DEFINITION Sequence 3 from Patent WO0107082.
ACCESSION AX076855
VERSION AX076855.1 GI:13121526
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Knick,V.C., Stimmel,J.B. and Thurmond,L.M.
TITLE Combination of an anti-ep-cam antibody with a chemotherapeutic agent
JOURNAL Patent: WO 0107082-A 3 01-FEB-2001;

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/product="Ig kappa light chain (VJC)"
61..360
V_region
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J_segment
/notes="J-Kappa 1"
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Query Match 79.8%; Score 277.6; DB 9; Length 410;
Best Local Similarity 87.4%; Pred. No. 5.6e-80;
Matches 304; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCCCTGGAGAGCGGCTCC 60
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QY 61 ATCTCTCTGCTCGAGTAGAGTCTCTCTATTAAGGATGGGAAGACATATTTGAATTGG 120
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QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTGATGTCCACCCCGGCA 180
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QY 181 TCAGGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 241 TCCGGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTGATAGTATCCA 300
Db 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTGATAGTATCCA 360
QY 301 TTCAGCTTCGGCCAAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 348
Db 361 TGGAGCTTCGGCCAAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 408

RESULT 8
HSA272080 353 bp mRNA linear PRI 16-NOV-2001
LOCUS
DEFINITION Homo sapiens partial mRNA for immunoglobulin light chain variable
region -Anti-F(ab')2 autoantibody (IGVL gene), isolate SN3.
ACCESSION AJ272080.1 GI:7024356
VERSION AJ272080.1
KEYWORDS anti-F(ab')2; autoantibody; IGVL gene; immunoglobulin; light chain;
variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Elagib,K.E., Borretzen,M., Vatn,I., Natvig,J.B. and Thompson,K.M.
TITLE Characterization and V(H) sequences of human monoclonal
anti-F(ab')2 autoantibodies from normals and Sjogren's syndrome
patients
JOURNAL Clin. Immunol. 98 (1), 62-69 (2001)
MEDLINE 20581399
PUBMED 11141328
REFERENCE 2 (bases 1 to 353)
AUTHORS Elagib,K.E.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2000) Elagib K.E., Laboratory for Rheumatology
Research, Institute of Immunology, Fr. Vamsgate 1, N-172 Oslo,
NORWAY
FEATURES
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50

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 /isolate="SN3"
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 <1..353
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 /function="Anti-F(ab')2 autoantibody"
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 /db_xref="GI:7024357"
 /translations="DIVMTQSPISLPVTGPEPASISCRSSQSLHSGNYLDWYLOK
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ORIGIN

Query Match 79.3%; Score 276; DB 9; Length 353;
 Best Local Similarity 87.1%; Pred. No. 1.9e-79;
 Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 QY 1 GATATTGTGACTCAGTCTCCACTCTCCCTGCGCTCACCCCTGGAGAGCGGCTCC 60
 Db 1 GATATTGTGACTCAGTCTCCACTCTCCCTGCGCTCACCCCTGGAGAGCGGCTCC 60
 QY 61 ATCTCTGTCGCTCAGTCTCCTCTATAGGATGGAGACATACCTTGAATTGG 120
 Db 61 ATCTCTGTCGCTCAGTCTCCTCTATAGGATGGAGACATACCTTGAATTGG 120
 QY 121 TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGGCA 180
 Db 121 TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGGGTTCTATCGGCC 180
 QY 181 TCAGGGTCTCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTACATGAAATC 240
 Db 181 TCAGGGTCTCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTACATGAAATC 240
 QY 241 AGCAGAGTGGAGGTGAGGATGTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
 Db 241 AGCAGAGTGGAGGTGAGGATGTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
 QY 301 TTCACGTTTCGGCCCAAGGACCAAGTGGAGATCAACAGTACGGTGGCT 348
 Db 301 CGTACGTTTCGGCCCAAGGACCAAGTGGAGATCAACAGTACGGTGGCT 348

RESULT 9

HSTOP003 360 bp mRNA linear PRI 25-NOV-1998
 LOCUS H.sapiens mRNA for kappa immunoglobulin light chain (V-J-C region;
 clone HSTOP003).

ACCESSION

X93771.1 GI:3928404
 VERSION constant region; immunoglobulin; immunoglobulin kappa chain;
 immunoglobulin light chain; joining region; variable region.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 360)
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

Barington,T., Hough,L., Juul,L., Madsen,H.O., Ryder,L.P.,
 Heilmann,C. and Svejgaard,A.
 The progeny of a single virgin B cell predominates the human recall
 B cell response to the capsular polysaccharide of Haemophilus
 influenzae type b
 J. Immunol. 157 (9), 4016-4027 (1996)

JOURNAL

MEDLINE

PUBMED

REFERENCE

2 (bases 1 to 360)
 Barington,T.

TITLE Direct Submission
 JOURNAL Submitted (01-DEC-1995) Torben Barrington, Tissue Typing Laboratory
 7631, Rigshospitalet, National University Hospital, Tagensvej 20,
 DK-2200 Copenhagen N, DENMARK
 COMMENT On Nov 26, 1998 this sequence version replaced gi:1296757.
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 1..360
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 <1..339
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 /product="immunoglobulin kappa light chain"
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 340..360
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 /notes="constant region"

SOURCE

Query Match 79.3%; Score 276; DB 9; Length 360;
 Best Local Similarity 87.1%; Pred. No. 1.9e-79;
 Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 QY 1 GATATTGTGACTCAGTCTCCACTCTCCCTGCGCTCACCCCTGGAGAGCGGCTCC 60
 Db 1 GATATTGTGACTCAGTCTCCACTCTCCCTGCGCTCACCCCTGGAGAGCGGCTCC 60
 QY 61 ATCTCTGTCGCTCAGTCTCCTCTATAGGATGGAGACATACCTTGAATTGG 120
 Db 61 ATCTCTGTCGCTCAGTCTCCTCTATAGGATGGAGACATACCTTGAATTGG 120
 QY 121 TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGGCA 180
 Db 121 TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGGGTTCTATCGGCC 180
 QY 181 TCAGGGTCTCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTACATGAAATC 240
 Db 181 TCAGGGTCTCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTACATGAAATC 240
 QY 241 AGCAGAGTGGAGGTGAGGATGTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
 Db 241 AGTAGAGTGGAGGTGAGGATGTGGGGTTTATTACTGTCAACAGCTGTACAAACCCCA 300
 QY 301 TTCACGTTTCGGCCCAAGGACCAAGTGGAGATCAACAGTACGGTGGCT 348
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ORIGIN

Query Match 79.3%; Score 276; DB 9; Length 360;
 Best Local Similarity 87.1%; Pred. No. 1.9e-79;
 Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 QY 1 GATATTGTGACTCAGTCTCCACTCTCCCTGCGCTCACCCCTGGAGAGCGGCTCC 60
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 Db 61 ATCTCTGTCGCTCAGTCTCCTCTATAGGATGGAGACATACCTTGAATTGG 120
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 Db 121 TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGGGTTCTATCGGCC 180
 QY 181 TCAGGGTCTCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTACATGAAATC 240
 Db 181 TCAGGGTCTCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTACATGAAATC 240
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 Db 241 AGTAGAGTGGAGGTGAGGATGTGGGGTTTATTACTGTCAACAGCTGTACAAACCCCA 300
 QY 301 TTCACGTTTCGGCCCAAGGACCAAGTGGAGATCAACAGTACGGTGGCT 348
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RESULT 10

HSTOP016 360 bp mRNA linear PRI 25-NOV-1998
 LOCUS H.sapiens mRNA for kappa immunoglobulin light chain (V-J-C region;
 clone HSTOP016).

ACCESSION

X93774.1 GI:3928407
 VERSION constant region; immunoglobulin; immunoglobulin kappa chain;
 immunoglobulin light chain; joining region; variable region.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 360)
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Barington,T., Hough,L., Juul,L., Madsen,H.O., Ryder,L.P.,
 Heilmann,C. and Svejgaard,A.
 The progeny of a single virgin B cell predominates the human recall
 B cell response to the capsular polysaccharide of Haemophilus

JOURNAL

MEDLINE

PUBMED

REFERENCE

2 (bases 1 to 360)
 Barington,T.

influenzae type b
J. Immunol. 157 (9), 4016-4027 (1996)
97047794
PUBMED
8892635
REFERENCE
AUTHORS
JOURNAL
TITLE
Barrington, T.
Direct Submission
Submitted (01-DEC-1995) Torben Barrington, Tissue Typing Laboratory
7631, Rigshospitalet, National University Hospital, Tagensvej 20,
DK-2200 Copenhagen N, DENMARK
On Nov 26, 1998 this sequence version replaced gi:1296760.

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Best Local Similarity 87.1%; Pred. No. 1.9e-79;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCGCTCACCCCTGGAGAGCGGCTCC 60
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DB 121 TACCTGAGAGCCAGGAGCTCCACAGCTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 180
QY 181 TCAGGGTCTCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 181 TCAGGGTCTCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATCTGTCAACAGCTGGTAGATATCCA 300
DB 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATCTGTCAACAGCTGGTAGATATCCA 300
QY 301 TTCACGTTGGCCAAAGGACCAAGCTGAGATCAACAGTACGTTGGCT 348
DB 301 TTCACGTTGGCCAAAGTGGATATCAACAGTACGTTGGCT 348

RESULT 11
HSTOP019
LOCUS
DEFINITION
H.sapiens mRNA for kappa immunoglobulin light chain (V-J-C region;
clone HSTOP019).
ACCESSION
X93776
VERSION
X93776.1 GI:3928409
KEYWORDS
constant region; immunoglobulin; immunoglobulin kappa chain;
immunoglobulin light chain; joining region; variable region.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
8892635
REFERENCE
AUTHORS
JOURNAL
TITLE
Barrington, T.
Direct Submission
Submitted (01-DEC-1995) Torben Barrington, Tissue Typing Laboratory
7631, Rigshospitalet, National University Hospital, Tagensvej 20,
DK-2200 Copenhagen N, DENMARK
On Nov 26, 1998 this sequence version replaced gi:1296762.

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ORIGIN
Query Match 79.3%; Score 276; DB 9; Length 360;
Best Local Similarity 87.1%; Pred. No. 1.9e-79;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCGCTCACCCCTGGAGAGCGGCTCC 60
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCGCTCACCCCTGGAGAGCGGCTCC 60
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DB 61 ATCTCTCTGCTCGAGTAAAGTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120
QY 121 TACCTGAGAGCCAGGAGCTCCACAGCTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 180
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QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATCTGTCAACAGCTGGTAGATATCCA 300
DB 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATCTGTCAACAGCTGGTAGATATCCA 300
QY 301 TTCACGTTGGCCAAAGGACCAAGCTGAGATCAACAGTACGTTGGCT 348
DB 301 TTCACGTTGGCCAAAGTGGATATCAACAGTACGTTGGCT 348

RESULT 12
HSTOP220
LOCUS
DEFINITION
H.sapiens mRNA for kappa immunoglobulin light chain (V-J-C region;
clone HSTOP220).
ACCESSION
X93792

Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 360)
Barrington, T., Houge, L., Juul, L., Madsen, H.O., Ryder, L.P.,
Heilmann, C., and Svejgaard, A.
The progeny of a single virgin B cell predominates the human recall
B cell response to the capsular polysaccharide of Haemophilus
influenzae type b
J. Immunol. 157 (9), 4016-4027 (1996)
97047794
PUBMED
8892635
REFERENCE
AUTHORS
JOURNAL
TITLE
Barrington, T.
Direct Submission
Submitted (01-DEC-1995) Torben Barrington, Tissue Typing Laboratory
7631, Rigshospitalet, National University Hospital, Tagensvej 20,
DK-2200 Copenhagen N, DENMARK
On Nov 26, 1998 this sequence version replaced gi:1296762.

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/gene="V-kappa-A3/A19 and J-kappa-3"
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340..>360
/genes="V-kappa-A3/A19 and J-kappa-3"
/note="constant region"

ORIGIN
Query Match 79.3%; Score 276; DB 9; Length 360;
Best Local Similarity 87.1%; Pred. No. 1.9e-79;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCGCTCACCCCTGGAGAGCGGCTCC 60
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCGCTCACCCCTGGAGAGCGGCTCC 60
QY 61 ATCTCTCTGCTCGAGTAAAGTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120
DB 61 ATCTCTCTGCTCGAGTAAAGTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120
QY 121 TACCTGAGAGCCAGGAGCTCCACAGCTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 180
DB 121 TACCTGAGAGCCAGGAGCTCCACAGCTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 180
QY 181 TCAGGGTCTCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 181 TCAGGGTCTCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATCTGTCAACAGCTGGTAGATATCCA 300
DB 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATCTGTCAACAGCTGGTAGATATCCA 300
QY 301 TTCACGTTGGCCAAAGGACCAAGCTGAGATCAACAGTACGTTGGCT 348
DB 301 TTCACGTTGGCCAAAGTGGATATCAACAGTACGTTGGCT 348

RESULT 12
HSTOP220
LOCUS
DEFINITION
H.sapiens mRNA for kappa immunoglobulin light chain (V-J-C region;
clone HSTOP220).
ACCESSION
X93792

VERSION X93792.1 GI:3928425
 KEYWORDS constant region; immunoglobulin; immunoglobulin kappa chain; immunoglobulin light chain; joining region; variable region.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 360)
 AUTHORS Barington, T., Houghs, L., Juul, L., Madsen, H.O., Ryder, L.P., Heilmann, C. and Svejgaard, A.
 TITLE The progeny of a single virgin B cell predominates the human recall B cell response to the capsular polysaccharide of Haemophilus influenzae type b
 JOURNAL J. Immunol. 157 (9), 4016-4027 (1996)
 MEDLINE 97047794
 PUBMED 8892635
 REFERENCE 2 (bases 1 to 360)
 AUTHORS Barington, T.
 TITLE Direct Submission
 JOURNAL Submitted (01-DEC-1995) Torben Barrington, Tissue Typing Laboratory 7631, Rigshospitalet, National University Hospital, Tagensvej 20, DK-2200 Copenhagen N, DENMARK
 COMMENT On Nov 26, 1998 this sequence version replaced gi:1296778.
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="2"
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 /tissue_type="peripheral blood"
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 <1..339
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 /product="immunoglobulin kappa light chain"
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 /note="constant region"
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 Query Match 79.3%; Score 276; DB 9; Length 360;
 Best Local Similarity 87.1%; Pred. No. 1.9e-79;
 Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCAACCCCTGGAGCGGCTCC 60
 DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCAACCCCTGGAGCGGCTCC 60
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 QY 121 TACCTGCAGAACGACGAGCTCCACAGCTCCTGATCTATTGTGATGTCACCCGGGCA 180
 DB 121 TACCTGCAGAACGACGAGCTCCACAGCTCCTGATCTATTGTGATGTCACCCGGGCA 180
 QY 181 TCAGGGGTCCCTGCACAGGTTCACTGTCAGTGGATCAGGCACAGATTTTACCTGAAATC 240
 DB 181 TCAGGGGTCCCTGCACAGGTTCACTGTCAGTGGATCAGGCACAGATTTTACCTGAAATC 240
 QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
 DB 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
 QY 301 TTCACGCTTCGGCCCAAGGACCAAGGTGGAGATCAAAAGTACGGTGGCT 348
 DB 301 TTCACGCTTCGGCCCAAGGACCAAGGTGGAGATCAAAAGTACGGTGGCT 348

RESULT 13
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 LOCUS H. sapiens mRNA for kappa immunoglobulin light chain (V-J-C region; clone HSTOP305).
 DEFINITION X93805.1 GI:3928439
 VERSION constant region; immunoglobulin; immunoglobulin kappa chain; immunoglobulin light chain; joining region; variable region.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 360)
 AUTHORS Barington, T., Houghs, L., Juul, L., Madsen, H.O., Ryder, L.P., Heilmann, C. and Svejgaard, A.
 TITLE The progeny of a single virgin B cell predominates the human recall B cell response to the capsular polysaccharide of Haemophilus influenzae type b
 JOURNAL J. Immunol. 157 (9), 4016-4027 (1996)
 MEDLINE 97047794
 PUBMED 8892635
 REFERENCE 2 (bases 1 to 360)
 AUTHORS Barington, T.
 TITLE Direct Submission
 JOURNAL Submitted (01-DEC-1995) Torben Barrington, Tissue Typing Laboratory 7631, Rigshospitalet, National University Hospital, Tagensvej 20, DK-2200 Copenhagen N, DENMARK
 COMMENT On Nov 26, 1998 this sequence version replaced gi:1296791.
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="2"
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 /tissue_type="peripheral blood"
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 /gene="V-kappa-A3/A19 and J-kappa-3"
 <1..339
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 /product="immunoglobulin kappa light chain"
 /note="variable region and joining region"
 340..>360
 /gene="V-kappa-A3/A19 and J-kappa-3"
 /note="constant region"
 ORIGIN
 Query Match 79.3%; Score 276; DB 9; Length 360;
 Best Local Similarity 87.1%; Pred. No. 1.9e-79;
 Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCAACCCCTGGAGCGGCTCC 60
 DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCAACCCCTGGAGCGGCTCC 60
 QY 61 ATCTCTGTGCTCGAGTAAAGTCTCCTGTATAAGGATGGGAGACATCTTGAATTGG 120
 DB 61 ATCTCTGTGAGGCTCTAGTCAGAGCCCTCCTGCATAGTAATGGCAACATCTATTTCGATTGG 120
 QY 121 TACCTGCAGAACGACGAGCTCCACAGCTCCTGATCTATTGTGATGTCACCCGGGCA 180
 DB 121 TACCTGCAGAACGACGAGCTCCACAGCTCCTGATCTATTGTGATGTCACCCGGGCA 180
 QY 181 TCAGGGGTCCCTGCACAGGTTCACTGTCAGTGGATCAGGCACAGATTTTACCTGAAATC 240
 DB 181 TCAGGGGTCCCTGCACAGGTTCACTGTCAGTGGATCAGGCACAGATTTTACCTGAAATC 240
 QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
 DB 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300

Qy 121 TACCTGCAGAACCCAGGGCAGTCTCCACAGCTCCTGATCTATTGTGATGTCCACCCGGGCA 180
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Db 150 TACCTGCAGAACCCAGGGCAGTCTCCACAGCTCCTGATCTATTGTGGTTCTAATCGGGCC 209
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Qy 181 TCAGGGGTCCCTGACACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
|||
Db 210 TCCGGGGTCCCAGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 269
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Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
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Db 270 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGCATGCAAGTTTACAAATCCG 329
|||
Qy 301 TTCACGTTTCGGCCCAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348
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Db 330 CTCACTTTCGGCGCGGGACCAAGGTGGAGATCAAAACGAACTGTGGCT 377
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Job time : 1546.75 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 1365.64 Seconds
(without alignments)
9699.731 Million cell updates/sec

Title: US-09-674-716B-17

Perfect score: 348

Sequence: 1 gatattgtgatcactcagtc.....agatcaaacgtacgtggct 348

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_ges1.*
9: gb_ges2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	277.6	79.8	597	6	CD689298 EST5820 h
2	277.6	79.8	743	6	CD987308 AGENCOURT
3	277.6	79.8	990	4	BI838327 601083265
4	276	79.3	600	6	CD700169 EST16693
5	276	79.3	605	6	CD698049 EST14572
6	276	79.3	817	6	CD957285 AGENCOURT
7	274.6	78.9	475	6	CD699289 EST15812
8	274.4	78.9	498	6	CD699812 EST16336
9	274.4	78.9	583	6	CD684087 EST607 hu
10	274.4	78.9	791	6	CD955891 AGENCOURT
11	274.4	78.9	830	6	CD985612 AGENCOURT
12	272.8	78.4	454	2	AW406883 UI-HF-BL0
13	272.8	78.4	524	6	CD700306 EST16830
14	272.8	78.4	616	6	CD703137 EST19728
15	272.8	78.4	700	6	CD987545 AGENCOURT
16	272.8	78.4	771	6	CD956254 AGENCOURT
17	272.8	78.4	995	5	BQ712430 AGENCOURT
18	271.2	77.9	522	4	BM511309 iJ46b08.y
19	271.2	77.9	731	6	CD985070 AGENCOURT
20	271.2	77.9	757	6	CD985283 AGENCOURT
21	271.2	77.9	773	6	CD959401 AGENCOURT
22	271.2	77.9	815	6	CD985592 AGENCOURT
23	269.6	77.5	569	6	CD705909 EST22436
24	269.6	77.5	734	6	CD957433 AGENCOURT

25	269.6	77.5	739	6	CB986287
26	269.6	77.5	743	6	CB956921
27	269.6	77.5	751	4	BG542438 602569513
28	268.6	77.2	554	6	CD696178 EST12701
29	268.2	77.1	363	1	AA464313 zX78C12.f
30	268	77.0	442	1	AA405415 zu56D02.f
31	268	77.0	488	2	AW405725 UI-HF-BL0
32	268	77.0	512	6	CD707724 EST24251
33	268	77.0	565	6	CD691296 EST7819 h
34	268	77.0	623	6	CD694404 EST10927
35	268	77.0	634	4	BM783161 K-EST0061
36	268	77.0	658	6	CB958484 AGENCOURT
37	268	77.0	719	6	CB958133 AGENCOURT
38	268	77.0	731	6	CB955606 AGENCOURT
39	268	77.0	743	6	CB957183 AGENCOURT
40	268	77.0	766	6	CB956983 AGENCOURT
41	268	77.0	839	6	CB986712 AGENCOURT
42	267	76.7	491	2	BF174573 MYE3409a
43	266.4	76.6	456	2	AW404683 UI-HF-BL0
44	266.4	76.6	500	6	CD696096 EST12619
45	266.4	76.6	512	6	CD709518 EST26045

ALIGNMENTS

RESULT 1

LOCUS CD689298 597 bp mRNA linear EST 25-JUN-2003
DEFINITION EST5820 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD689298
VERSION CD689298.1 GI:32208911
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 597)
AUTHORS Liu,X.-O., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center

Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsus.edu.cn.

Location/Qualifiers
1..597
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN
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Best Local Similarity 87.4%; Pred. No. 2.1e-72;
Matches 304; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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110 GATATTGTGATGCTCAGTCTCCACTCTCCCTCCCGTCACCCCTGAGAGCGGCTCC 169
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61 ATCTCTCTGCTCGCTAGAGTCTCCTGTATAAGGATGGGAAGACATCTTGAATTGG 120
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170 ATCTCTCTGAGGCTTAGTCAGAGCCCTCTGCATAGTAATGATACAACTATTTGGATTGG 229
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121 TACCTGCAGAAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTATTGATGTCCACCCCGGCA 180
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Db 230 TACCTGAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGGTCTTAATCGGCG 289
 Qy 181 TCAGGGGTCCCTGACAGGTTCAAGTGGGATCAGGACAGATTTTACATGAAATC 240
 Db 290 TCGGGGTCCCTGACAGGTTCAAGTGGGATCAGGACAGATTTTACATGAAATC 349
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 Db 350 AGCAGAGTGAGGCTGAGATGTTGGGTTTATTACTGTCACAGCTGCTAGATATCCA 409
 Qy 301 TTCACGTTGGCCCAAGGACCAAGGTGGAGATCAAAACGTACGTTGGCT 348
 Db 410 TACACGTTGGCCCAAGGACCAAGGTGGAGATCAAAACGTACGTTGGCT 457

RESULT 2
 CB987308 743 bp mRNA linear EST 01-MAY-2003
 LOCUS
 DEFINITION
 AGENCOURT_13643139 NIH_MGC_184 Homo sapiens cDNA clone
 IMAGE:30328074 5', mRNA sequence.

CB987308 1 GI:30281828
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 743)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDCM138 row: b column: 19
 High quality sequence stop: 557.

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 /clone_lib="NIH_MGC_184"
 /notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
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 Library is oligo-dT primed and directionally cloned. cDNA
 was prepared from a glandular pool of tissues from thyroid,
 parathyroid, adrenal, cortex and pineal gland. 5' and 3'
 adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGACGCGGCGGCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.38
 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN
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 Best Local Similarity 87.4%; Pred. No. 2.2e-72;
 Matches 304; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCACCCCTGAGAGCGGCTCC 60
 Db 94 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCACCCCTGAGAGCGGCTCC 153

Qy 61 ATCTCTGCTGCTCGAGTAAGAGTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120
 Db 154 ATCTCTGCTGCTGAGTCTAGTCAGAGCTCTGTATAGTATATGATACACTTATTGGATGG 213
 Qy 121 TACCTGCAGAAAGCCAGGCGAGTCTCCACAGCTCTGATCTATTTGATGTCCACCCGGGCA 180
 Db 214 TACCTGCAGAAAGCCAGGCGAGTCTCCACAGCTCTGATCTATTTGGTCTTAAATCGGGCC 273
 Qy 181 TCAGGGTCCCTGACAGGTTCAAGTGGGATCAGGCACAGATTTTACACTGAAATC 240
 Db 274 TCCGGGTCCCTGACAGGTTCAAGTGGGATCAGGCACAGATTTTACACTGAAATC 333
 Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
 Db 334 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 393
 Qy 301 TTCAGTTCGGCCCAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348
 Db 394 CTCACCTTTCCGGCGGAGGACCAAGGTGGAGATCAAAACGTGGCT 441

RESULT 3
 BI838327 990 bp mRNA linear EST 04-OCT-2001
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 DEFINITION
 603083265F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222297 5',
 mRNA sequence.

BI838327 1 GI:15949877
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 990)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM1559 row: a column: 18
 High quality sequence stop: 740.

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 /db_xref="taxon:9606"
 /clone="IMAGE:5222297"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_120"
 /note="Organ: pooled pancreas and spleen; Vector:
 pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 source anonymous pool of spleen and pancreas from 28 yo
 male. Library is oligo-dT primed and directionally cloned
 (EcoRV site is destroyed upon cloning). Average insert
 size 1.5 kb, insert size range 1-2.5 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen) Research Genetics
 tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 79.8%; Score 277.6; DB 4; Length 990;
 Best Local Similarity 87.4%; Pred. No. 2.4e-72;
 Matches 304; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCACCCCTGAGAGCGGCTCC 60


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Db      87  GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCTGGAGAGCGGCGCTCC 146
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Qy      121  TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGGCA 180
Db      207  TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCTTAATCGGGCC 266
Qy      181  TCAGGGTCTCCCTGACAGTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 240
Db      267  TCGGGGTCTCTGACAGTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 326
Qy      241  AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db      327  AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCCGTGAGTCTTACAAACCCG 386
Qy      301  TTCAGTTCGGCCCAAGGACCAAGGTGGAGATCAACAGTACGGTGGCT 348
Db      387  CTCACCTTCGGCGAGGACCAAGGTGGAGATCAACAGTACGGTGGCT 434

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RESULT 4
LOCUS CD700169 600 bp mRNA linear EST 25-JUN-2003
DEFINITION EST16693 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD700169
VERSION CD700169.1 GI:32230142
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 600)
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.

FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
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/notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN
Query Match 79.3%; Score 276; DB 6; Length 600;
Best Local Similarity 87.1%; Pred. No. 6.5e-72;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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Qy      61  ATCTCTCTGCTCGCTCGAGTAAGAGTCTCTGTATAAGGATGGGAAGACATACCTTGAATTGG 120
Db      173  ATCTCTCTGAGGTCTAGTACAGAGCTCTCTGATAGGAATGGATACAACTATTGGATTGG 232
Qy      121  TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGGCA 180
Db      233  TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGGTTCTTAATCGGGCC 292

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Qy      181  TCAGGGTCTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
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Db      353  AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTGATGCAAGCTCTTACAACTCCT 412
Qy      301  TTCACGTTCCGGCCCAAGGACCAAGGTGGAGATCAACAGCTACGGTGGCT 348
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RESULT 5
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DEFINITION EST14572 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD698049
VERSION CD698049.1 GI:32226103
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 605)
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.

TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.

FEATURES
source
1. .605
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN
Query Match 79.3%; Score 276; DB 6; Length 605;
Best Local Similarity 87.1%; Pred. No. 6.5e-72;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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Qy      1  GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCTGGAGAGCGGCGCTCC 60
Db      112  GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCTGGAGAGCGGCGCTCC 171
Qy      61  ATCTCTCTGCTCGCTCGAGTAAGAGTCTCTGTATAAGGATGGGAAGACATACCTTGAATTGG 120
Db      172  ATCTCTCTGAGGTCTAGTACAGAGCTCTCTGTATAGTAATGGACACAGTATTGGATTGG 231
Qy      121  TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGGCA 180
Db      232  TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGGTTCTACTCGGGCC 291
Qy      181  TCAGGGTCTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db      292  TCGGGGTCTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 351
Qy      241  AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db      352  ACCAGAGTGGAGGCTGACGATGTTGGGTTTATTACTGTGATGCGGCGCTACAAATCCT 411
Qy      301  TTCACGTTCCGGCCCAAGGACCAAGGTGGAGATCAACAGTACGGTGGCT 348

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Db 412 CCCACTTTCCGGCGGAGGACCAAGGTGGAGATCAACAGCACTGTGGCT 459
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CB957285 817 bp mRNA linear EST 29-APR-2003
AGENCOURT 13666811 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30354094 5', mRNA sequence.
CB957285
CB957285 1 GI:30213402
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 817)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs@emall.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM155 row: n column: 23
High quality sequence stop: 534.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30354094"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccattggcc); Site 2: SfiI (ggcgctggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATATGCCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

Db 412 CCCACTTTCCGGCGGAGGACCAAGGTGGAGATCAACAGCACTGTGGCT 459
|||||
CB957285 817 bp mRNA linear EST 29-APR-2003
AGENCOURT 13666811 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30354094 5', mRNA sequence.
CB957285
CB957285 1 GI:30213402
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 817)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs@emall.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM155 row: n column: 23
High quality sequence stop: 534.
FEATURES
source
Location/Qualifiers
1..817
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30354094"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccattggcc); Site 2: SfiI (ggcgctggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATATGCCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

Query Match 79.3%; Score 276; DB 6; Length 817;
Best Local Similarity 87.1%; Pred. No. 7e-72;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCCCTGGAGAGCGGCTCC 60
DB 96 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCCCTGGAGAGCGGCTCC 155
QY 61 ATCTCTGTGCTCGAGTAAAGTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 120
DB 156 ATCTCTGTGCTCGAGTAAAGTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 215
QY 121 TACCTGAGAGAGCCAGGCGGAGTCTCCACAGCTCTCTGATCTATTTGATGTCCACCCCGGCA 180
DB 216 TACCTGAGAGAGCCAGGCGGAGTCTCCACAGCTCTCTGATCTATTTGGTTCTATCGGCC 275
QY 181 TCAGGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGACAGATTTTACATGAAATC 240
DB 276 TCCGGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGACAGATTTTACATGAAATC 335

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QY 241 ACCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
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QY 301 TTCAGTTTCGGCCCAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348
DB 396 CTCACCTTTCGGGGAGGAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 443
RESULT 7
CD699289 475 bp mRNA linear EST 25-JUN-2003
LOCUS EST15812 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION CD699289
ACCESSION CD699289
VERSION CD699289.1 GI:32228425
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 475)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzaums.edu.cn.
FEATURES
source
Location/Qualifiers
1..475
/organism="Homo sapiens"
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/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

Query Match 78.9%; Score 274.6; DB 6; Length 475;
Best Local Similarity 87.2%; Pred. No. 1.6e-71;
Matches 301; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCCCTGGAGAGCGGCTCC 60
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DB 191 ATCTCTGTGCTCGAGTAAAGTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 250
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DB 251 TACCTGAGAGAGCCAGGCGGAGTCTCCACAGCTCTCTGATCTATTTGGTTCTAATCGGCC 310
QY 181 TCAGGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGACAGATTTTACATGAAATC 240
DB 311 TCCGGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGACAGATTTTACATGAAATC 370
QY 241 ACCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
DB 371 ACCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 430
QY 301 TTCACGTTCCGGCAAGGACCAAGGTGGAGATCAAAACGTACGGTGG 345
DB 431 CCGACGTTCCGGCAAGGACCAAGGTGGAGATCAAAACGTACGGTGG 475

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RESULT 8
CD699812          498 bp  mRNA  linear  EST 25-JUN-2003
LOCUS             EST16336 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION         CD699812
VERSION           CD699812.1 GI:32229450
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 498)
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE
Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL
COMMENT
Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
FEATURES
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/notes="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"
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Query Match 78.9%; Score 274.4; DB 6; Length 498;
Best Local Similarity 86.8%; Pred. No. 1.9e-71;
Matches 302; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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Db 233 TACCTGAGAGCCAGCGAGTCTCCACAGTCTCTGATCTATTGTGGGTTCTAATCGGGCC 292
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Qy 241 AGCAGAGTGGAGGTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 353 AGTAGAGTGGAGGTGAGGATGTTGGGGTTTATTACTGTCTTGTCAATCTCTACAAATTCG 412
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LOCUS             EST607 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION         CD684087
VERSION           CD684087.1 GI:32198747
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 583)
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE
Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL
COMMENT
Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
FEATURES
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/notes="ESTs generated from a normal nasopharynx cDNA
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Query Match 78.9%; Score 274.4; DB 6; Length 583;
Best Local Similarity 86.8%; Pred. No. 1.9e-71;
Matches 302; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCCCTGAGAGCGCGCTCC 60
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Db 181 ATCTCTGCTCGATGCTAGTCAGAGCTCTCTGATAGTAAAGAAACAGCAATTTGGATTGG 240
Qy 121 TACCTGAGAGCCAGCGAGTCTCCACAGTCTCTGATCTATTGTATGTCACCCCGGCA 180
Db 241 TACCTGAGAGCCAGCGAGTCTCCACAGTCTCTGATCTATTGTGGTTCTAATCGGGCC 300
Qy 181 TCAGGGGTCCCTGCAGCTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 240
Db 301 TCCGGGGTCCCTGCAGCTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 360
Qy 241 AGCAGAGTGGAGCTCAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 361 AGCAGAGTGGAGCTCAGGATGTTGGGGTTTATTACTGTATGCAAGTCTCAAAATTCG 420
Qy 301 TTCACGTTCCGGCCNAGGACCAAGTGGAGATCAAACTACGTTGGCT 348
Db 421 TACACTTTCGGCCNAGGACCAAGTGGAGATCAAACTACGTTGGCT 468

RESULT 10
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LOCUS             AGENCOURT 13777308 NIH MGC 184 Homo sapiens cDNA clone
DEFINITION
IMAGE:30350668 5', mRNA sequence.
ACCESSION         CB955891
VERSION           CB955891.1 GI:30212009
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 791)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.

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cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM146 row: p column: 05
 High quality sequence stop: 520.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
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 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 184"
 /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
 SfiI (ggccattatggcc); Site 2: SfiI (ggccgctcgcc);
 Library is oligo-dr primed and directionally cloned. cDNA
 was prepared from a glandular pool of tissues from thyroid,
 parathyroid, adrenal, cortex and pineal gland. 5' and 3'
 adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.38
 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 78.9%; Score 274.4; DB 6; Length 791;
 Best Local Similarity 86.8%; Pred. No. 2.1e-71;
 Matches 302; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 60
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 QY 61 ATCTCTGCTGCTCGAGTAGAGTCTCCTGTATAGGATGGGAGACATCTTGATTGG 120
 DB 155 ATCTCTGCTGCTCGAGTAGAGTCTCCTGTATAGGATGGGAGACATCTTGATTGG 214
 QY 121 TACTCTGAGAAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGTATGTCACCCGGGCA 180
 DB 215 TACTCTGAGAAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGTACTTCTAATCGGCC 274
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 QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTGGCT 348
 DB 335 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTGGCT 394
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 AGENCOURT 13459280 NIH_MGC_184 Homo sapiens cDNA clone
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 CB985612
 CB985612.1 GI:30280136
 EST.
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 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 830)
 AUTHORS
 NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE JOURNAL COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM133 row: g column: 11
 High quality sequence stop: 412.

FEATURES

Location/Qualifiers
 1. 830

/organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone="IMAGE:30326266"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 184"
 /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
 SfiI (ggccattatggcc); Site 2: SfiI (ggccgctcgcc);
 Library is oligo-dr primed and directionally cloned. cDNA
 was prepared from a glandular pool of tissues from thyroid,
 parathyroid, adrenal, cortex and pineal gland. 5' and 3'
 adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGGAGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.38
 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 78.9%; Score 274.4; DB 6; Length 830;
 Best Local Similarity 86.8%; Pred. No. 2.1e-71;
 Matches 302; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 60
 DB 94 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 153
 QY 61 ATCTCTGCTGCTCGAGTAAGAGTCTCCTGTATAGGATGGGAGACATCTTGAAATTGG 120
 DB 154 ATCTCTGCTGCTCGAGTAAGAGTCTCCTGTATAGGATGGGAGACATCTTGAAATTGG 213
 QY 121 TACTCTGAGAAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGTATGTCACCCGGGCA 180
 DB 214 TACTCTGAGAAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGGGTTCTAATCGGGCC 273
 QY 181 TCAGGGGTCTCCGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 240
 DB 274 TCCGGGGTCTCCGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 333
 QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTGGATATCCA 300
 DB 334 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTGGATATCCA 393
 QY 301 TTACGTTCCGGCCAAAGGCAAGGTCGAGATCAAAAGCTACCGTGGCT 348
 DB 394 AGGACGTTCCGGCCAAAGGCAAGGTCGAGATCAAAAGCTACCGTGGCT 441

RESULT 12
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 IMAGE:3061493 5', mRNA sequence.
 AW406883
 AW406883.1 GI:6925940
 EST.

AW406883 454 bp mRNA linear EST 16-FEB-2000
 UI-HF-BL0-adg-h-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
 IMAGE:3061493 5', mRNA sequence.
 AW406883
 AW406883.1 GI:6925940
 EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 454)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
1..454
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3061493"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_37"
/notes="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldi, Ph.D. and M. Bento Soares, Ph.D."

Query Match 78.4%; Score 272.8; DB 2; Length 454;
Best Local Similarity 86.5%; Pred. No. 5.6e-71;
Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 60
Db 16 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 75

QY 61 ATCTCTGTCGTCGAGTAGAGTCTCTGTATAGGATGGGAGACATATTTGAATTGG 120
Db 76 ATCTCTGTCAGGTTCTAGTCAGAGCTCTGCATAGTAAGGATACAACTATTTGGATTGG 135

QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTGATCTATTATTGATGTCCACCCGGGCA 180
Db 136 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTGATCTATTATTGGTTCTAATCGGGC 195

QY 181 TCAGGGGTCCCTCAGAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 196 TCCGGGGTCCCTCAGAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 255

QY 241 AGCAGAGTGAGGCTGAGGATGTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 256 AACAAAGTGAGGCTGAGGATGTGGGTTTATTACTGTCAACAGCTGTACAAATCTCT 315

QY 301 TTCACGTTCCGGCCAAAGGACCAAGGTGGAGATCAAAACGTACCGTGGCT 348
Db 316 CAGACGTTCCGGCCAAAGGACCAAGGTGGAAATCAACAGCACTGTGGCT 363

RESULT 13
LOCUS CD700306
DEFINITION EST16830 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD700306
VERSION CD700306.1 GI:32230410
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 524)
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yzeng@gzsums.edu.cn
Location/Qualifiers
1..524
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

Query Match 78.4%; Score 272.8; DB 6; Length 524;
Best Local Similarity 86.5%; Pred. No. 5.9e-71;
Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 60
Db 116 GATATTGTGATGAGGAGTCTCCACTCTCTCTGCCGTCACCCCTGGAGAGCGGCTCC 175

QY 61 ATCTCTGTCGTCGAGTAGAGTCTCTGTATAGGATGGGAGACATATTTGAATTGG 120
Db 176 ATCTCTGTCAGGTTCTAGTCAGAGCTCTCTTATAGTAATGGATACACCTATTTGGATTGG 235

QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTGATCTATTATTGATGTCCACCCGGGCA 180
Db 236 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTGATCTATTATTGATGTCCACCCGGG 295

QY 181 TCAGGGGTCCCTCAGAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 296 TCCGGGGTCCCTCAGAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGCAATC 355

QY 241 AGCAGAGTGAGGCTGAGGATGTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 356 AGCAGAGTGAGGCTGAAGATGTGGGTTTATTACTGTCAACAGCTGTACAGACTCCC 415

QY 301 TTCACGTTCCGGCCAAAGGACCAAGGTGGAGATCAAAACGTACCGTGGCT 348
Db 416 CTCACGTTCCGGCCAAAGGACCAAGGTGGAAATCAAAACGAACTGTGGCT 463

RESULT 14
LOCUS CD703137
DEFINITION EST19728 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD703137
VERSION CD703137.1 GI:32233831
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 616)
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng

Cancer Center
 Sun Yat-sen University
 651 Dongfeng Road East, Guangzhou 510060, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzeng@zsu.edu.cn.

FEATURES
 source
 Location/Qualifiers
 1. .616
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="normal nasopharynx"
 /clone_lib="human nasopharynx"
 /note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN
 Query Match 78.4%; Score 272.8; DB 6; Length 616;
 Best Local Similarity 86.5%; Pred. No. 6e-71;
 Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 60
 DB 123 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 182
 QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCCTGTATAGGATGGAGACATACCTGGAATTGG 120
 DB 183 ATCTCTGTGCTCGAGTCTCAGAGCCCTTGCATACCTAAATGGATACAACTATTITGGATTGG 242
 QY 121 TACTCTGAGAGCAGGAGAGTCTCCACAGCTCCTGATCTATTGTATGTCACCCCGGCA 180
 DB 243 TACTCTGAGAGCAGGAGAGTCTCCACAGCTCCTGATCTATTGTGTTCTAATCGGGC 302
 QY 181 TCAGGGGTCCCTGACAGGTTCACTGAGTGGATAGGACAGATTTTACCTGAAATC 240
 DB 303 TCCGGGGTCCCTGACAGGTTCACTGAGTGGATAGGACAGATTTTACCTGAAATC 362
 QY 241 AGCAGATGAGGCTGAGGATGTTGGGTTTATTACTGTCACAGCTGGTAGAGTATCCA 300
 DB 363 AGCAGATGAGGCTGAGGATGTTGGGTTTATTACTGATGATGATCTTACAACTCG 422
 QY 301 TTCACGTTCCGCAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348
 DB 423 TACACTTTGGCCAGTGGACCAAGCTGGAGATCAACGAACTGTGGCT 470

RESULT 15
 CB987545
 LOCUS
 DEFINITION
 AGENCOURT 13647879 NIH_MGC_184 Homo sapiens cDNA clone
 IMAGE:30328321 5', mRNA sequence.

ACCESSION
 VERSION
 CB987545.1 GI:30282065
 KEYWORDS
 EST.

SOURCE
 Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 700)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs@mail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDCM138 row: m column: 02
 High quality sequence stop: 542.

FEATURES
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 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clones="IMAGE:30328321"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_184"
 /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: SfiI (ggccattatggc); Site_2: SfiI (ggccgcttcggcc); cDNA library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 78.4%; Score 272.8; DB 6; Length 700;
 Best Local Similarity 86.5%; Pred. No. 6.2e-71;
 Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 60
 DB 94 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 153
 QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCCTGTATAGGATGGAGACATACCTTGAATTGG 120
 DB 154 ATCTCTGTGCTCGAGTCTACTCAGAGCTCTCTTATATAGATACAACTATTITGGATTGG 213
 QY 121 TACTCTGAGAGCAGGAGGAGTCTCCACAGCTCTGATCTATTGTATGTCACCCGGCA 180
 DB 214 TACCTGACAGAGCAGGAGGAGTCTCCACAGCTCTCTTGGGTCTAATCGGGC 273
 QY 181 TCAGGGGTCCCTGACAGGTTCACTGAGTGGATAGGACAGATTTTACACTGAAATC 240
 DB 274 TCCGGGGTCCCTGACAGGTTCACTGAGTGGATAGGACAGATTTTACACTGAAATC 333
 QY 241 AGCAGATGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
 DB 334 AGCAGATGAGGCTGAGGATGTTGGGTTTATTACTGATGATGATCTTACAAATTCCT 393
 QY 301 TTCACGTTCCGCAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348
 DB 394 CGGACGTTCCGCAAGGACCAAGGTGGAGATCAAAACGAACTGTGGCT 441

Search completed: April 18, 2005, 17:28:39
 Job time : 1367.64 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 195.759 Seconds
(without alignments)
10523.523 Million cell updates/sec

Title: US-09-674-716B-17

Perfect score: 348
Sequence: 1 gatattgtgatcactcagtc.....agatcaaacgtacgttgct 348

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	348	100.0	348	AAZ34747	Aaz34747 Humanised
2	292	83.9	740	AAF63377	Aaf63377 Anti-Ep-C
3	292	83.9	740	AAF63373	Aaf63373 Humanised
4	277.6	79.8	720	AD28460	Ade28460 Human ant
5	276	79.3	772	AAZ24418	Aaz24418 Human bla
6	274.4	78.9	720	AD28404	Ade28404 Human ant
7	274	78.7	720	AAAI3927	Aaai3927 Human PTH
8	273	78.4	720	AAAI3924	Aaai3924 Human PTH
9	272.8	78.4	720	AAAI3925	Aaai3925 Human PTH
10	272.8	78.4	720	AD28468	Ade28468 Human ant
11	272.8	78.4	720	AD28464	Ade28464 Human ant
12	272.8	78.4	1081	ABSS1811	Abss1811 Human mdd
13	272.4	78.3	720	AAAI3928	Aaai3928 Human PTH
14	271.8	78.1	720	AAAI3920	Aaai3920 Human PTH
15	271.2	77.9	649	ABZ22313	Abz22313 S: pneumo
16	271.2	77.9	720	AD28396	Ade28396 Human ant
17	270.8	77.8	720	AAAI3926	Aaai3926 Human PTH
18	269.8	77.5	337	AD28436	Ade28436 Human ant
19	269.8	77.5	337	AD007296	Ado07296 Human A3-
20	269.6	77.5	720	AAAI3921	Aaai3921 Human PTH

21	269.6	77.5	720	10	AD28494	Ade28494 Human ant
22	269.6	77.5	720	10	AD28476	Ade28476 Human ant
23	268.8	77.2	336	12	AD122057	Adi22057 Anti-plat
24	268.2	77.1	720	3	AAAI3923	Aaai3923 Human PTH
25	268	77.0	720	10	AD28420	Ade28420 Human ant
26	267.8	77.0	720	3	AAAI3929	Aaai3929 Human PTH
27	266.6	76.6	720	3	AAAI3922	Aaai3922 Human PTH
28	266	76.4	339	9	ADA89235	Ada89235 Human ant
29	265.6	76.3	336	10	AD28486	Ade28486 Human ant
30	265.6	76.3	336	10	AD28408	Ade28408 Human ant
31	265.6	76.3	336	12	AD122060	Adi22060 Anti-plat
32	265.6	76.3	336	12	AD122067	Adi22067 Anti-plat
33	265.6	76.3	336	12	AD122065	Adi22065 Anti-plat
34	265.6	76.3	336	12	AD122066	Adi22066 Anti-plat
35	265.6	76.3	336	12	AD122059	Adi22059 Anti-plat
36	265	76.1	337	10	AD28440	Ade28440 Human ant
37	265	76.1	337	10	AD28444	Ade28444 Human ant
38	264.8	76.1	720	12	ADH34603	Adh34603 O11 light
39	264	75.9	336	12	AD122058	Adi22058 Anti-plat
40	263.6	75.7	375	6	ABQ92702	Abq92702 Human imm
41	263.4	75.7	1076	11	ACN90285	Acn90285 Breast ca
42	263.2	75.6	720	12	ADH34604	Adh34604 O21 light
43	263.2	75.6	963	4	AAF44895	Aaf44895 Human bre
44	263	75.6	1143	4	AAD20732	Aad20732 Human biv
45	263	75.6	1143	10	ABX79087	Abx79087 DNA encod

ALIGNMENTS

RESULT 1

AAZ34747
ID AAZ34747 standard; cDNA; 348 BP.
XX
AC AAZ34747;
XX
DT 15-FEB-2000 (first entry)
XX
DE Humanised anti-CD23 Mab C11 light chain variable region cDNA.

XX CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
KW therapy; ds.
XX
OS Homo sapiens.
OS Synthetic.

XX WO9958679-A1.
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-GB001434.
XX
XX 09-MAY-1998; 98GB-00009839.
XX (GLAX) GLAXO GROUP LTD.

XX Bonney JUMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
PI WPI; 2000-053101/04.
XX P-PSDB; AAY32362.
XX Cell receptor specific antibodies useful for treating e.g. arthritis,
XX diabetes, multiple sclerosis and psoriasis.
XX Claim 17; Fig 3; 81pp; English.

XX This DNA sequence encodes the light chain variable region (VL) of
CC humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of a human
CC framework (H5IGKV11) and the light chain complementarity determining
CC regions (see AY32254-56) of murine antibody C11. The DNA was constructed
CC by splice overlap PCR. The invention provides altered antibodies, such as
CC chimeric or humanised antibodies, which comprise sufficient of the amino
CC acid sequences of the C11 light and heavy chain complementarity
CC determining regions to render them capable of binding to the CD23 type II
CC molecule expressed on haematopoietic cells. The antibodies are used to
CC block soluble CD23 formation in human therapy, for the treatment of
CC arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic asthma,
CC intrinsic asthma, acute asthmatic exacerbation, rhinitis, eczema, graft-
CC versus-host disease, COPD, insulinitis, bronchitis (particularly chronic
CC bronchitis) or diabetes (particularly type 1 diabetes), and B-cell
CC malignancies (claimed). They are also useful for studying interactions
CC between CD23 and various ligands and determining the binding agents
XX

XX Sequence 348 BP; 81 A; 87 C; 97 G; 83 T; 0 U; 0 Other;

Query Match 100.0%; Score 348; DB 3; Length 348;
Best Local Similarity 100.0%; Pred. No. 9e-97;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCGGCTCC 60
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCGGCTCC 60

QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCTGTATAGGATGGGAGACATCTTGAATTGG 120
DB 61 ATCTCTGTGCTCGAGTAAGAGTCTCTGTATAGGATGGGAGACATCTTGAATTGG 120

QY 121 TACTCTGCAGAACGCCAGGAGTCTCCACAGCTCTCTGATCTATTGTGATGCCACCGGGCA 180
DB 121 TACTCTGCAGAACGCCAGGAGTCTCCACAGCTCTCTGATCTATTGTGATGCCACCGGGCA 180

QY 181 TCAGGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACATGAAATC 240
DB 181 TCAGGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACATGAAATC 240

QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300

QY 301 TTCACGTTTCGGCCCAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348
DB 301 TTCACGTTTCGGCCCAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348

RESULT 2
AAF63377/c
ID AAF63377 standard; DNA; 740 BP.
XX
AC AAF63377;
XX
DT 10-MAY-2001 (first entry)
XX
DE Anti-Ep-CAM antibody related DNA sequence SEQ ID 3.
XX
KW Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer; ds.
XX
OS Unidentified.
XX
FN WO200107082-A1.
XX
PD 01-FEB-2001.
XX
PF 23-JUL-1999; 99WO-EP005271.
XX

PR 23-JUL-1999; 99WO-EP005271.
XX (GLAX) GLAXO GROUP LTD.
XX Knick VC, Stimmel JB, Thurmond LM;
XX WPI; 2001-182729/18.
XX Combination for treating cancer (e.g. breast, gastric or prostate
PT cancers), or in the manufacture of a medicament for anti-cancer therapy,
PT comprises an anti-Ep-cyclic adenosine monophosphate antibody with a
PT chemotherapeutic agent.
XX
XX Disclosure; Page 66; 103pp; English.
PS This invention relates to a combination of an anti-Ep-CAM (cyclic
XX adenosine monophosphate) antibody with a chemotherapeutic agent, that is
XX capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
XX phase or the second growth phase (M) of cell enlargement (G2)/DNA
XX replication. The antibody exhibits cytostatic activity and is useful in
XX the manufacture of a medicament for use in anti-cancer therapy.
XX characterised in that a chemotherapeutic agent, which is capable of
XX arresting Ep-CAM antigen expressing cells in S or in G2/M, is co-
XX administered to a patient with an anti-Ep-CAM antibody. The combination
XX is useful for treating cancer, particularly colorectal cancer, breast
XX cancer, gastric cancer, prostate cancer or non-small-cell lung cancer.
XX The present sequence represents DNA related to the anti-Ep-CAM antibody
XX used in the combination of the invention

XX Sequence 740 BP; 165 A; 187 C; 201 G; 187 T; 0 U; 0 Other;

Query Match 83.9%; Score 292; DB 4; Length 740;
Best Local Similarity 89.9%; Pred. No. 2e-79;
Matches 313; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCGGCTCC 60
DB 660 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCGGCTCC 601

QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCTGTATAGGATGGGAGACATCTTGAATTGG 120
DB 600 ATCTCTGTGCTCGAGTAAGAGTCTCTGTATAGGATGGGAGACATCTTGAATTGG 541

QY 121 TACTCTGCAGAACGCCAGGAGTCTCCACAGCTCTCTGATCTATTGTGATGCCACCGGGCA 180
DB 540 TACTCTGCAGAACGCCAGGAGTCTCCACAGCTCTCTGATCTATTGTGATGCCACCGGGCA 481

QY 181 TCAGGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACATGAAATC 240
DB 480 TCAGGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACATGAAATC 421

QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 420 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 361

QY 301 TTCACGTTTCGGCCCAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348
DB 360 CGGACGTTTCGGCCCAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 313

RESULT 3
AAF63373
ID AAF63373 standard; cDNA; 740 BP.
XX
AC AAF63373;
XX
DT 10-MAY-2001 (first entry)
XX
DE Humanised 323/A3 (IgG1) antibody light chain cDNA sequence.
XX
KW Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
KW light chain; ss.
XX

XX Mus sp.
OS Homo sapiens.
XX WO200107082-A1.
XX 01-FEB-2001.
XX 23-JUL-1999; 99WO-EP005271.
XX 23-JUL-1999; 99WO-EP005271.
XX (GLAX) GLAXO GROUP LTD.
XX Knick VC, Stimmel JB, Thurmond LM;
XX WPI; 2001-182729/18.
XX P-PSDB; AAB72227.
XX Combination for treating cancer (e.g. breast, gastric or prostate
PT cancers), or in the manufacture of a medicament for anti-cancer therapy,
PT comprises an anti-Ep-cyclic adenosine monophosphate antibody with a
PT chemotherapeutic agent.
XX
XX Example 6; Fig 15; 103pp; English.
XX
XX This invention relates to a combination of an anti-Ep-CAM (cyclic
CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is
CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
CC phase or the second growth phase (M) of cell enlargement (G2)/DNA
CC replication. The antibody exhibits cytostatic activity and is useful in
CC the manufacture of a medicament for use in anti-cancer therapy,
CC characterised in that a chemotherapeutic agent, which is capable of
CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is co-
CC administered to a patient with an anti-Ep-CAM antibody. The combination
CC is useful for treating cancer, particularly colorectal cancer, breast
CC cancer, gastric cancer, prostate cancer or non-small-cell lung cancer.
CC The present sequence represents cDNA encoding the light chain of anti-Ep-
CC CAM antibody known as humanised 323/A3 (IgG1) which can be used in the
CC combination of the invention
XX
XX Sequence 740 BP; 187 A; 201 C; 187 G; 165 T; 0 U; 0 Other;
Query Match 83.9%; Score 292; DB 4; Length 740;
Best Local Similarity 89.9%; Pred. No. 2e-79;
Matches 313; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCCGTCACTCCCTGGAGCGCGCTCC 60
DB 81 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCCGTCACTCCCTGGAGCGCGCTCC 140
QY 61 ATCTCTGTCGCTCGAGTAGAGTCTCTGTATAAGGATGGGAAGACATCTTGAATTGG 120
DB 141 ATCTCTGTAGGTCTAGTAGAATCTCTGTATAGTAATGGCATCTTATTGTATTGG 200
QY 121 TACCTCGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTATGTCACCCGGGCA 180
DB 201 TACCTCGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATCAGATGTCACCTTGGC 260
QY 181 TCAGGGGTCTCTACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACATGAAATC 240
DB 261 TCAGGGGTCTCTACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACATGAAATC 320
QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGTGAGATATCCA 300
DB 321 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCTCAAAATCTAGAGATCTCT 380
QY 301 TTCACGTTCCGCCCAAGGCAAGAGTGGAGATCAAAACGTACCGTGGCT 348
DB 381 CGGACGTTCCGCCCAAGGCAAGAGTGGAGATCAAAACGTACCGTGGCT 428

RESULT 4

ADE28460

ID ADE28460 standard; cDNA; 720 BP.

XX AC ADE28460;

XX DT 29-JAN-2004 (first entry)

XX DE Human anti-CD40 antibody 23-28-1 variable region light chain cDNA.

XX KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;

XX KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;

XX KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;

XX KW human; variable region light chain; ss; gene; 23-28-1.

XX OS Homo sapiens.

XX PN WO2003040170-A2.

XX PD 15-MAY-2003.

XX PF 08-NOV-2002; 2002WO-US036107.

XX PR 09-NOV-2001; 2001US-0348980P.

XX PA (PFIZ) PFIZER PROD INC.

XX PA (ABGE-) ABGENIX INC.

XX PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;

XX WPI; 2003-441521/41.

XX DR P-PSDB; ADE28461.

XX PT New chimeric or human monoclonal antibody or its antigen-binding portion

XX PT that specifically binds to and activates human CD40, useful for enhancing

XX PT an immune response in a human, or treating cancer, HIV, neutropenia or

XX PT viral infections.

XX XX

XX Claim 24; SEQ ID NO 67; 177pp; English.

XX The invention relates to a novel chimeric or human monoclonal antibody or

XX its antigen-binding portion that specifically binds to and activates

XX human CD40. The anti-CD40 antibody of the invention demonstrates

XX cytostatic, virucide, antibacterial, immunostimulant and anti-HIV

XX activities and may be useful for treating a hyperproliferative disorder

XX such as cancer, viral and bacterial infection or genetic, primary or

XX combined immunodeficiency conditions including neutropenia or HIV

XX infection. The anti-CD40 antibodies may also be useful for detecting CD40

XX in a biological sample in vitro or in vivo, as well as during gene

XX therapy procedures. The current sequence is that of the human anti-CD40

XX antibody variable region light chain cDNA of the invention.

XX XX

XX Query Match 79.8%; Score 277.6; DB 10; Length 720;

XX Best Local Similarity 87.4%; Pred. No. 5.4e-75;

XX Matches 304; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCCGTCACTCCCTGGAGCGCGCTCC 60

DB 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCCGTCACTCCCTGGAGCGCGCTCC 120

QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCTGTATAAGGATGGGAAGACATCTTGAATTGG 120

DB 121 ATCTCTGTCGAGTCTAGTCAGAGTGTCTGTATAGTAATGGATACACTATTGTGATTGG 180

QY 121 TACCTCGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTATGTCACCCGGGCA 180

DB 181 TACCTCGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTGTTCTAATCGGGCC 240

QY 181 TCAGGGGTCTCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACATGAAATC 240

DB 241 TCCGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACATGAAATC 300

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 300
 DB 301 ACCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 360
 QY 301 TTACAGCTTGGCCCAAGGACCAAGAGTGGAGATCAACAGCTGTAGAGTATCCA 348
 DB 361 TTACAGCTTGGCCCTGGGACCAAGTGGATATCAACAGCTGTAGAGTATCCA 408

RESULT 5

AAZ24418
 ID AAZ24418 standard; cDNA; 772 BP.
 XX
 AC AAZ24418;
 XX
 DT 14-FEB-2000 (first entry)
 XX
 DE Human bladder tumour cDNA library derived EST 30.

XX Expressed sequence tag; human; bladder; tumour; cancer; cytostatic;
 KW treatment; gene therapy; EST; ss.
 XX

OS Homo sapiens.

XX DE19818619-A1.

XX 28-OCT-1999.

XX 21-APR-1998; 98DE-01018619.

XX 21-APR-1998; 98DE-01018619.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
 PI WPI; 1999-612028/53.

XX New nucleic acid sequences expressed in bladder tumor tissue, and derived
 PT polypeptides, for treatment of bladder tumor and identification of
 PT therapeutic agents.

XX Claim 3; Page 84; 132pp; German.

XX This invention describes novel polypeptide fragments (I) and the
 CC polynucleotides (II) that encode them that are highly expressed in a
 CC human bladder tumour and which have cytostatic activity. (II) are used
 CC for recombinant expression of (I) and to isolate complete genes. (I) are
 CC used to identify agents suitable for treatment of bladder cancer, to
 CC directly treat this form of cancer (including expression from gene
 CC therapy vectors) or are used in a preparation for cancer treatment. (I)
 CC is also used for the generation of specific antibodies. (II) are
 CC identified by assembling ESTs (expressed sequence tags) from a particular
 CC tissue type before comparison of expression patterns. This allows a
 CC significantly longer fragment of the gene to be revealed, and therefore
 CC reduces the number of failures associated with the fact that ESTs from
 CC different libraries may represent different parts of the same unknown
 CC gene, distorting the estimated frequency of occurrence in a particular
 CC tissue. AAZ3260-243309 represent expressed sequence tag (EST) fragments
 CC isolated from a human bladder tumour cDNA library which encode the
 CC proteins represented in AAY66143-Y66198

XX Sequence 772 BP; 181 A; 210 C; 206 G; 175 T; 0 U; 0 Other;

Query Match 79.3%; Score 276; DB 2; Length 772;

Best Local Similarity 87.1%; Pred. No. 1.7e-74;

Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCGGCTCC 60

DB 87 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCGGCTCC 146

QY 61 ATCTCCTGCTCGAGTAAGAGTCTCTGTATTAAGGATGGGAAGACATCTTGAATTGG 120

DB 147 ATCTCCTGAGGCTCTAGTCCAGAGCTCTCTGATAGTAATGATACAACTATTGGATTGG 206
 QY 121 TACCTGCAGAGCCAGGCGCAGTCTCCACAGCTCTCTGATCTATTGTTGATGTCACCGGGCA 180
 DB 207 TACCTGCAGAGCCAGGCGCAGTCTCCACAGCTCTCTGATCTATTGTTGATGTCACCGGGCC 266
 QY 181 TCAGGGGTCCCTGCACAGGTTTCAGTGGCGATGATCAGGCACAGATTTTACACTGAAAATC 240
 DB 267 TCCGGGGTCCCTGCACAGGTTTCAGTGGCGATGATCAGGCACAGATTTTACACTGAAAATC 326
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 300
 DB 327 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 386
 QY 301 TTCAGGTTCCGCCAAGGACCAAGTGGAGATCAACAGCTGTAGAGTATCCA 348
 DB 387 CTCAGTTTCGGCGGAGGACCAAGTGGAGATCAACAGCTGTAGAGTATCCA 434

RESULT 6

ADE28404

ID ADE28404 standard; cDNA; 720 BP.

XX ADE28404;

XX 29-JAN-2004 (first entry)

XX Human anti-CD40 antibody 7-1-2 variable region light chain cDNA.

XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
 KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
 KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
 KW human; variable region light chain; ss; gene; 7-1-2.

XX Homo sapiens.

XX WO2003040170-A2.

XX 15-MAY-2003.

XX 08-NOV-2002; 2002WO-US036107.

XX 09-NOV-2001; 2001US-0348980P.

XX (PFIZ) PFIZER PROD INC.

XX (ABGE-) ABGENIX INC.

XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;

XX WPI; 2003-441521/41.

XX P-PSDB; ADE28405.

XX New chimeric or human monoclonal antibody or its antigen-binding portion
 PT that specifically binds to and activates human CD40, useful for enhancing
 PT an immune response in a human, or treating cancer, HIV, neutropenia or
 PT viral infections.

XX Claim 24; SEQ ID NO 11; 177pp; English.

XX The invention relates to a novel chimeric or human monoclonal antibody or
 CC its antigen-binding portion that specifically binds to and activates
 CC human CD40. The anti-CD40 antibody of the invention demonstrates
 CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
 CC activities and may be useful for treating a hyperproliferative disorder
 CC such as cancer, viral and bacterial infection or genetic, primary or
 CC combined immunodeficiency conditions including neutropenia or HIV
 CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
 CC in a biological sample in vitro or in vivo, as well as during gene
 CC therapy procedures. The current sequence is that of the human anti-CD40
 CC antibody variable region light chain cDNA of the invention.

XX Sequence 720 BP; 173 A; 195 C; 192 G; 160 T; 0 U; 0 Other;

Query Match 78.9%; Score 274.4; DB 10; Length 720;
 Best Local Similarity 86.8%; Pred. No. 5.3e-74;
 Matches 302; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTCACCCTCGAGAGCGGCTCC 60
 DB 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTCACCCTCGAGAGCGGCTCC 120

QY 61 ATCTCTCTGCTCGCTGAGTCTCTCTGTATAGGATGGAGACATATCTTGAATTGG 120
 DB 121 ATCTCTCTGCTGAGTCTCTGTATAGGATGGAGACATATCTTGAATTGG 180

QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGTATAGGATGGAGAGCGGCGCA 180
 DB 181 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGTATAGGATGGAGAGCGGCGCC 240

QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 240
 DB 241 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 300

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
 DB 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 360

QY 301 TTCACGTTTCGGCCCAAGGACCAAGGTGGAGATCAAACTGCGTGGCT 348
 DB 361 CGGACGTTTCGGCCCAAGGACCAAGGTGGAGATCAAACTGCGTGGCT 408

RESULT 7

AAAL13927
 ID AAA13927 standard; DNA; 720 BP.
 AC AAA13927;
 XX
 XX 02-AUG-2000 (first entry)
 DE Human PTHrP monoclonal antibody clone 3G4-3 DNA SEQ ID NO:17.
 XX
 XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis;
 KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;
 KW antiarthritic; cytostatic; antiinflammatory; ds.
 XX
 OS Homo sapiens.
 XX
 XX JP2000080100-A.
 XX
 XX 21-MAR-2000.
 XX
 XX 12-OCT-1998; 98JP-00304793.
 XX
 XX 17-JUN-1998; 98JP-00188196.
 PR 26-JUN-1998; 98JP-00196729.
 XX
 XX (NISR) JAPAN TOBACCO INC.
 XX
 XX WPI; 2000-286723/25.
 DR P-PSDB; AAY82617.

A human monoclonal antibody to parathyroid hormone related protein. -
 useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 including metastasis, and pain.

Example 10; Page 50; 89pp; Japanese.

The present invention describes a human monoclonal antibody to
 parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 its fragments, following the stimulation of PTHrP has the following
 properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 the release of calcium from bone; or (c) inhibits elevation of blood

CC calcium content. The monoclonal antibody can be used in the treatment of
 CC hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a human
 CC PTHrP monoclonal antibody clone nucleotide sequence from the present
 CC invention

XX
 SQ Sequence 720 BP; 174 A; 191 C; 188 G; 163 T; 0 U; 4 Other;

Query Match 78.7%; Score 274; DB 3; Length 720;
 Best Local Similarity 86.5%; Pred. No. 7e-74;
 Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTCACCCTCGAGAGCGGCTCC 60
 DB 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTCACCCTCGAGAGCGGCTCC 120

QY 61 ATCTCTCTGCTCGCTGAGTCTCTCTGTATAGGATGGAGACATATCTTGAATTGG 120
 DB 121 ATCTCTCTGCTGAGTCTCTGTATAGGATGGAGACATATCTTGAATTGG 180

QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGTATAGGATGGAGAGCGGCGCA 180
 DB 181 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGTATAGGATGGAGAGCGGCGCC 240

QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 240
 DB 241 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 300

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
 DB 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 360

QY 301 TTCACGTTTCGGCCCAAGGACCAAGGTGGAGATCAAACTGCGTGGCT 348
 DB 361 TTCACGTTTCGGCCCAAGGACCAAGGTGGAGATCAAACTGCGTGGCT 408

RESULT 8

AAAL13924
 ID AAA13924 standard; DNA; 720 BP.
 XX
 XX AAA13924;
 XX
 XX 02-AUG-2000 (first entry)
 DT Human PTHrP monoclonal antibody clone 2F8-10-3 DNA SEQ ID NO:11.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis;
 KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;
 KW antiarthritic; cytostatic; antiinflammatory; ds.

OS Homo sapiens.

XX JP2000080100-A.

XX 21-MAR-2000.

XX 12-OCT-1998; 98JP-00304793.

XX 17-JUN-1998; 98JP-00188196.

XX 26-JUN-1998; 98JP-00196729.

XX (NISR) JAPAN TOBACCO INC.

XX WPI; 2000-286723/25.

XX P-PSDB; AAY82614.

PT A human monoclonal antibody to parathyroid hormone related protein. -

PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain.

XX Example 10; Page 41-42; 88pp; Japanese.

XX The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment of
 CC hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a human
 CC PTHrP monoclonal antibody clone nucleotide sequence from the present
 CC invention

XX Sequence 720 BP; 174 A; 190 C; 188 G; 163 T; 0 U; 5 Other;

SQ Query Match 78.4%; Score 273; DB 3; Length 720;

Best Local Similarity 86.2%; Pred. No. 1.4e-73;

Matches 300; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCACCTCTGGAGCGGCTCC 60

Db 61 GATATTGTGATGANTCAGTNTCCACTCTCCCTGCGGTCACCTCTGGAGCGGCTCC 120

QY 61 ATCTCTGTGCTCGAGTAAAGTCTCCTGTATAGGATGGGAGACATCTTGAATTGG 120

Db 121 ATCTCTGTGAGTCTTAGTCAGACCTCTCTGATGTAATGGAACAACATTTGGATTGG 180

QY 121 TACCTGCGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGTATGTCACCCCGGCA 180

Db 181 TACCTGCGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGTGTTCTAATCGGGC 240

QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240

Db 241 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300

QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300

Db 301 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 360

QY 301 TTCACGTTTCGGCCAAAGCCAAAGTGGAGATCAAAACGTCACGTTGGCT 348

Db 361 TTCACGTTTCGGCCCTGGGACCAAGTGGATATCAAAACGAACTGTGGCT 408

RESULT 9

AAAL13925

ID AAAL13925 standard; DNA; 720 BP.

XX AC AAAL13925;

XX 02-AUG-2000 (first entry)

XX Human PTHrP monoclonal antibody clone 1C1-3 DNA SEQ ID NO:13.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis;
 KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;
 KW antiarthritic; cytostatic; antiinflammatory; ds.

XX Homo sapiens.

XX JP2000080100-A.

XX 21-MAR-2000.

XX 12-OCT-1998; 98JP-00304793.

XX 17-JUN-1998; 98JP-00188196.
 PR 26-JUN-1998; 98JP-00196729.

XX (NISR) JAPAN TOBACCO INC.

XX WPI: 2000-286723/25.

DR P-PSDB; AY82615.

XX A human monoclonal antibody to parathyroid hormone related protein. -
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain.

XX Example 10; Page 44-45; 88pp; Japanese.

XX The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment of
 CC hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a human
 CC PTHrP monoclonal antibody clone nucleotide sequence from the present
 CC invention

XX Sequence 720 BP; 172 A; 197 C; 190 G; 160 T; 0 U; 1 Other;

Query Match 78.4%; Score 272.8; DB 3; Length 720;

Best Local Similarity 86.5%; Pred. No. 1.6e-73;

Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCACCTCTGGAGCGGCTCC 60

Db 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCACCTCTGGAGCGGCTCC 120

QY 61 ATCTCTGTGCTCGAGTAAAGTCTCCTGTATAGGATGGGAGACATCTTGAATTGG 120

Db 121 ATCTCTGTGAGTCTTAGTCAGACCTCTCTGATGTAATGGAACAACATTTGGATTGG 180

QY 121 TACCTGCGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGTATGTCACCCCGGCA 180

Db 181 TACCTGCGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGTGTTCTAATCGGGC 240

QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240

Db 241 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300

QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300

Db 301 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 360

QY 301 TTCACGTTTCGGCCAAAGCCAAAGTGGAGATCAAAACGTCACGTTGGCT 348

Db 361 TTCACGTTTCGGCCCTGGGACCAAGTGGATATCAAAACGAACTGTGGCT 408

RESULT 10

ADE28468

ID ADE28468 standard; cDNA; 720 BP.

XX ADE28468;

XX 29-JAN-2004 (first entry)

XX Human anti-CD40 antibody 23-29-1 variable region light chain cDNA.

XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
 KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
 KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;

KW human; variable region light chain; ss; gene; 23-29-1.

XX Homo sapiens.

OS WO2003040170-A2.

PN PD 15-MAY-2003.

XX 08-NOV-2002; 2002WO-US036107.

XX 09-NOV-2001; 2001US-0348980P.

XX (PFIZ) PFIZER PROD INC.

XX (ABGE-) ABGENIX INC.

XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;

XX WPI; 2003-441521/41.

XX P-PSDB; ADE28469.

XX New chimeric or human monoclonal antibody or its antigen-binding portion
PT that specifically binds to and activates human CD40, useful for enhancing
PT an immune response in a human, or treating cancer, HIV, neutropenia or
PT viral infections.

XX Claim 24; SEQ ID NO 75; 177pp; English.

XX The invention relates to a novel chimeric or human monoclonal antibody or
CC its antigen-binding portion that specifically binds to and activates
CC human CD40. The anti-CD40 antibody of the invention demonstrates
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC activities and may be useful for treating a hyperproliferative disorder
CC such as cancer, viral and bacterial infection or genetic, primary or
CC combined immunodeficiency conditions including neutropenia or HIV
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC in a biological sample in vitro or in vivo, as well as during gene
CC therapy procedures. The current sequence is that of the human anti-CD40
CC antibody variable region light chain cDNA of the invention.

XX Sequence 720 BP; 173 A; 196 C; 192 G; 157 T; 0 U; 2 Other;

Query Match 78.4%; Score 272.8; DB 10; Length 720;

Best Local Similarity 86.5%; Pred. No. 1.6e-73;

Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCCACCCCTGGAGAGCGGCTCC 60

DB 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCCACCCCTGGAGAGCGGCTCC 120

QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCTGTATAAGGATGGGAGACATATTGAATTGG 120

DB 121 ATCTCTGTCGAGGTCTAGTCAGAGCTCTCTGCTGTAATGATACAACTATTGGATTGG 180

QY 121 TACTTCGAGAAGCCAGGCGAGTCTCCACAGCTCTGTATTTGATGTCACCCCGGCGCA 180

DB 181 TACTTCGAGAAGCCAGGCGAGTCTCCACAGCTCTGTATTTGATGTCACCCCGGCGCC 240

QY 181 TCAGGGTCTCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240

DB 241 TCCGGGTCTCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300

QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300

DB 301 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 360

QY 301 TTACGTTTCGGCCAGGAGCAAGAGTGGAGATCAACAGTACGGTGGCT 348

DB 361 CGGACGTTTCGGCCAGGAGCAAGAGTGGAGATCAACAGTACGGTGGCT 408

RESULT 11

ADE28464

ID ADE28464 standard; cDNA; 720 BP.

XX

AC

XX

DT

XX

DE

XX

KW

KW

KW

KW

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OS

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PN

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PD

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PF

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PR

XX

PA

PA

XX

PI

XX

DR

DR

XX

PT

PT

PT

PT

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

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CC

CC

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CC

CC

CC

CC

ADE28464;

29-JAN-2004 (first entry)

Human anti-CD40 antibody 23-28-1 full length light chain cDNA.

anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
human; light chain; ss; gene; 23-28-1.

Homo sapiens.

WO2003040170-A2.

15-MAY-2003.

08-NOV-2002; 2002WO-US036107.

09-NOV-2001; 2001US-0348980P.

(PFIZ) PFIZER PROD INC.

(ABGE-) ABGENIX INC.

Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;

WPI; 2003-441521/41.

P-PSDB; ADE28465.

New chimeric or human monoclonal antibody or its antigen-binding portion
PT that specifically binds to and activates human CD40, useful for enhancing
PT an immune response in a human, or treating cancer, HIV, neutropenia or
PT viral infections.

Claim 24; SEQ ID NO 71; 177pp; English.

The invention relates to a novel chimeric or human monoclonal antibody or
its antigen-binding portion that specifically binds to and activates
human CD40. The anti-CD40 antibody of the invention demonstrates
cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
activities and may be useful for treating a hyperproliferative disorder
such as cancer, viral and bacterial infection or genetic, primary or
combined immunodeficiency conditions including neutropenia or HIV
infection. The anti-CD40 antibodies may also be useful for detecting CD40
in a biological sample in vitro or in vivo, as well as during gene
therapy procedures. The current sequence is that of the human anti-CD40
antibody full length light chain cDNA of the invention.

Sequence 720 BP; 172 A; 195 C; 191 G; 161 T; 0 U; 1 Other;

Query Match 78.4%; Score 272.8; DB 10; Length 720;

Best Local Similarity 86.5%; Pred. No. 1.6e-73;

Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCCACCCCTGGAGAGCGGCTCC 60

DB 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCCACCCCTGGAGAGCGGCTCC 120

QY 61 ATCTCTGTCGCTCGAGTAAGAGTCTCTGTATAAGGATGGGAGACATATTGAATTGG 120

DB 121 ATCTCTGTCGAGGTCTAGTCAGAGCTCTCTGTATAGTATGATATTAATTTGGATTGG 180

QY 121 TACTTCGAGAAGCCAGGCGAGTCTCCACAGCTCTGTATTTGATGTCACCCCGGCGCA 180

DB 181 TACTTCGAGAAGCCAGGCGAGTCTCCACAGCTCTGTATTTGATGTCACCCCGGCGCC 240

QY 181 TCAGGGTCTCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240

DB 241 TCCGGGTCTCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300

QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300

DB 301 AGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 360

QY 301 TTACGTTTCGGCCAGGAGCAAGAGTGGAGATCAACAGTACGGTGGCT 348

DB 361 CGGACGTTTCGGCCAGGAGCAAGAGTGGAGATCAACAGTACGGTGGCT 408

RESULT 11

ADE28464

ID ADE28464 standard; cDNA; 720 BP.

Db 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAAACTCCT 360
 QY 301 TTCACGTTTGGCCCAAGGACCAAGGTGGAGATCAAAAGCTACGGTGGCT 348
 Db 361 CGGACGTTTGGCCCAAGGACCAAGGTGGAGATCAAAAGCTACGGTGGCT 408

RESULT 12

ABSS1811
 ID ABSS1811 standard; cDNA; 1081 BP.

AC
 XX
 XX
 XX
 DT 21-OCT-2002 (first entry)

XX
 DE Human mdmt cDNA Incyte ID No: LI:1171219.2:2001JAN12.
 XX

KW Human; molecule for disease detection and treatment; MDDT; cancer;
 KW cell proliferative disorder; arteriosclerosis; cirrhosis; asthma;
 KW autoimmune disorder; inflammatory disorder; Crohn's disease;
 KW multiple sclerosis; cytostatic; antiarteriosclerotic; antiinflammatory;
 KW hepatotropic; immunosuppressive; antiasthmatic; gene therapy; gene; ss.
 XX
 OS Homo sapiens.

XX
 XX WO200255738-A2.

PN
 XX
 PD 18-JUL-2002.

XX
 PF 09-JAN-2002; 2002WO-US0001008.

XX
 PR 12-JAN-2001; 2001US-0261622P.

PR 16-JAN-2001; 2001US-0261865P.

PR 17-JAN-2001; 2001US-0262208P.

PR 17-JAN-2001; 2001US-0262209P.

PR 17-JAN-2001; 2001US-0262326P.

PR 19-JAN-2001; 2001US-0263063P.

PR 19-JAN-2001; 2001US-0263065P.

PR 19-JAN-2001; 2001US-0263329P.

XX
 XX (INCY-) INCYTE GENOMICS INC.

XX Panzer SR, Lincoln SE, Altus CM, Dufour GE, Hillman JL, Jones AL;
 PI Dam TC, Liu TP, Harris B, Flores V, Daffo A, Marwaha R, Chen AJ;
 PI Chang SC, Gerstin EH, Peralta CH, David MH, Lewis SA;
 XX
 DR WPI; 2002-590679/63.
 DR P-PSDB; ABG70338.

XX
 XX New disease detection and treatment molecule (MDDT) polynucleotides and
 PT polypeptides, useful in diagnosing, studying, preventing or treating
 PT diseases associated with MDDT expression, e.g. autoimmune or inflammatory
 PT disorders.

XX
 XX Claim 1; Page 105; 129pp; English.

XX
 CC The present invention relates to the isolation of novel human molecules
 CC for disease detection and treatment (MDDT), and the polynucleotide
 CC sequences (mdmt) encoding them. The MDDT polypeptides may be used to
 CC screen for molecules that bind to, or are bound by the encoded
 CC polypeptides, and to develop a transcript image of a tissue or cell type.
 CC Probes comprising at least 20 nucleotides of the mdmt polynucleotide may
 CC be used to assess the toxicity of a test compound. The MDDT polypeptides
 CC and mdmt polynucleotides are useful in the diagnosis, study, prevention
 CC and treatment of diseases associated with the expression of molecules for
 CC disease detection and treatment. Such disorders include cell
 CC proliferative disorders (e.g. arteriosclerosis, cirrhosis, or cancers),
 CC and autoimmune/inflammatory disorders (e.g. asthma, Crohn's disease, or
 CC multiple sclerosis). The mdmt polynucleotides may also be used as
 CC molecule markers, in microarrays, and in somatic or germline gene
 CC therapy. ABSS1779-ABSS1814 encode the MDDT proteins of the invention
 XX
 XX Sequence 1081 BP; 255 A; 303 C; 276 G; 247 T; 0 U; 0 Other;

Query Match 78.4%; Score 272.8; DB 6; Length 1081;
 Best Local Similarity 86.5%; Pred. No. 1.9e-73;
 Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCTCC 60
 Db 87 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCTCC 146
 QY 61 AFTCTCTGTGCTCGAGTAAGAGTCTCTGTATTAAGGATGGAGACATATTGAATTGG 120
 Db 147 ATCTCTCTGAGGTCTAGTCAGAGGCTCTCTGATAGTAATGGAACAACATATTGGATTGG 206
 QY 121 TACCTGCAAGAGCCAGGCGAGTCTCCACAGCTCCCTGATCTATTGATGTCACCCCGGCA 180
 Db 207 TTCTTGCAGAGCCAGGCGAGGCTCCACAGCTCTCTGATCTATTGCGGTCTAGTCGGGCC 266
 QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
 Db 267 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 326
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 300
 Db 327 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGTGTAGTACAAATACCT 386
 QY 301 TTCACGTTTGGCCCAAGGACCAAGGTGGAGATCAAAAGCTACGGTGGCT 348
 Db 387 TCCATTTCCGGCGGAGGACCAAGGTGGAGATCAAAAGCTACGGTGGCT 434

RESULT 13

AAAL3928

ID AAAL3928 standard; DNA; 720 BP.

XX AC AAAL3928;

XX DT 02-AUG-2000 (first entry)

XX DE Human PTHrP monoclonal antibody clone 4B4-6-21 DNA SEQ ID NO:19.

XX KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingivitis; sepsis;
 KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;
 KW antiarthritic; cytostatic; antiinflammatory; ds.

XX OS Homo sapiens.

XX PN JP2000080100-A.

XX PD 21-MAR-2000.

XX PF 12-OCT-1998; 98JP-00304793.

XX PR 17-JUN-1998; 98JP-00188196.

XX PR 26-JUN-1998; 98JP-00196729.

XX PA (NIBS) JAPAN TOBACCO INC.

XX DR WPI; 2000-286723/25.

XX DR P-PSDB; AAY82618.

XX PT A human monoclonal antibody to parathyroid hormone related protein.
 XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 XX including metastasis, and pain.

XX Example 10; Page 53-54; 88pp; Japanese.

XX PS The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood

CC calcium content. The monoclonal antibody can be used in the treatment of
 CC hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a human
 CC PTHrP monoclonal antibody clone nucleotide sequence from the present
 CC invention
 XX
 SQ Sequence 720 BP; 174 A; 191 C; 186 G; 162 T; 0 U; 7 Other;
 Query Match 78.3%; Score 272.4; DB 3; Length 720;
 Best Local Similarity 86.2%; Pred. No. 2.2e-73;
 Matches 300; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
 QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCTCACCCTCGAGAGCGGCTCC 60
 DB 61 GATATTGTGATGANTCAGTTCACCTCTCCCTGCGCTCACCCTCGAGAGCGGCTCC 120
 QY 61 ATCTCTGTCTCGAGTAAAGTCTCTCTATAAGGATGGGAAGACATATCTTGAATTGG 120
 DB 121 ATCTCTGTGAGTCTAGTCAGAGCTCTCTGAATAGTAATGATACAACTATTTTCGATTGG 180
 QY 121 TACTTCGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCCGGCA 180
 DB 181 TACTTCGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGAGTCTTAATCGGGCC 240
 QY 181 TCAGGGGTCTCTGACAGTTCAGTGGCGAGTGGATCAGGCACAGATTTTACACTGAAATC 240
 DB 241 TCCGGGTCTCTGACAGTTCAGTGGCGAGTGGATCAGGCACAGATTTTACACTGAAATC 300
 QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
 DB 301 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 360
 QY 301 TTCAGTTTCGGCCAGGACCAAGTGGAGATCAACAGTACGGTGGCT 348
 DB 361 TTCACTTTTCGGCCCTGGGACCAAGTGGATATCAACAGCACTGGCT 408
 RESULT 14
 AA13920
 ID AAA13920 standard; DNA; 720 BP.
 AC AAA13920;
 XX
 DT 02-AUG-2000 (first entry)
 XX
 DE Human PTHrP monoclonal antibody clone 15H7-8-3 DNA SEQ ID NO:3.
 XX
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis;
 KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;
 KW antiarthritic; cytostatic; antiinflammatory; ds.
 XX
 OS Homo sapiens.
 XX
 PN JP2000080100-A.
 XX
 PD 21-MAR-2000.
 XX
 PF 12-OCT-1998; 98JP-00304793.
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 PR 17-JUN-1998; 98JP-00188196.
 PR 26-JUN-1998; 98JP-00196729.
 XX
 PA (NISB) JAPAN TOBACCO INC.
 XX
 DR WPI; 2000-286723/25.
 DR P-PSDB; AAY82610.
 XX
 PT A human monoclonal antibody to parathyroid hormone related protein. -

PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain.
 XX
 PS Example 10; Page 31-32; 88pp; Japanese.
 XX
 CC The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment of
 CC hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a human
 CC PTHrP monoclonal antibody clone nucleotide sequence from the present
 CC invention
 XX
 SQ Sequence 720 BP; 174 A; 191 C; 188 G; 164 T; 0 U; 3 Other;
 Query Match 78.1%; Score 271.8; DB 3; Length 720;
 Best Local Similarity 86.2%; Pred. No. 3.3e-73;
 Matches 300; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
 QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCTCACCCTCGAGAGCGGCTCC 60
 DB 61 GATATTGTGATGACTCAGTCTCCCTGCGCTCACCCTCGAGAGCGGCTCC 120
 QY 61 ATCTCTGTCTCGAGTAAAGTCTCTCTATAAGGATGGGAAGACATATCTTGAATTGG 120
 DB 121 ATTTCTGTCAGGTTTGTAGTCAGAGCTCTCTGCAATAGTAATGGAACAACTATTGATTGG 180
 QY 121 TACTTCGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCCGGCA 180
 DB 181 TACTTCGAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGAGTCTTAATCGGGCC 240
 QY 181 TCAGGGGTCTCTGACAGTTCAGTGGCGAGTGGATCAGGCACAGATTTTACACTGAAATC 240
 DB 241 TCCGGGTCTCTGACAGTTCAGTGGCGAGTGGATCAGGCACAGATTTTACACTGAAATC 300
 QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
 DB 301 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 360
 QY 301 TTCAGTTTCGGCCAGGACCAAGTGGAGATCAACAGTACGGTGGCT 348
 DB 361 TTCACTTTTCGGCCCTGGGACCAAGTGGATATCAACAGCACTGGCT 408
 RESULT 15
 AB222313
 ID AB222313 standard; DNA; 649 BP.
 XX
 AC AB222313;
 XX
 DT 20-MAR-2003 (first entry)
 XX
 DE S. pneumoniae PPS-3 antibody A7 light chain DNA sequence SEQ ID NO:8.
 XX
 KW Antipneumococcal; antibody; monoclonal antibody; infection; PPS-3;
 KW Streptococcus pneumoniae; capsular polysaccharide; gene; ds.
 XX
 OS Streptococcus pneumoniae.
 OS Synthetic.
 XX
 PN WO200292017-A2.
 XX
 PD 21-NOV-2002.
 XX
 PF 16-MAY-2002; 2002WO-US018363.
 XX
 PR 16-MAY-2001; 2001US-0291492P.

```
XX (PIRO/) PIROFSKY L.
PA (ZHON/) ZHONG Z.
PA (CHAN/) CHANG Q.
XX
XX Pirofsky L, Zhong Z, Chang Q;
XX
XX WPI; 2003-120598/11.
XX
XX New antibody or its antigen-binding fragment that specifically binds the
PT capsular polysaccharide of Streptococcus pneumoniae serotype 3, useful
PT for treating, inhibiting or preventing S. pneumoniae infections.
XX
XX Claim 27; Fig 6C; 56pp; English.
XX
XX The present invention describes an antibody or its antigen-binding
CC fragment (I) that specifically binds the capsular polysaccharide of
CC Streptococcus pneumoniae serotype 3 (S. pneumoniae PPS-3), comprising a
CC heavy and/or light chain amino acid sequence. (I) has antibacterial
CC activity and can be used in vaccines. The anti-S. pneumoniae PPS-3
CC antibody or its antigen-binding fragment is useful for treating,
CC inhibiting or preventing S. pneumoniae infections or conditions or
CC disorders caused by the infection. Methods from the present invention can
CC be used for preventing or reducing the severity of conditions or
CC disorders caused by S. pneumoniae serotype 3 infection, or for increasing
CC the resistance of a subject to infection by S. pneumoniae serotype 3. The
CC present sequence represents a S. pneumoniae PPS-3 antibody light chain
CC DNA sequence from the present invention
XX
XX Sequence 649 BP; 167 A; 182 C; 160 G; 137 T; 0 U; 3 Other;
SQ
Query Match 77.9%; Score 271.2; DB 8; Length 649;
Best Local Similarity 86.2%; Pred. No. 4.9e-73;
Matches 300; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACTCCCTGGAGCGCGCTCC 60
DB 1 GATATTGAGCTCACTCAGTCTCCACTCTCCCTGCCGTCACTCCCTGGAGCGCGCTCC 60
QY 61 ATCTCCTGTGGCTCGAGTAAAGTCTCCTGTATAGGATGGGAAGACATACCTTGAATTGG 120
DB 61 ATCTCCTGCAGGTCTAGTCAGAGCTCTCTGCATAGTAATGGATACAACTATTGGATTGG 120
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCCGGCA 180
DB 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTTGGTCTTAATCGGGCC 180
QY 181 TCAGGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 240
DB 181 TCAGGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 240
QY 241 AGCAGAGTGGAGCTCAGAGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
DB 241 AGCAGAGTGGAGCTCAGAGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
QY 301 TTCACGTTCGGCCAGGCGAGGTCAGATGAGATCAACAGCTACGGTGGCT 348
DB 301 CGGACGTTCCGCCAAGGCGAGGTCAGATGAGATCAACAGCTACGGTGGCT 348
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Job time : 196.759 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 14:42:49 ; Search time 947.356 Seconds
(without alignments)
2228.534 Million cell updates/sec

Title: US-09-674-716B-17

Perfect score: 348

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277.6	79.8	720	17	US-10-292-088-39
2	274.4	78.9	720	17	US-10-292-088-15
3	272.8	78.4	720	17	US-10-292-088-55
4	272.8	78.4	720	17	US-10-292-088-63
5	272.8	78.4	1081	17	US-10-466-164-33
6	271.2	77.9	649	19	US-10-714-079C-8
7	271.2	77.9	720	17	US-10-292-088-7
8	269.8	77.5	337	17	US-10-292-088-35
9	269.8	77.5	337	19	US-10-638-265-11
10	269.8	77.5	337	19	US-10-638-265-31
11	269.6	77.5	720	17	US-10-292-088-79
Sequence 39, Appl					
Sequence 15, Appl					
Sequence 55, Appl					
Sequence 63, Appl					
Sequence 33, Appl					
Sequence 8, Appl					
Sequence 7, Appl					
Sequence 35, Appl					
Sequence 11, Appl					
Sequence 31, Appl					
Sequence 79, Appl					

ALIGNMENTS

RESULT 1

US-10-292-088-39
; Sequence 39, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-292-088-39

Query Match 79.8%; Score 277.6; DB 17; Length 720;
Best Local Similarity 87.4%; Pred. No. 1.1e-84;
Matches 304; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCCGTCAACCCCTGGAGACGGGCTCC 60
Db 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTCCCGTCAACCCCTGGAGACGGGCTCC 120
QY 61 ATCTCTCTGTCGTCGAGTAAGAGTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120

Sequence 101, Appl
Sequence 7, Appl
Sequence 67, Appl
Sequence 31, Appl
Sequence 217, Appl
Sequence 218, Appl
Sequence 35, Appl
Sequence 47, Appl
Sequence 79, Appl
Sequence 11, Appl
Sequence 93, Appl
Sequence 50, Appl
Sequence 52, Appl
Sequence 54, Appl
Sequence 50, Appl
Sequence 52, Appl
Sequence 51, Appl
Sequence 59, Appl
Sequence 243, Appl
Sequence 23, Appl
Sequence 27, Appl
Sequence 39, Appl
Sequence 43, Appl
Sequence 51, Appl
Sequence 71, Appl
Sequence 11435, A
Sequence 36, Appl
Sequence 36, Appl
Sequence 6, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 25, Appl
Sequence 3, Appl

Db 121 ATCTCTCGAGGCTAGTCAGAGTGTCTGTATAGTAATGATACAACTATTGGATTGG 180
QY 121 TACCTCGAAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGATGTCCACCCGGGCA 180
Db 181 TACCTCGAAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGGGTTCTAATCGGGCC 240
QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 241 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300
QY 241 AGCAGAGTGGAGGCTCAGGATGTTGGGGTTTATTAAGTCAACAGCTGGTAGAGTATCCA 300
Db 301 AGCAGAGTGGAGGCTCAGGATGTTGGGGTTTATTAAGTCAACAGCTGGTAGAGTATCCA 360
QY 301 TTCAGGTTGGCCAAAGGACCAAGTGGAGATCAAAAGTACGTTACGGTGGCT 348
Db 361 TTCAGTTCGGCCCTGGACCAAGTGGATATCAAAAGCAACTGTGGCT 408

RESULT 2

US-10-292-088-15

; Sequence 15, Application US/10292088

; Publication No. US20030211100A1

; GENERAL INFORMATION:

; APPLICANT: BEDIAN, VAHE

; APPLICANT: GLADUE, RONALD P.

; APPLICANT: CORVALAN, JOSE

; APPLICANT: JIA, XIAO-CHI

; APPLICANT: FENG, XIAO

; TITLE OF INVENTION: ANTIBODIES TO CD40

; FILE REFERENCE: ABX-PF/3 US

; CURRENT APPLICATION NUMBER: US/10/292,088

; CURRENT FILING DATE: 2003-03-14

; PRIOR FILING DATE: 2001-11-09

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 15

; LENGTH: 720

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-292-088-15

Query Match 78.9%; Score 274.4; DB 17; Length 720;
Best Local Similarity 86.8%; Pred. No. 1.4e-83;
Matches 302; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCTCC 60
Db 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCTCC 120
QY 61 ATCTCTGTCGCTCGAGTAAGTCTCTGTATAGTAAGTGGAGACATACTTGAATTGG 120
Db 121 ATCTCTGTCGAGTCTAGTCAGAGCTCTGTATAGTAAGTGGAGACATACTTGAATTGG 180
QY 121 TACCTCGAAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGATGTCCACCCGGGCA 180
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QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 241 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300
QY 241 AGCAGAGTGGAGGCTCAGGATGTTGGGGTTTATTAAGTCAACAGCTGGTAGAGTATCCA 300
Db 301 AGCAGAGTGGAGGCTCAGGATGTTGGGGTTTATTAAGTCAACAGCTGGTAGAGTATCCA 360
QY 301 TTCAGGTTGGCCAAAGGACCAAGTGGAGATCAAAAGTACGTTACGGTGGCT 348
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RESULT 3

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; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-292-088-55

Query Match 78.4%; Score 272.8; DB 17; Length 720;
Best Local Similarity 86.5%; Pred. No. 5.1e-83;
Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCTCC 60
Db 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCTCC 120
QY 61 ATCTCTGTCGCTCGAGTAAGTCTCTGTATAGTAAGTGGAGACATACTTGAATTGG 120
Db 121 ATCTCTGTCAGTCTAGTCAGAGCTCTCTGTATAGTAAGTGGAGATTAATCTTTGGATTGG 180
QY 121 TACCTCGAAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGATGTCCACCCGGGCA 180
Db 181 TACCTCGAAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGGGTTCTAATCGGGCC 240
QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 241 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300
QY 241 AGCAGAGTGGAGGCTCAGGATGTTGGGGTTTATTAAGTCAACAGCTGGTAGAGTATCCA 300
Db 301 AGCAGAGTGGAGGCTCAGGATGTTGGGGTTTATTAAGTCAACAGCTGGTAGAGTATCCA 360
QY 301 TTCAGGTTGGCCAAAGGACCAAGTGGAGATCAAAAGTACGTTACGGTGGCT 348
Db 361 CGGACGTTCCGCCAAGGACCAAGTGGAGATCAAAAGCAACTGTGGCT 408

RESULT 4

US-10-292-088-63

; Sequence 63, Application US/10292088

; Publication No. US20030211100A1

; GENERAL INFORMATION:

; APPLICANT: BEDIAN, VAHE

; APPLICANT: GLADUE, RONALD P.

; APPLICANT: CORVALAN, JOSE

; APPLICANT: JIA, XIAO-CHI

; APPLICANT: FENG, XIAO

; TITLE OF INVENTION: ANTIBODIES TO CD40

; FILE REFERENCE: ABX-PF/3 US

; CURRENT APPLICATION NUMBER: US/10/292,088

; CURRENT FILING DATE: 2003-03-14

; PRIOR APPLICATION NUMBER: 60/348,980

; PRIOR FILING DATE: 2001-11-09

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 63

; LENGTH: 720

; TYPE: DNA

```
; ORGANISM: Homo sapiens
US-10-292-088-63

Query Match      78.4%; Score 272.8; DB 17; Length 720;
Best Local Similarity 86.5%; Pred. No. 5.1e-83;
Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCCCTGGAGAGCGGCGCTCC 60
DB 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCCCTGGAGAGCGGCGCTCC 120
QY 61 ATCTCTGTCGTCGAGTAAGTCTCTCTGATTAAGGATGGGAAGACATACCTTGAATTGG 120
DB 121 ATCTCTGTCGAGGTCTAGTCAGAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 121 TACTCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCCGGCA 180
DB 181 TACTCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCCGGCA 240
QY 181 TCAGGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 240
DB 241 TCAGGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 300
QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 301 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 360
QY 301 TTCACGTTTCGGCCAAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 348
DB 361 CGGACGTTTCGGCCAAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 408

RESULT 5
US-10-466-164-33
; Sequence 33, Application US/10466164
; Publication No. US20040058365A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; PANZER, Scott R.;
; APPLICANT: LINCOLN, Stephen E.; ALTUS, Christina M.;
; APPLICANT: DUFOUR, Gerard E.; JACKSON, Jennifer L.;
; APPLICANT: JONES, Anissa L.; DAM, Tam C.;
; APPLICANT: LIU, Tommy F.; HARRIS, Bernard;
; APPLICANT: FLORES, Vincent Z.; DAPFO, Abel;
; APPLICANT: MARWAHA, Rakesh; CHEN, Alice J.;
; APPLICANT: CHANG, Simon C.; GERSTIN, Jr., Edward H.;
; APPLICANT: PERALTA, Careyna H.; DAVID, Marie H.;
; APPLICANT: LEWIS, Samantha A.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1215 PCT
; CURRENT APPLICATION NUMBER: US/10/466,164
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/US02/01008
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/261,865
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/263,065
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/263,329
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/262,209
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,326
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/263,063
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/261,622
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 1081

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20040058365A1 LI:1171219.2:2001JAN12
US-10-466-164-33

Query Match      78.4%; Score 272.8; DB 17; Length 1081;
Best Local Similarity 86.5%; Pred. No. 5.9e-83;
Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCCCTGGAGAGCGGCGCTCC 60
DB 87 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCAACCCCTGGAGAGCGGCGCTCC 146
QY 61 ATCTCTGTCGTCGAGTAAGTCTCTCTGATTAAGGATGGGAAGACATACCTTGAATTGG 120
DB 147 ATCTCTGTCGAGGTCTAGTCAGAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 206
QY 121 TACTCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCCGGCA 180
DB 207 TACTCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCCGGCA 266
QY 181 TCAGGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 240
DB 267 TCAGGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 326
QY 241 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 327 AGCAGAGTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 386
QY 301 TTCACGTTTCGGCCAAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 348
DB 387 TCCACTTTCGGCGGAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 434

RESULT 6
US-10-714-079C-8
; Sequence 8, Application US/10714079C
; Publication No. US20050014931A1
; GENERAL INFORMATION:
; APPLICANT: PIROFSKI, LIISE-ANNE
; APPLICANT: ZHONG, ZHAOJING
; APPLICANT: CHANG, QING
; TITLE OF INVENTION: HUMAN ANTIPNEUMOCOCCAL ANTIBODIES FROM NON-HUMAN
; TITLE OF INVENTION: ANIMALS
; FILE REFERENCE: ABX-AE1 CON
; CURRENT APPLICATION NUMBER: US/10/714,079C
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: PCT/US02/18363
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/291,492
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 649
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (462)
; OTHER INFORMATION: a, t, c, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (495)
; OTHER INFORMATION: a, t, c, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (513)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-714-079C-8
```

Query Match 77.9%; Score 271.2; DB 19; Length 649;
Best Local Similarity 86.2%; Pred. No. 1.8e-82;
Matches 300; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGAGCGGCTCC 60
DB 1 GATATTGAGCTACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGAGCGGCTCC 60

QY 61 ATCTCTGTGCTCGAGTAAAGTCTCCTGTATAGGATGGGAAGACATACCTTGAATTGG 120
DB 61 ATCTCTGAGGTCTAGTCAGAGCTCTCCGTAGTAATAGGATACAACTATTGGATTGG 120

QY 121 TACCTGAGAAGCCAGGCGAGTCTCCACAGCTCTCTATTTGATGTCCACCGGGCA 180
DB 121 TACCTGAGAAGCCAGGCGAGTCTCCACAGCTCTCTATTTGGGTTCTAATCGGGC 180

QY 181 TCAGGGGTCTCCGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 181 TCAGGGGTCTCCGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240

QY 241 AGCAGAGTGAGGCTCAGAGTGTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
DB 241 AGCAGAGTGAGGCTCAGAGTGTGGGTTTATTACTGTCAACAGCTGTACAACTCCT 300

QY 301 TTCAGGTTCCGCAAGGACCAAGGTGGAGATCAAACTACGTTGGCT 348
DB 301 CGGAGTTTCGGCAAGGACCAAGGTGGAGATCAAACTACGTTGGCT 348

RESULT 7

US-10-292-088-7
; Sequence 7, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens

Query Match 77.9%; Score 271.2; DB 17; Length 720;
Best Local Similarity 86.2%; Pred. No. 1.8e-82;
Matches 300; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGAGCGGCTCC 60
DB 61 GATATTGTGCTGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGAGCGGCTCC 120

QY 61 ATCTCTGTGCTCGAGTAAAGTCTCCTGTATAGGATGGGAAGACATACCTTGAATTGG 120
DB 121 ATCTCTGAGGTCTAGTCAGAGCTCTGTATAGTAATAGGATACAACTTTTGGATTGG 180

QY 121 TACCTGAGAAGCCAGGCGAGTCTCCACAGCTCTCTATTTGATGTCCACCGGGCA 180
DB 181 TACCTGAGAAGCCAGGCGAGTCTCCACAGCTCTCTATTTGGGTTCTAATCGGGC 240

QY 181 TCAGGGGTCTCCGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 241 TCAGGGGTCTCCGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300

QY 241 AGCAGAGTGAGGCTCAGAGTGTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 301 AGCAGATTGGAGGCTCAGAGTGTGGGTTTATTACTGTCAACAGCTGTACAACTCCT 360

QY 301 TTCAGTTCGGCCAAAGGACCAAGGTGGAGATCAAACTACGTTGGCT 348
DB 361 CGGAGTTTCGGCCAAAGGACCAAGGTGGAGATCAAACTACGTTGGCT 408

RESULT 8

US-10-292-088-35
; Sequence 35, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homo sapiens

Query Match 77.5%; Score 269.8; DB 17; Length 337;
Best Local Similarity 87.5%; Pred. No. 4.3e-82;
Matches 295; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGAGCGGCTCC 60
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGAGCGGCTCC 60

QY 61 ATCTCTGTGCTCGAGTAAAGTCTCCTGTATAGGATGGGAAGACATACCTTGAATTGG 120
DB 61 ATCTCTGCTGAGTCTAGTCAGAGTCTCTGTATAGTAATAGGATACAACTATTGGATTGG 120

QY 121 TACCTGAGAAGCCAGGCGAGTCTCCACAGCTCTCTATTTGATGTCCACCGGGCA 180
DB 121 TACCTGAGAAGCCAGGCGAGTCTCCACAGCTCTCTATTTGGGTTCTAATCGGGC 180

QY 181 TCAGGGGTCTCCGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 181 TCAGGGGTCTCCGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240

QY 241 AGCAGAGTGAGGCTCAGAGTGTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 241 AGCAGAGTGAGGCTCAGAGTGTGGGTTTATTACTGTCAACAGCTTTTACAACTCCA 300

QY 301 TTCAGTTCGGCCAAAGGACCAAGGTGGAGATCAAACTACGTTGGCT 337
DB 301 TTCAGTTCGGCCCTGGGACCAAGGTGGATATCAAACT 337

RESULT 9

US-10-638-265-11
; Sequence 11, Application US/10638265
; Publication No. US20050031614A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Foltz, Ian
; APPLICANT: King, Chadwick
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
; TITLE OF INVENTION: HORMONE (PTH) AND USES THEREOF
; FILE REFERENCE: ABGENIX.092A

; CURRENT APPLICATION NUMBER: US/10/638,265
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homosapien
US-10-638-265-11

Query Match 77.5%; Score 269.8; DB 19; Length 337;
Best Local Similarity 87.5%; Pred. No. 4.3e-82;
Matches 295; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACAGCTCTCTGATCTTATTTGGGTTCTAATCGGCTCC 60
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACAGCTCTCTGATCTTATTTGGGTTCTAATCGGCTCC 60
QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCTGTATTAAGGATGGGAAGACATATTTGAATTGG 120
DB 61 ATCTCTGTGCTCGAGTCTAGTCAGAGCTCTCTGTATAGTAATGATACAAATATTTGGATTGG 120
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTTATTTGGGTTCTAATCGGCTCC 180
DB 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTTATTTGGGTTCTAATCGGCTCC 180
QY 181 TCAGGGGTCTCCGTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 181 TCAGGGGTCTCCGTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTTACTGTCAACAGCTGGTAGAGTATCCA 300
QY 301 TTCACGTTGGCCCAAGGACCAAGTGGAGATCAAAAC 337
DB 301 TGGACGTTGGCCCAAGGACCAAGTGGAGATCAAAAC 337

RESULT 10

US-10-638-265-31
; Sequence 31, Application US/10638265
; Publication No. US20050031614A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Foltz, Ian
; APPLICANT: King, Chadwick
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
; FILE REFERENCE: HORMONE (PTH) AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/638,265
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homosapien
US-10-638-265-31

Query Match 77.5%; Score 269.8; DB 19; Length 337;
Best Local Similarity 87.5%; Pred. No. 4.3e-82;
Matches 295; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACAGCTCTCTGATCTTATTTGGGTTCTAATCGGCTCC 60
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACAGCTCTCTGATCTTATTTGGGTTCTAATCGGCTCC 60
QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCTGTATTAAGGATGGGAAGACATATTTGAATTGG 120
DB 61 ATCTCTGTGCTCGAGTCTAGTCAGAGCTCTCTGATAGTAATGATACAAATATTTGGATTGG 120
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTTATTTGGGTTCTAATCGGCTCC 180

DB 121 TTCTCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTTATTTGGGTTCTAATCGGCTCC 180
QY 181 TCAGGGGTCTCCGTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 181 TCAGGGGTCTCCGTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTTACTGTCAACAGCTGGTAGAGTATCCA 300
QY 301 TTCACGTTGGCCCAAGGACCAAGTGGAGATCAAAAC 337
DB 301 TGGACGTTGGCCCAAGGACCAAGTGGAGATCAAAAC 337

RESULT 11

US-10-292-088-79
; Sequence 79, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-292-088-79

Query Match 77.5%; Score 269.6; DB 17; Length 720;
Best Local Similarity 85.9%; Pred. No. 6.5e-82;
Matches 299; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACAGCTCTCTGATCTTATTTGGGTTCTAATCGGCTCC 60
DB 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACAGCTCTCTGATCTTATTTGGGTTCTAATCGGCTCC 120
QY 61 ATCTCTGTGCTCGAGTAAGAGTCTCTGTATTAAGGATGGGAAGACATATTTGAATTGG 120
DB 121 ATCTCTGTGCTCGAGTCTAGTCAGAGCTCTCTGCTGGTAATGGATCAACTATTTGGATTGG 180
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTTATTTGGTCCACCCGGGCA 180
DB 181 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTTATTTGGGTTCTAATCGGCTCC 240
QY 181 TCAGGGGTCTCCGTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 241 TCAGGGGTCTCCGTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTTACTGTCAACAGCTGGTAGAGTATCCA 360
QY 301 TTCACGTTGGCCCAAGGACCAAGTGGAGATCAAAACGTCACGGTGGCT 348
DB 361 CGGACGTTGGCCCAAGGACCAAGTGGAGATCAAAACGTCACGGTGGCT 408

RESULT 12

US-10-292-088-101
; Sequence 101, Application US/10292088
; Publication No. US20030211100A1

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; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-292-088-101

Query Match 77.5%; Score 269.6; DB 17; Length 720;
Best Local Similarity 85.9%; Pred. No. 6.5e-82;
Matches 299; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCTCC 60
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCTCC 60
QY 61 ATCTCTCGTCTCGAGTAAGAGTCTCCTGTATAGGATGGGAACACATATCTTGAATTGG 120
DB 61 ATCTCTCGAGGTCTTAGTCAGAGCCCTCTCGATAGTAAATGATACAAATATTTGGATTGG 120
QY 121 TACCTGCAGAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTTGATGTCCACCCGGGCA 180
DB 121 TTCTCTGCAGAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTTGGGTCTTATTCGGGCC 180
QY 181 TCAGGGGTCCCTGACAGGTTGAGTGGCAGTGGATCAGGCACACAGATTTTACACTGAAATC 240
DB 181 TCCGGGGTCCCTGACAGGTTGAGTGGCAGTGGATCAGGCACACAGATTTTACACTGAAATC 240
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 241 AGCAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
QY 301 TTCAGGTTGGGCCAAGGACCAAGGTGGAGATCAAAAC 337
DB 301 TGGACGTTTGGGCCAAGGACCAAGGTGGAAATCAAAAC 337

RESULT 14
US-10-638-265-67
; Sequence 67, Application US/10638265
; Publication No. US20050031614A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Foltz, Ian
; APPLICANT: King, Chadwick
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
; FILE REFERENCE: ABGENIX.092A
; CURRENT APPLICATION NUMBER: US/10/638,265
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homosapien
US-10-638-265-67

Query Match 77.1%; Score 268.2; DB 19; Length 337;
Best Local Similarity 87.2%; Pred. No. 1.5e-81;
Matches 294; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCTCC 60
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCTCC 60
QY 61 ATCTCTCTCGCTCGAGTAAGAGTCTCCTGTATAGGATGGGAACACATATCTTGAATTGG 120
DB 61 ATCTCTCGAGGTCTTAGTCAGAGCCCTCTCGATAGTAAATGATACAAATATTTGGATTGG 120
QY 121 TACCTGCAGAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTTGATGTCCACCCGGGCA 180
DB 121 TACCTGCAGAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTTGGGTCTTATTCGGGCC 180
QY 181 TCAGGGGTCCCTGACAGGTTGAGTGGCAGTGGATCAGGCACACAGATTTTACACTGAAATC 240
DB 181 TCCGGGGTCCCTGACAGGTTGAGTGGCAGTGGATCAGGCACACAGATTTTACACTGAAATC 240
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 241 AGCAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
QY 301 TTCAGGTTGGGCCAAGGACCAAGGTGGAGATCAAAAC 337
DB 301 TGGACGTTTGGGCCAAGGACCAAGGTGGAAATCAAAAC 337

RESULT 13
US-10-638-265-7
; Sequence 7, Application US/10638265
; Publication No. US20050031614A1
; GENERAL INFORMATION:
; APPLICANT: Roskos, Lorin
; APPLICANT: Foltz, Ian
; APPLICANT: King, Chadwick
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
; FILE REFERENCE: ABGENIX.092A
; CURRENT APPLICATION NUMBER: US/10/638,265
; CURRENT FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homosapien
US-10-638-265-7

Query Match 77.1%; Score 268.2; DB 19; Length 337;
Best Local Similarity 87.2%; Pred. No. 1.5e-81;
Matches 294; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCTCC 60
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCTCC 60
QY 61 ATCTCTCTCGCTCGAGTAAGAGTCTCCTGTATAGGATGGGAACACATATCTTGAATTGG 120
DB 61 ATCTCTCGAGGTCTTAGTCAGAGCCCTCTCGATAGTAAATGATACAAATATTTGGATTGG 120
QY 121 TACCTGCAGAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTTGATGTCCACCCGGGCA 180
DB 121 TACCTGCAGAGCCAGGGCAGTCTCCACAGCTCTCTGATCTATTTGGGTCTTATTCGGGCC 180
QY 181 TCAGGGGTCCCTGACAGGTTGAGTGGCAGTGGATCAGGCACACAGATTTTACACTGAAATC 240
DB 181 TCCGGGGTCCCTGACAGGTTGAGTGGCAGTGGATCAGGCACACAGATTTTACACTGAAATC 240
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 241 AGCAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
QY 301 TTCAGGTTGGGCCAAGGACCAAGGTGGAGATCAAAAC 337
DB 301 TGGACGTTTGGGCCAAGGACCAAGGTGGAAATCAAAAC 337
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Db 301 TGGAGGTTGGCCCAAGGACCAAGGTGGAATCAAAAC 337

RESULT 15

US-10-292-088-31
; Sequence 31, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-292-088-31

Query Match 77.0%; Score 268; DB 17; Length 720;
Best Local Similarity 85.6%; Pred. No. 2.3e-81;
Matches 298; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCCCTCACCCCTGGAGAGCCGGCCTCC 60
Db |||||||
Qy 61 ATCTCCTGTGCTCGAGTAGAGTCTCCTGTATAGGATGGGAAGACATATCTGAATGG 120
Db |||||||
Qy 121 ATCTCCTGCAAGTCTAGTCAGAGCCTCTACATACTAATGATACAACTATTTTCGATTGG 180
Db |||||||
Qy 121 TACCTGCAGAACCCAGGGCAGTCTCCACAGCTCCTGATCTATTGTGATGCCACCCGGGCA 180
Db |||||||
Qy 181 TACCTGCAGAACCCAGGGCAGTCTCCACAACTCCTGATCTATTGGGTTCTAATCGGGCC 240
Db |||||||
Qy 181 TCAGGGGTCCCTGCACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 240
Db |||||||
Qy 241 TCGGGGTCCCTGCACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 300
Db |||||||
Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db |||||||
Qy 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAATGCAAGCTCTACAAACTCCG 360
Db |||||||
Qy 301 TTCACGTTCCGCCAAGGGACCAAGTGGAGATCAAACTACGGTGGCT 348
Db |||||||
Qy 361 TACAGTTTGGCCAGGGGACCAAGCTGGAGATCAAACTACGGTGGCT 408
Db |||||||

Search completed: April 19, 2005, 00:13:29
Job time : 948.356 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 67.129 Seconds
(without alignments)
8482.539 Million cell updates/sec

Title: US-09-674-716B-17

Perfect score: 348

Sequence: 1 gatattgtgatcactcagtc.....agatcaaacgtacggtgct 348

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
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- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	261.2	75.1	339	1	US-08-082-623-2
2	256.8	73.8	968	4	US-10-000-489-7
3	252.8	72.6	336	3	US-09-000-088-1
4	252	72.4	336	3	US-09-240-274-99
5	249.4	71.7	339	1	US-08-264-093-9
6	244	70.1	420	3	US-09-214-095D-111
7	244	70.1	464	1	US-08-438-123-15
8	243.6	70.0	339	2	US-08-672-345C-88
9	243.6	70.0	339	3	US-09-214-095D-99
10	240.4	69.1	368	2	US-08-672-345C-86
11	240.4	69.1	368	3	US-09-214-095D-107
12	239.2	68.7	368	2	US-08-672-345C-90
13	239.2	68.7	368	3	US-09-214-095D-103
14	239.2	68.7	666	4	US-09-479-614-25
15	239.2	68.7	666	4	US-09-479-614-27
16	239.2	68.7	726	4	US-09-479-614-23
17	239.2	68.7	726	4	US-09-479-614-24
18	239.2	68.7	954	4	US-09-479-614-19
19	239.2	68.7	954	4	US-09-479-614-21
20	238.8	68.6	339	3	US-09-406-532-13
21	231.6	66.6	375	1	US-08-482-882-65
22	231.6	66.6	375	1	US-08-482-882-65
23	231.6	66.6	375	2	US-08-487-113D-65
24	231.6	66.6	375	2	US-08-473-503-65
25	231.6	66.6	375	2	US-08-483-932-65
26	231.6	66.6	375	2	US-08-720-420A-65
27	231.6	66.6	375	3	US-08-714-017-65

28	231.6	66.6	375	3	US-08-475-680-65
29	228.8	65.7	336	3	US-08-483-749A-3
30	228.6	65.7	344	4	US-09-840-459-98
31	228.6	65.7	344	4	US-09-840-459-105
32	228.6	65.7	344	4	US-09-497-625A-98
33	228.6	65.7	344	4	US-09-497-625A-105
34	227.6	65.4	419	4	US-09-472-087-52
35	227.4	65.3	373	3	US-08-732-708C-40
36	226	64.9	399	1	US-08-253-877C-9
37	226	64.9	399	2	US-08-452-164A-9
38	226	64.9	399	3	US-08-603-024-3
39	226	64.9	399	4	US-08-450-809-2
40	225.2	64.7	882	1	US-08-392-419-3
41	224.8	64.6	720	3	US-08-487-550-5
42	224.8	64.6	720	4	US-09-526-098-5
43	224.8	64.6	720	4	US-09-383-916-5
44	222.2	63.9	1095	3	US-08-875-811-52
45	222.2	63.9	1098	3	US-08-875-811-54

ALIGNMENTS

RESULT 1
US-08-082-623-2
; Sequence 2, Application US/08082623
; Patent No. 5750106
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO
; CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082, 623
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010,228
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-055-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..339
; OTHER INFORMATION: /standard_name= "Nucleotide
; OTHER INFORMATION: Sequence of the V-1 region of SDZ MSL 109"
; Patent No. 5750106

US-08-082-623-2

Query Match 75.1%; Score 261.2; DB 1; Length 339;
Best Local Similarity 85.8%; Pred. No. 6.7e-77;
Matches 290; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGCGCTCC 60
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGCGCTCC 60

QY 61 ATCTCTCTCGCTCGAGTAAAGTCTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 120
DB 61 ATCTCTCTCGAGTCTAGTCAGAGCTCTCTGATACATACTAATGGATACAACTATTGGATTGG 120

QY 121 TACCTCGAAGCAGCGGAGCTCTCCAGAGCTCTGATCTATTTGATGTCCACCGGGCA 180
DB 121 TAGCTGCAAGCAGCGGAGCTCTCCAGAGCTCTGATCTATCTGCTTCTAATCGGGCC 180

QY 181 TCAGGGGTCCTGACAGGTTTCAGTGGCAGTCAGGACAGATTTTACACTGAAAATC 240
DB 181 TCAGGGGTCCTGACAGGTTTCAGTGGCAGTCAGGACAGATTTTACACTGAAAATC 240

QY 241 AGCAGAGTGGAGCTCAGGATGTTGGGGTTTATCTGTCAACAGCTGGTAGAGTATCCA 300
DB 241 AGCAGAGTGGAGCTCAGGATGTTGGGGTTTATCTGTCAACAGCTGGTAGAGTATCCA 300

QY 301 TTCACGTTCCGCAAGGACCAAGGTGGAGATCAAAACG 338
DB 301 CGGACGTTCCGCCAAGGACCAAGGTGGAGATCAAAACG 338

RESULT 2

US-10-000-489-7

; Sequence 7, Application US/10000489
; Patent No. 6794363
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.056.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 7
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..31
; NAME/KEY: CDS
; LOCATION: 32..748
; NAME/KEY: 3'UTR
; LOCATION: 749..968
; NAME/KEY: polyA_signal
; LOCATION: 928..933
; NAME/KEY: polyA_site
; LOCATION: 953..968
US-10-000-489-7

Query Match 73.8%; Score 256.8; DB 4; Length 968;
Best Local Similarity 83.6%; Pred. No. 3.1e-75;
Matches 291; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGCGCTCC 60
DB 92 GATATTGTGATGACTCAGTCTCCACTCTCTCTGCCGTCACCCCTGGAGAGCGCGCTCC 151

QY 61 ATCTCTCTCGCTCGAGTAAAGTCTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 120
DB 152 ATCTCTCTCGAGTCTAGTCAGAGCTCTGATCTTCAAGGGTCCAACTATTGGATTGG 211

QY 121 TACCTGCAAGCAGCGGAGCTCTCCAGAGCTCTCTGATCTATTTGATGTCCACCGGGCA 180
DB 212 TACCAACAGAGCAGCGGAGCTCTCCAACTCTCTGATATATTTGGGTTCTAATCGGGCC 271

QY 181 TCAGGGGTCCTGACAGGTTTCAGTGGCAGTCAGGACAGATTTTACACTGAAAATC 240
DB 272 TCAGGGGTCCTGACAGGTTTCAGTGGCAGTCAGGACAGATTTTACACTGAAAATC 331

QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATCTGTCAACAGCTGGTAGAGTATCCA 300
DB 332 AGTAGAGTGGAGGCTGAGGATGTTGGGGTTTATCTGTCAACAGCTGGTAGAGTATCCA 391

QY 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAAACG 348
DB 392 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAAAACG 439

RESULT 3

US-09-000-088-1

; Sequence 1, Application US/09000088
; Patent No. 6146629
; GENERAL INFORMATION:
; APPLICANT: DAGAN, Shlomo
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST HEPATITIS B VIRUS
; TITLE OF INVENTION: SURFACE ANTIGEN (HBVSAg)
; FILE REFERENCE: DAGAN=1
; CURRENT APPLICATION NUMBER: US/09/000,088
; CURRENT FILING DATE: 1998-01-22
; EARLIER APPLICATION NUMBER: PCT/IL97/00183
; EARLIER FILING DATE: 1997-06-10
; EARLIER APPLICATION NUMBER: IL96/118626
; EARLIER FILING DATE: 1996-06-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 336
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(336)
US-09-000-088-1

Query Match 72.6%; Score 252.8; DB 3; Length 336;
Best Local Similarity 84.5%; Pred. No. 4.2e-74;
Matches 284; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGCGCTCC 60
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGCGCTCC 60

QY 61 ATCTCTCTCGCTCGAGTAAAGTCTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 120
DB 61 ATCTCTCTCGAGTCTAGTCAGAGCTCTCTGATAGTCTGGAACAACTATTGGATTGG 120

QY 121 TACCTGCAAGCAGCGGAGCTCTCCAGAGCTCTCTGATCTATTTGATGTCCACCGGGCA 180
DB 121 TACCTGCAAGCAGCGGAGCTCTCCAGAGCTCTCTGATCTATGTGGTTCTAATCGGGCC 180

QY 181 TCAGGGGTCCTGACAGGTTTCAGTGGCAGTCAGGACAGATTTTACACTGAAAATC 240
DB 181 TCAGGGGTCCTGACAGGTTTCAGTGGCAGTCAGGACAGATTTTACACTGAAAATC 240

Db 181 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGAGTATACACTGAAATC 240
Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 241 AGTAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Qy 301 TTCAGTTTCGGCCAGGAGCAGAGTGGAGATCAAA 336
Db 301 CGGACTTTTGGCCAGGAGCAGAGTGGAGATCAAA 336

RESULT 4

US-09-240-274-99
; Sequence 99, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain G01
US-09-240-274-99

Query Match 72.4%; Score 252; DB 3; Length 336;
Best Local Similarity 84.9%; Pred. No. 7.7e-74;
Matches 282; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
Qy 7 GTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCGGCTCCATCTCC 66
Db 4 GAGCTCACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCGGCTCCATCTCC 63
Qy 67 TGTGCTCGAGTAAAGTCTCTGTATAAGGATGGGAAGACATCTTGAATTCGTACCTG 126
Db 64 TGCAGTCTAGTCAGAGCTCTCTGCATAGTAGTGGATCACTTTTGGATTTGGTACCTG 123
Qy 127 CAGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTATGTCACCCGGGATCAGGG 186
Db 124 CAGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATATGGTTCTAATCGGGCTCCGGG 183
Qy 187 GTCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACATGAAATCAGCAGA 246
Db 184 GTCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACATGAAATCAGCAGA 243
Qy 247 GTGAGGCTCAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCAATTCAG 306
Db 244 GTGAGGCTCAGGATGTTGGGGTTTATTACTGTCAACAGCTTACAAATTCCTCTCACT 303
Qy 307 TTCGGCCAGGAGCAGGAGTGGAGATCAAAACG 338
Db 304 TTCGGCGAGGAGCAGGAGTGGAGATCAAAACG 335

RESULT 5

US-08-264-093-9
; Sequence 9, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE

; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; STREET: 101 Richmond Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-08-264-093-9

Query Match 71.7%; Score 249.4; DB 1; Length 339;
Best Local Similarity 85.5%; Pred. No. 5.7e-73;
Matches 290; Conservative 0; Mismatches 46; Indels 3; Gaps 1;
Qy 1 GATATTGTGATCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCGGCTCC 60
Db 1 GATATTGTGATCAGGAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCGGCTCC 60
Qy 61 ATCTCTCTGCTCGAGTAAAGTCTCTGTATA---AGGATGGGAAGACATCTTGAAT 117
Db 61 ATCTCTCTGAGTCTAGTCAGAGCTCTTGGATAGTAGTATGGAACACCTATTGGAC 120
Qy 118 TGGTACCTGCAGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTGATGCCCGG 177
Db 121 TGGTACCTGCAGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATACGCTTCTATCGG 180
Qy 178 GCATCAGGGGTCCTGCAGAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAA 237
Db 181 GCCTCTGGAGTCCCAAGACAGAGTTCAGTGGCAGTGGGTGAGGACATGATTTTCACTGAAA 240
Qy 238 ATCAGCAGAGTGGAGCTCAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTAT 297
Db 241 ATCAGCAGGTTGAGGCTGAGGATGTTGGAGTTTATTCTGATGCAACGATGATAGAGTTT 300
Qy 298 CCAATTCACGTTCCGGCCAGGAGCAGGAGTGGAGATCAAA 336
Db 301 CTTTTCACGTTCCGGCGAGGAGCAGGAGTGGAGATCAAA 339

RESULT 6

US-09-214-095D-111
; Sequence 111, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D

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; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 111
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: V segment
; LOCATION: (1) - (403)
; OTHER INFORMATION: n at any position represents any nucleotide including c,g,t,a,u
; US-09-214-095D-111

Query Match 70.1%; Score 244; DB 3; Length 420;
Best Local Similarity 81.3%; Pred. No. 3,9e-71;
Matches 283; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGCGCTCC 60
    |||||
Db 53 GATATGGTGATGAGCGAGGATGAACCTCCAACTCCTGTCACTTCTGGAGATCAGTTTCC 112
    |||||

Qy 61 ATCTCTGTGCTCGAGTGAAGAGTCTCTGTATAAGATGGGAAGACATATCTGAATTGG 120
    |||||
Db 113 ATCTCTGCGAGTCTAGTAGGAGTCTCTATATAGGGATGGGAAGACATATCTGAATTGG 172
    |||||

Qy 121 TACCTCGAAGCCAGGGGAGTCTCCACAGCTCCTGATCTATTTGATGTCACCCGGGCA 180
    |||||
Db 173 TTTCTCGAGAGACGAGGACGATCTCTCAACTCCTGATCTATTTGATGTCACCCGGTGA 232
    |||||

Qy 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGATCAGGCACAGATTTTACACTGAAATC 240
    |||||
Db 233 TCAGGAGTCTCAGACCGGTTTATGTGAGTGCGGTGAGGATCAGGAACAGATTTCACTGGAATC 292
    |||||

Qy 241 AGCAGAGTGGAGGCTGAGGATGTGTGGGGTTTATTACTGTCAACAGCTGCTAGAGTATCCA 300
    |||||
Db 293 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAACACTTTGTAGACTATCCA 352
    |||||

Qy 301 TTCACGTTTCGGCCAAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348
    |||||
Db 353 TTCACGTTTCGGTTCGGGGCAAAAGTTGGAGATAAACCGGTTGATGCT 400
    |||||

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-438-123-15

Query Match 70.1%; Score 244; DB 1; Length 464;
Best Local Similarity 81.3%; Pred. No. 4.le-71;
Matches 283; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGAGCGGCTCC 60
Db 102 GATATTGTGATGACTCAGGCTGCACCCCTCTGTACTCTGTCACTCTCTGGAGAGTCAGTATCC 161
Qy 61 ATCTCTCTGTCGTCGATAGAGTCTCTCTATATAGGATGGAGACATACTTGAATTGG 120
Db 162 ATCTCTGTCAGGTCTAGTAAGAGTCTCTGCAAGTAAATGGCAACCTTACTTTATTTGG 221
Qy 121 TACCTGCAGAAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTATGTCCACCCGGGCA 180
Db 222 TTCTCTGCAGAGGCCAGGCCAGTCTCCTCAGCTCTGATATATCGGATGTCCAACTTTGTC 281
Qy 181 TCAGGGGTTCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 282 TCAGGAGTCCGACAGGTTTCAGTGGCAGTGGGTTCAGGAACTGCTTTCACTAGAGAATC 341
Qy 241 AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGTCAAACAGCTGGTAGAGTATCCA 300
Db 342 AGTAGAGTGGAGGCTGAGGATGTTGGGTGTTTATCTGTCTGCACATCTAGAGTATCCG 401
Qy 301 TTCACGTTCCGCCCAAGGACCAAGGTGGAGATCAAAAGTACGGTGGCT 348
Db 402 TTCACGTTCCGTTCTGGGACCAAGCTCGAGCTGAAACGGGCTGATGCT 449

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RESULT 7
 US-08-438-123-15
 ; Sequence 15, Application US/08438123
 ; Patent No. 5552293
 ; GENERAL INFORMATION:
 ; APPLICANT: Lindholm et al
 ; TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lowe, Price, Leblanc & Becker
 ; STREET: Suite 300, 99 Canal Center Plaza
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22314
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: DOS Text File
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/438,123
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/906,350
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: J.G. Mullins
 ; REGISTRATION NUMBER: 33073
 ; REFERENCE/DOCKET NUMBER: 149-011

RESULT 8
 US-08-672-345C-88
 ; Sequence 88, Application US/08672345C
 ; Patent No. 5948658
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry Donald, W.
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; NUMBER OF SEQUENCES: 108
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper and Durham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/672,345C
 ; FILING DATE: 24-JUN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 0575/51400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 88:
 ; SEQUENCE CHARACTERISTICS

Qy	241	AGCAGAGTGGAGGCTCAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA	300
Db	241	AGTAGAGTGAAGGCTGAGGATGCTGGGTGTGTATTACTGTCAACACTTTGTAGAGTATCCA	300
Qy	301	TTACAGTTCGGCCAAAGGACCAAGGTGGAGATCAAAACG	338
Db	301	TTACAGTTCGGCTCGGGACAAAGTTGGAGATAAAACG	338
RESULT 10			
US-08-672-345C-86			
; Sequence 86, Application US/08672345C			
; Patent No. 5948658			
; GENERAL INFORMATION:			
; APPLICANT: Landry Donald, W.			
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY			
; NUMBER OF SEQUENCES: 108			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Cooper and Dunham LLP			
; STREET: 1185 Avenue of the Americas			
; CITY: New York			
; STATE: New York			
; COUNTRY: USA			
; ZIP: 10036			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/672,345C			
; FILING DATE: 24-JUN-1996			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; NAME: White, John P.			
; REGISTRATION NUMBER: 28,678			
; REFERENCE/DOCKET NUMBER: 0575/51400			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 212-278-0400			
; TELEFAX: 212-391-0525			
; INFORMATION FOR SEQ ID NO: 86:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 368 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: cDNA			
; US-08-672-345C-86			
Query Match 69.1%; Score 240.4; DB 2; Length 368;			
Best Local Similarity 82.0%; Pred. No. 5.9e-70;			
Matches 277; Conservative 0; Mismatches 61; Indels 0; Gaps 0			
Qy	1	GATATTGTGATGACTCAGTCTCCA	60
Db	1	GATATGGTGATGACGCAAGACGA	60
Qy	61	ATCTCTCTGCTCGAGTAAAGATCTCTGTATGAAGATGGGAAGACATATCTGAATTGG	120
Db	61	ATCTCTCTGCGTCTAGTAAAGATCTCTATATGAGGATGGGAAGACATATCTGAATTGG	120
Qy	121	TACCTGCAGAGCCAGGCGCAGTCTCCA	180
Db	121	TTTCTGACAGACACAGGCAATCTCCT	180
Qy	181	TCAGGGGTCCCTGCAGCAGGTT	240
Db	181	TCAGGAGTCTCAGACCGGTT	240
Qy	241	AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA	300
Db	241	AGTAGAGTGAAGGCTGAGGATGCTGGGTGTGTATTACTGTCAACAAATTTGTAGAGTATCCA	300

QY 301 TTCACGTTCCGCAAGGACCAAGGTGGAGATCAACG 338
DB 301 TTCACGTTCCGCTCGGGGCAAAAGTTGGAATAAGACG 338

RESULT 11

US-09-214-095D-107

; Sequence 107, Application US/09214095D

; Patent No. 6280987

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 51400-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/214,095D

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 107

; LENGTH: 368

; TYPE: DNA

; ORGANISM: Murine

US-09-214-095D-107

Query Match 69.1%; Score 240.4; DB 3; Length 368;

Best Local Similarity 82.0%; Pred. No. 5.9e-70; Mismatches 61; Indels 0; Gaps 0;

Matches 277; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGGCGCTCC 60

DB 1 GATATGGTATGACGCAAGCAAGCAACTCTCCAACTCTGTCACCTCTGAGAGATCAGTTTCC 60

QY 61 ATCTCTGTCGTCGAGTAAGTCTCCTGTATAGGATGGGAAGACATACCTTGAATTGG 120

DB 61 ATCTCTGTCGAGTCTAGTAAGTCTCCTATATAGGATGGGAAGACATACCTTGAATTGG 120

QY 121 TACCTCAGAACGACGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCGCGGCA 180

DB 121 TTTCTCAGAGACGACGACAATCTCTCCTCTGATCTATTGATGTCACCCGCGGCA 180

QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTACACTGAAATC 240

DB 181 TCAGGAGTCTCAGACCGTTTAGTGGCAGTGGGTGAGAACAGATTTACACTGAAATC 240

QY 241 AGCAGAGTGAGCTCAGATGTTGGGTTTATTACTGTCAACAGCTGTAGATATCCA 300

DB 241 AGTAGAGTGAAGCTCAGGATGTTGGTGGCTATTACTGTCAACAATTTGTAGATATCCA 300

QY 301 TTCACGTTCCGCAAGGACCAAGGTGGAGATCAACG 338

DB 301 TTCACGTTCCGCTCGGGGCAAAAGTTGGAATAAGACG 338

RESULT 12

US-08-672-345C-90

; Sequence 90, Application US/08672345C

; Patent No. 5948658

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald, W.

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; NUMBER OF SEQUENCES: 108

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper and Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/672,345C

; FILING DATE: 24-JUN-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/51400

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-278-0400

; TELEFAX: 212-391-0525

; INFORMATION FOR SEQ ID NO: 90:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 368 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-672-345C-90

Query Match 68.7%; Score 239.2; DB 2; Length 368;

Best Local Similarity 80.5%; Pred. No. 1.5e-69;

Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGGCGCTCC 60

DB 1 GATATGGTATGACGCAAGATGAACTCTCCAACTCTGTCACCTCTGAGAGATCAGTTTCC 60

QY 61 ATCTCTGTCGTCGAGTAAGTCTCCTGTATAGGATGGGAAGACATACCTTGAATTGG 120

DB 61 ATCTCTGTCGAGTCTAGTAGGAGTCTCCTATATAGGATGGGAAGACATACCTTGAATTGG 120

QY 121 TACCTGCAAGACGCGGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCGCGGCA 180

DB 121 TTTCTCAGAGACGAGGACGATCTCCTCACTCTGATCTATTGATGTCACCCGCGGCA 180

QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTACACTGAAATC 240

DB 181 TCAGGAGTCTCAGACCGTTTAGTGGCAGTGGGTGAGAACAGATTTACACTGAAATC 240

QY 241 AGCAGAGTGGAGCTGAGAGTGTGGGTTTATTACTGTCAACAGCTGTAGATATCCA 300

DB 241 AGTAGAGTGAAGCTGAGGATGTTGGTGGCTATTACTGTCAACAATTTGAGAGACTATCCA 300

QY 301 TTCACGTTCCGCAAGGACCAAGGTGGAGATCAACG 348

DB 301 TTCACGTTCCGCTCGGGGCAAAATTTGAGATCAACGCGGCTGATGCT 348

RESULT 13

US-09-214-095D-103

; Sequence 103, Application US/09214095D

; Patent No. 6280987

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 51400-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/214,095D

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 103

; LENGTH: 368

; TYPE: DNA

; ORGANISM: MURINE

US-09-214-095D-103

Query Match 68.7%; Score 239.2; DB 3; Length 368;

Best Local Similarity 80.5%; Pred. No. 1.5e-69;

Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCGGCGCTCC 60

Db 1 GATATGTGTAGTACGCAAGATGAATCTCTCAATCTCTGTCTCACTTTCTGGAGAAATCAGTTTCC 60
Qy 61 ATCTCTGTCTGCTCAGTAAGAGTCTCTGTATAAGGATGGGAAGACATATCTTGAATTGG 120
Db 61 ATCTCTGCAAGTCTAGTAGAGTCTCTGTATATAGGATGGGAAGACATATCTTGAATTGG 120
Qy 121 TACCTGCAAGAGCCAGGCGAGTCTCCACAGCTCTGTATCTTATTTGATGTCCACCCGGGCA 180
Db 121 TTTCTGCAGAGACCAGGACGATCTCTCAACTCTGTATCTTATTTGATGTCCACCCGGTCA 180
Qy 181 TCAGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACATGAAATC 240
Db 181 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTTCAGGAAACAGATTTTCACTTGGAAATC 240
Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 241 AGTAGAGTGAAGGCTGAGGATGTTGGGTGTATTTACTTTCAACACTTTGAGAGCTATCCA 300
Qy 301 TTCACGTTCCGCCCAAGGACCAAGGTGGAGATCAAACTACGGTGGCT 348
Db 301 TTCACGTTCCGGCTCGGGGACAAAATTTGGAGATAAAACGGGCTGATGCT 348

RESULT 14

US-09-479-614-25

; Sequence 25, Application US/09479614

; Patent No. 6573372

; GENERAL INFORMATION:

; APPLICANT: McCall, Catherine

; APPLICANT: Weber, Eric

; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

; FILE REFERENCE: P-1047

; CURRENT APPLICATION NUMBER: US/09/479,614

; EARLIER FILING DATE: 2000-01-07

; EARLIER FILING DATE: 1999-01-07

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 25

; LENGTH: 666

; TYPE: DNA

; ORGANISM: Felis catus

US-09-479-614-25

Query Match 68.7%; Score 239.2; DB 4; Length 666;
Best Local Similarity 80.5%; Pred. No. 1.9e-69;
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 1 GATATGTGTAGTACGCTCAGTCTCCACTCTCCCTGCCGTCAACCCCTGGAGAGCCGGCTCC 60
Db 1 GATATGTGTAGTACGAGACCCCTCTGTCTCTGCTCAACCCCTGGAGAGCCAGCTCA 60
Qy 61 ATCTCTGTCTGCTCAGTAAGAGTCTCTGTATAAGGATGGGAAGACATATCTTGAATTGG 120
Db 61 ATCTCTGCAAGGCGCAGGAGCTCTGTACAGTGTGAAATATCTTATCTGAATTGG 120
Qy 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTGTATCTTATTTGATGTCCACCCGGGCA 180
Db 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCGGTGTATCTTATTTTCCAAACCGGGAC 180
Qy 181 TCAGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACATGAAATC 240
Db 181 TCTGGGTTCCAGACAGGTTTCAGTGGCAGTGGGTTCAGGACAGATTTTCACTTGAATC 240
Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 241 AGCAGGGTGGAGGCTGACGACGCTCGGTGTTTATTACTCGGTTCAAGGTTTACAGCATCT 300
Qy 301 TTCACGTTCCGCCCAAGGACCAAGGTGGAGATCAAACTACGGTGGCT 348
Db 301 CTCACTTTCGGCCCGAGGTACCAAGCTGGAGATCAAAACGGAGTGTATGCT 348

RESULT 15

US-09-479-614-27/c

; Sequence 27, Application US/09479614

; Patent No. 6573372

; GENERAL INFORMATION:

; APPLICANT: McCall, Catherine

; APPLICANT: Weber, Eric

; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

; FILE REFERENCE: P-1047

; CURRENT APPLICATION NUMBER: US/09/479,614

; EARLIER FILING DATE: 2000-01-07

; EARLIER FILING DATE: 1999-01-07

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 27

; LENGTH: 666

; TYPE: DNA

; ORGANISM: Felis catus

US-09-479-614-27

Query Match 68.7%; Score 239.2; DB 4; Length 666;
Best Local Similarity 80.5%; Pred. No. 1.9e-69;
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 1 GATATGTGTAGTACGCTCAGTCTCCACTCTCCCTGCCGTCAACCCCTGGAGAGCCGGCTCC 60
Db 666 GATATGTGTAGTACGAGACCCCTCTGTCTCTGCTCAACCCCTGGAGAGCCAGCTCA 607
Qy 61 ATCTCTGTCTGCTCAGTAAGAGTCTCTGTATAAGGATGGGAAGACATATCTTGAATTGG 120
Db 606 ATCTCTGTGAGGCGCAGTCAGAGCCTCTGTACAGTGTGAAATATCTTATCTGAATTGG 547
Qy 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTGTATTTGATGTCCACCCGGGCA 180
Db 546 TACCTGCAGAGCCAGGCGAGTCTCCACGCGGCTTGTATCTTCTTTTCCAAACCGGGAC 487
Qy 181 TCAGGGTCTCTGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACATGAAATC 240
Db 486 TCTGGGTTCCAGACAGGTTTCAGTGGCAGTGGGTTCAGGACAGATTTTCACTTGAATC 427
Qy 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 426 AGCAGGGTGGAGGCTGACGACGTCGGTGTTTATTACTCGGTTCAAGGTTTACAGCATCT 367
Qy 301 TTCACGTTCCGCCCAAGGACCAAGGTGGAGATCAAACTACGGTGGCT 348
Db 366 CTCACTTTCGGCCCGAGGTACCAAGCTGGAGATCAAAACGGAGTGTATGCT 319

Search completed: April 18, 2005, 21:13:07

Job time : 68.129 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 5929.82 Seconds
(without alignments)
10908.879 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 1335

Sequence: 1 gaggtgcagctgtgtgagtc.....ccctgtctcgggtaaatga 1335

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1335	100.0	1335	6	BD232425 Antibody
2	1335	100.0	1335	6	BD232452 Antibody
3	1335	100.0	1335	6	AX010615 Sequence
4	1335	100.0	1335	6	AX010646 Sequence
5	1163.2	87.1	1626	9	AK129510 Homo sapi
6	1160.8	87.0	1639	9	AK130434 Homo sapi
7	1160.6	86.9	1685	9	BC065820 Homo sapi
8	1158	86.7	1645	9	CQ850293 Sequence
9	1158	86.7	1645	9	AK127409 Homo sapi
10	1156	86.6	1679	9	BC018747 Homo sapi
11	1154.6	86.5	1392	6	CQ774324 Sequence
12	1154.6	86.5	1392	6	CQ790351 Sequence
13	1154.6	86.5	1392	6	CQ812157 Sequence
14	1154.6	86.5	1392	6	CQ816433 Sequence
15	1154.6	86.5	1392	6	AX594307 Sequence
16	1154.6	86.5	1392	6	AX616608 Sequence
17	1154.6	86.5	1392	6	AX616908 Sequence
18	1154.6	86.5	9568	6	AX616611 Sequence
19	1149.2	86.1	1404	9	AF027159 Homo sapi

20	1149.2	86.1	1422	9	AB159728 Homo sapi
21	1149.2	86.1	1442	6	BD266675 Human mon
22	1147.8	86.0	1634	9	BC072419 Homo sapi
23	1147.2	85.9	1437	6	AR108865 Sequence
24	1147.2	85.9	1437	6	AR285199 Sequence
25	1147.2	85.9	1437	6	AR488221 Sequence
26	1147.2	85.9	1437	6	BD063037 Identific
27	1146.6	85.9	1630	9	BC024289 Homo sapi
28	1146.6	85.8	1659	9	BC014667 Homo sapi
29	1145.6	85.8	1694	9	EX640620 Homo sapi
30	1145	85.8	1694	9	HS080665 Sequence
31	1143.4	85.6	1416	6	CQ758863 Sequence
32	1142.8	85.6	6281	6	CQ758861 Sequence
33	1141.2	85.5	1620	6	BD266673 Human mon
34	1141.2	85.5	1620	6	CQ843166 Sequence
35	1141.2	85.5	1620	9	AK126132 Homo sapi
36	1139.4	85.3	19040	6	BD075127 Method fo
37	1139	85.3	1621	9	AK130844 Homo sapi
38	1137	85.2	1628	6	CQ758864 Sequence
39	1137	85.2	1628	6	CQ850299 Sequence
40	1136.2	85.1	1410	6	AK127415 Homo sapi
41	1136	85.1	1425	9	CQ758862 Sequence
42	1136	85.1	1430	6	AX172959 Homo sapi
43	1135	85.0	1347	6	AX419496 Sequence
44	1133.8	84.9	7521	6	BD222482 Human/rod
45	1131.2	84.7	1621	9	AX080951 Sequence
					BC064496 Homo sapi

ALIGNMENTS

RESULT 1	BD232425	1335 bp	DNA	linear	PAT 17-JUL-2003	
LOCUS	BD232425	Antibodies against CD23, derivatives thereof and therapeutic utilization of the same.				
DEFINITION	BD232425	utilization of the same.				
ACCESSION	BD232425	1	GI:33042195			
VERSION	BD232425	1	GI:33042195			
KEYWORDS	JP 2002514421-A/9.					
SOURCE	synthetic construct					
ORGANISM	synthetic construct					
REFERENCE	1 (bases 1 to 1335)					
AUTHORS	Bonnefoy,J.Y.M.P., Crowe,S.J., Ellis,J.H., Rapson,N.T. and Shearin,J.					
TITLE	Antibodies against CD23, derivatives thereof and therapeutic utilization of the same					
JOURNAL	Patent: JP 2002514421-A 9 21-MAY-2002;					
COMMENT	GLAXO GROUP LTD					
	OS Artificial Sequence					
	PN JP 2002514421-A/9					
	PD 21-MAY-2002					
	PF 07-MAY-1999 JP 2000548470					
	PR 09-MAY-1998 GB 9809839.5					
	PI JEAN YVES MARCEL PAUL BONNEFOY,SCOTT JAMES CROWE,JONATHAN PI HENRY ELLIS,					
	PI NICHOLAS TIMOTHY RAPSON,JEAN SHEARIN					
	PC C12N15/02,A61K39/395,C07K16/28,C12N15/00					
	CC Description of Artificial Sequence: Humanised anti-CD23 CC antibody heavy chain variable region.					
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RESULT 2
BD232452/c 1335 bp DNA linear PAT 17-JUL-2003
LOCUS Antibodies against CD23, derivatives thereof and therapeutic
DEFINITION utilization of the same.
ACCESSION BD232452
VERSION BD232452.1 GI:33042222
KEYWORDS JP 2002514421-A/36.
SOURCE synthetic construct
ORGANISM synthetic construct; artificial sequences.
REFERENCE 1 (bases 1 to 1335)
AUTHORS Bonnefoy,J.Y.M.P., Crowe,S.J., Ellis,J.H., Rapson,N.T. and Shearin,J.
TITLE Antibodies against CD23, derivatives thereof and therapeutic
JOURNAL utilization of the same
Patent: JP 2002514421-A 36 21-MAY-2002;
COMMENT GLAXO GROUP LTD
OS Artificial Sequence
PN JP 2002514421-A/36
PD 21-MAY-2002
PF 07-MAY-1999 JP 2000548470
PR 08-MAY-1998 GB 9809839.5
PI JEAN YVES MARCEL PAUL BONNEFOY,SCOTT JAMES CROWE,JONATHAN PI
HENRY ELLIS,
PI NICHOLAS TIMOTHY RAPSON,JEAN SHEARIN
PC Cl2N15/02,A61K39/395,C07K16/28,Cl2N15/00
CC Description of Artificial Sequence: Humanised anti-CD23 CC
antibody heavy
CC chain variable region
FH Key Location/Qualifiers
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Query Match 100.0%; Score 1335; DB 6; Length 1335;
Best Local Similarity 100.0%; Pred. No. 4.2e-264;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGTGCACTGGTGAAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
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AX010615
LOCUS 1335 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 18 from Patent WO9958679.
ACCESSION AX010615
VERSION AX010615.1 GI:9997427
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.
TITLE Antibodies to cd23, derivatives thereof, and their therapeutic uses
JOURNAL Patent: WO 9958679-A 18 NOV-1999;
Bonnefoy JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY (GB); SHEARIN JEAN (US)
FEATURES
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ORIGIN
Query Match 100.0%; Score 1335; DB 6; Length 1335;
Best Local Similarity 100.0%; Pred. No. 4.2e-264;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION	Sequence 49 from Patent WO958679.		
ACCESSION	AX010646		
VERSION	AX010646.1 GI:9997455		
KEYWORDS	synthetic construct		
SOURCE	synthetic constrcut		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Bonneyfoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.		
TITLE	Antibodies to cd23, derivatives thereof, and their therapeutic uses		
JOURNAL	Patent: WO 958679-A 49 18-NOV-1999;		
	BONNEYFOY JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY (GB); SHEARIN JEAN (US)		
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Db	855	ACCAGCGCGTGCACACCTTCCCCGGCTGTCTCTACAGTCTCTCAGACTCTACTCCCTCAGC	796
Qy	541	AGCGTGTGACCGTGGCCCTTCAGACGCTTGGGCAACCCAGACCTACATCTCGAACGTGAAT	600
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AUTHORS
TITLE
JOURNAL

COMMENT

FEATURES
source

CDS

ORIGIN

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Query Match 87.1%; Score 1163.2; DB 9; Length 1626;
Best Local Similarity 92.0%; Pred. No. 8.6e-229;
Matches 1247; Conservative 0; Mismatches 88; Indels 21; Gaps 1;

QY 1 GAGGTGCGAGCTGCTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
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DB 318 GAATCTGTCGCTGTGTGAAGGAGATTCACCATCTCAAGAGATGATTCCGAGGCTGTC 377
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DB 378 GCCTATCTTCAATGAACAGCTCTGAAACCGAGGACACAGCCATATATTACTGTACTAGA 437
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DB 438 GAGCCCATGAGACGCCACTGCTTTTGTATCTCTGGGGCCCAAGGGACATTTGGTTCACCGTCTCT 497
QY 340 TCAGCTCTCCACCAAGGGCCCATCGCTTCTCCCTCTGACCCCTCTCTCAAGAGACCTCT 399
DB 498 TCAGCTCTCCACCAAGGGCCCATCGCTTCTCCCTCTGACCCCTCTCTCTCAAGAGACCTCT 557
QY 400 GGGGGCACAGCGGCCCTCTGGGCTGCTTGGTCAAGGACTACTTCCCGCAACCGGTGACGGTG 459
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AUTHORS
TITLE
JOURNAL

COMMENT

FEATURES
source

CDS

ORIGIN

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Query Match 87.1%; Score 1163.2; DB 9; Length 1626;
Best Local Similarity 92.0%; Pred. No. 8.6e-229;
Matches 1247; Conservative 0; Mismatches 88; Indels 21; Gaps 1;

QY 1 GAGGTGCGAGCTGCTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
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QY 61 TCCTGTGCGAGTACGCGATTCACCTTTTCAGTGGCTTCTGGATGTCTTGGTCCGCGAGGCT 120
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QY 121 CCAGGGAAGGGGCTCGAGTGGGTTCGTAATTTAGATTGAATCTGATTAATTTATGCAACA 180
DB 258 CCGGGGAAGGGGCTGGAGTGGGTGGTTCATTTAGAGCCGAGGCTTATGTTGGGCAACA 317
QY 181 CATTATGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGA 240
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DB 378 GCCTATCTTCAATGAACAGCTCTGAAACCGAGGACACAGCCATATATTACTGTACTAGA 437
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DB 438 GAGCCCATGAGACGCCACTGCTTTTGTATCTCTGGGGCCCAAGGGACATTTGGTTCACCGTCTCT 497
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Qy	1168	ACACGCGCTCCGCTGTGACTCCGACGGCTCTTCTCTCTTCTACAGCAGCTCACCGTG	1227
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RESULT 7

BC065820 1685 bp mRNA linear PRI 03-FEB-2004

LOCUS Homo sapiens cDNA clone MGC:75197 IMAGE:6178926, complete cds.

DEFINITION BC065820

ACCESSION BC065820.1 GI:41351365

VERSION MGC.

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1685)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Deuge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullah,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Viallon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12477932

REFERENCE 2 (bases 1 to 1685)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (26-JAN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgapsof@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

info@cgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabh, Parvaneh Saeedi, JK Santos, Angeliq Schnerch, Ursula Skalska, Duane Smalus, Jeff Scott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 141 Row: B Column: 18

This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

Location/Qualifiers

1. .1685

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

FEATURES

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Query Match      86.9%; Score 1160.6; DB 9; Length 1685;
Best Local Similarity 91.6%; Pred. No. 2.9e-228;
Matches 1251; Conservative 0; Mismatches 84; Indels 30; Gaps 1;

QY 1 GAGGTGAGTGTGGAGTCTGGGGAGGCTTCGTAAAGCCCGGGGGTCCCTTAGACTC 60
DB 121 GAGGCGCACTGTGGAGTCTGGGGAGGCTTCGTAGCCCGGGGGTCCCTTAGACTC 180
QY 61 TCCTGTGACAGTACGAGATTCATTTTCAGTGGCTATGATGTCCTGGGTCGCCAGGCT 120
DB 181 TCCTGTACAGGTCTGGATTCACCTTCAGTGGCGCTGTGGTGGAGTGGGTCGCCAGGCT 240
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RESULT 8

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DEFINITION Sequence 762 from Patent EP1447413.
ACCESSION CQ850293
VERSION   CQ850293.1 GI:51508505
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
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RAB.

FEATURES

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Location/Qualifiers

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Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalilus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257
12477932
2 (bases 1 to 1679)
Strausberg, R.
Direct Submission
Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letitia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabh, Parvaneh Saedi, Jacqueline Schein, Duane Smalilus, Michael Smith, Lorraine Spence, Jeff Scott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 40 Row: i Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity to protein.

FEATURES

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ORGANISM other sequences; artificial sequences.
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AUTHORS Adolf, G., Baum, A. and Heider, K.H.
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Boehringer Ingelheim International GmbH (DE)
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AUTHORS

Compositions and methods for treating cancer using cytotoxic

TITLE

CD4antibody immunoconjugates and radiotherapy

JOURNAL

Patent: EP 1417974-A 7 12-MAY-2004;

JOURNAL

Boehringer Ingelheim International GmbH (DE)

FEATURES

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Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 7"

ORIGIN

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Best Local Similarity 92.5%; Pred. No. 5.1e-227;
Matches 1240; Conservative 0; Mismatches 89; Indels 12; Gaps 2;

QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
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VERSION
CQ816433.1
KEYWORDS
synthetic construct
synthetic construct
other sequences; artificial sequences.

SOURCE
ORGANISM
REFERENCE
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AUTHORS
Adolf, G., Baumann, M. and Heider, K. H.
TITLE
Compositions and methods for treating cancer using cytotoxic
cd4antibody immunoconjugates and radiotherapy
JOURNAL
Patent: WO 2004041307-A 7 21-MAY-2004;
Boehringer Ingelheim International GmbH (DE)

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Best Local Similarity 92.5%; Pred. No. 5.1e-227;
Matches 1240; Conservative 0; Mismatches 89; Indels 12; Gaps 2;

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QY 181 CATTATTCGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGA 240
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QY 298 ---GATTTCTAGACTGGGGCCAGGGAACACTAGTACCGTCTCCTCAGCTCCACCAAG 354
DB 352 CAGGGGTGGACTACTGGGGTCCAGGAACCTTAGTACCGTCTCCTCAGTACGACCAAG 411

QY 355 GGCCCATCGGTCTTCCCTCCCTGGCACCTCTCCCAAGACACCTCTCGGGGACAGGGGCC 414
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DB 652 GTGAATCACAAGCCCAAGCAACCAAGGTGGACAAGAAAGTGGAGCCCAAAATTTGTGAC 711

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Qy 655 AAAAATCACAATGCAATGCAAGCAACCTGAGTCAACCTGCGGGGGCACCGTCACTCTTC 714
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Qy 715 CTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCGAGCCCTGAGGTCAACATGC 774
Db 772 CTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCGAGCCCTGAGGTCAACATGC 831
Qy 775 GTGGTGTGACGTGACGACCAAGAACCTCTGAGTCAAGTTCACTGGTACGTGAGCGC 834
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RESULT 15
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LOCUS AX594307 1392 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 7 from Patent EP1258255.
ACCESSION AX594307
VERSION AX594307.1 GI:28396232
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Adolf, G., Heider, K.H., Patzelt, B. and Sproll, M.
TITLE Conjugates of an antibody to cd44 and a maytansinoid
JOURNAL Patent: EP 1258255-A 7 20-NOV-2002;
Boehringer Ingelheim International GmbH (DE)
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ORIGIN
Query Match 86.5%; Score 1154.6; DB 6; Length 1392;
Best Local Similarity 92.5%; Pred. No. 5.1e-227;
Matches 1240; Conservative 0; Mismatches 89; Indels 12; Gaps 2;
Qy 1 GAGGTGACGCTGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 5238.89 Seconds
(without alignments)
9699.731 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 1335

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gses1:*

9: gb_gses2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	985.4	73.8	1022	3	CR611254 full-leng
2	985.4	73.8	1048	3	CR595172 full-leng
3	985.4	73.8	1090	3	CR612308 full-leng
4	985.4	73.8	1091	3	CR604961 full-leng
5	985.4	73.8	1093	3	CR616804 full-leng
6	985.4	73.8	1098	3	CR626477 full-leng
7	985.4	73.8	1100	3	CR612813 full-leng
8	985.4	73.8	1102	3	CR601777 full-leng
9	985.4	73.8	1102	3	CR625051 full-leng
10	985.4	73.8	1103	3	CR595194 full-leng
11	985.4	73.8	1104	3	CR591904 full-leng
12	985.4	73.8	1106	3	CR613460 full-leng
13	985.4	73.8	1106	3	CR620071 full-leng
14	985.4	73.8	1107	3	CR598548 full-leng
15	985.4	73.8	1109	3	CR614200 full-leng
16	985.4	73.8	1109	3	CR619687 full-leng
17	985.4	73.8	1111	3	CR606782 full-leng
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ALIGNMENTS

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DEFINITION full-length cDNA clone CS0DE007YJ17 of Placenta of Homo sapiens (human).
ACCESSION CR611254
VERSION CR611254.1 GI:50492061
KEYWORDS HTC; CNSIT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1022)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
REFERENCE 2 (bases 1 to 1022)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Query Match 73.8%; Score 985.4; DB 3; Length 1022;
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RESULT 2

CR595172

LOCUS

DEFINITION

ACCESSION

VERSION

CR595172 1048 bp mRNA linear HTC 21-JUL-2004
 full-length cDNA clone CS0D1040YA16 of Placenta Cot 25-normalized
 of Homo sapiens (human).
 CR595172
 CR595172.1 GI:50475979

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

ORIGIN

-Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

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QY

Db

QY

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QY

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QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

HTC; CNSLT cDNA.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1048)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue

2 (bases 1 to 1048)

Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

Location/Qualifiers

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/organism="Homo sapiens"

/no_type="mRNA"

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/clone="CS0D1040YA16"

/tissue type="Placenta Cot 25-normalized"

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-Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

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Db

QY

Db

QY

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QY

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QY

Db


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  full-length cDNA clone CS0D1009YJ10 of Placenta Cot 25-normalized
  of Homo sapiens (human)
ACCESSION
  CR604961
VERSION
  CR604961.1 GI:50485768
KEYWORDS
  HTC; CNSLT_CDNA
SOURCE
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ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished
  Contact : Feng Liang Email : fliang@lifetech.com URL :
  http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
  Paraday Avenue
  2 (bases 1 to 1091)
  Genoscope.
  Direct Submission
  Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
  BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
  - Web : www.genoscope.cns.fr)
  1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
  end enriched, double-strand cDNA was digested with Not I and cloned
  into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
  was normalized. Library was constructed by Life Technologies, a
  division of Invitrogen.
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  Best Local Similarity 99.4%; Pred. No. 1.1e-244;
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  QY 581 CCTACATCTGCAAGTGAATCAAGCCCAAGCCAGCAACACCAAGGTGGACAAGAAAGTGGAGC 640
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  QY 641 CCAAACTTTGTGACAAAACTCACAATGCCACCGTCCAGCAGCACTGAACTCGCGGGGG 700
  DB 312 CCAAACTTTGTGACAAAACTCACAATGCCACCGTCCAGCAGCACTGAACTCGTGGGGG 371
  QY 701 CACGCTCAGTCTTCTCTCCCTCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCC 760
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  QY 761 CTGAGGTCACATGCGTGGTGGAGCGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACT 820
  DB 432 CTGAGGTCACATGCGTGGTGGAGCGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACT 491
  QY 821 GGTAGTGGACCGGTGGAGGTGCATATATCCAAAGAACCGCGGGAGGAGCAGTACA 880
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  QY 1301 CGCAGAAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1335
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  CR616804 1093 bp mRNA linear HTC 21-JUL-2004
  full-length cDNA clone CS0D1048YC07 of Placenta Cot 25-normalized
  of Homo sapiens (human)
  CR616804
  CR616804.1 GI:50497611
  HTC; CNSLT_CDNA
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  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished
  Contact : Feng Liang Email : fliang@lifetech.com URL :
  http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
  Faraday Avenue
  2 (bases 1 to 1093)
  Genoscope.
  Direct Submission
  Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
  BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
  - Web : www.genoscope.cns.fr)
  1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
  end enriched, double-strand cDNA was digested with Not I and cloned
  into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
  was normalized. Library was constructed by Life Technologies, a
  division of Invitrogen.
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Db	972	CACAGAAGACCTCTCCCTGTCTCCGGTAAATGA	1006
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DEFINITION	full-length cDNA clone CS0CAP001Y113 of Thymus of Homo sapiens (human).		
ACCESSION	CR626477		
VERSION	CR626477.1	GI:50507284	
KEYWORDS	HTC; CNS1T cDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished		
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/InvitroGen Corporation 1600 Paraday Avenue		
REFERENCE	2 (bases 1 to 1098)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)		
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.		
FEATURES	Location/Qualifiers		
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Query Match	73.8%	Score 985.4;	DB 3; Length 1098;
Best Local Similarity	99.4%;	Pred. No. 1.1e-244;	
Matches	989; Conservative	0; Mismatches	6; Indels 0; Gaps 0;
QY	341	CAGCCTCCACGAGGCCCATCGGTCTTCCCTGCGACCTCTCTCAAGAGCACCTCTG	400
Db	12	CAGCCTCCACGAGGCCCATCGGTCTTCCCTGCGACCTCTCTCAAGAGCACCTCTG	71
QY	401	GGGGCAGCGGGCCCTGGCTGCTGTCAGAGACTCTTCCCGAACCGGTGACGGTGT	460
Db	72	GGGGCAGCAGGACCTTGGCTGCTGTCAGAGACTCTTCCCGAACCGGTGACGGTGT	131
QY	461	CGTGGAACTCAGCGCCCTGACAGCGGGCTGCACACCTTCGGGCTGTCTTACAGTCC	520
Db	132	CGTGGAACTCAGCGCCCTGACAGCGGGCTGCACACCTTCGGGCTGTCTTACAGTCC	191
QY	521	CAGGACTCTACTCCCTCAGCAGGGTGTGACCGTGCCTCCAGCAGCTTTGGGCACCCAGA	580
Db	192	CAGGACTCTACTCCCTCAGCAGGGTGTGACCGTGCCTCCAGCAGCTTTGGGCACCCAGA	251
QY	581	CCTACATCTGCAACGTGAATCAACAAGCCAGCAACCAAGGTGGACAAGAAAGTGGAGC	640
Db	252	CCTACATCTGCAACGTGAATCAACAAGCCAGCAACCAAGGTGGACAAGAAAGTGGAGC	311
QY	641	CCAAATCTTGTGACAAAACCTCACATGCCCCCGGTGCCAGCACTCTGACCTCGCGGGG	700

Db 312 CCAATCTTGTGAAAACTCACACATGCCACCGTGCCAGCACCTGAACTCTCTGGGG 371
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Db 372 GACCGTCAGTCTTCTTCTTCCCGCCAAACCCAGGACACCTCATGATCTCCCGACCC 431
QY 761 CTGAGTTCACATCGCTGGTGGAGCTGAGCCACGAAGACCTCGAGGTCAAGTTCAACT 820
Db 432 CTGAGTTCACATCGCTGGTGGAGCTGAGCCACGAAGACCTCGAGGTCAAGTTCAACT 491
QY 821 GGTACGTGACGCGCTGGAGTGCATTAATGCCAAGCAAAAGCCGCGGAGGAGCAGTACA 880
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QY 881 ACAGCAGTACCGCTGGTGGAGCTGAGCTCTACCGCTGTCACAGGACTGGTGAATGGCA 940
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RESULT 7
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LOCUS 1100 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0D1081YF02 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR612813
VERSION 1
KEYWORDS HTG; CNSLT; cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1100)
AUTHORS Li, W. B., Gruber, C., Jesse, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Redwood City, CA 94063
Genoscope.
REFERENCE 2 (bases 1 to 1100)
AUTHORS Direct Submission
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
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Query Match 73.8%; Score 985.4; DB 3; Length 1100;
Best Local Similarity 99.4%; Pred. No. 1.1e-244; Indels 0; Gaps 0;
Matches 989; Conservative 0; Mismatches 6;
QY 341 CAGCCTCCACCAAGGCGCCATCGGTCTTCCCTCGGCACCCCTCTCCAGAGCACCCTCTG 400
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REFERENCE
AUTHORS
TITLE
JOURNAL
2 (bases 1 to 1102)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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Query Match 73.8%; Score 985.4; DB 3; Length 1102;
Best Local Similarity 99.4%; Pred. No. 1.le-244;
Matches 989; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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DB 12 CAGCCTCCACCAAGGCGCCATCGGTCTTCCCTGGCAGCCCTCTCTCAAGAGCACCTCTG 71
QY 401 GGGGACAGGGCCCTGGGTCTGGTCAAGACTACTTCCCGAACCGGTGACGGTGT 460
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QY 521 CAGGACTCTACTCCCTCAGCAGCGGTGTGACCGGTGTCACACCTTCCCGGTGCTCTACAGTCT 580
DB 192 CAGGACTCTACTCCCTCAGCAGCGGTGTGACCGGTGTCACACCTTCCCGGTGTCACAGTCT 251
QY 581 CTTACATCTGCAACGTGAATCAACGCCAGCAACACCAAGGTGGGCAAGAAAGTGGAGC 640
DB 252 CTTACATCTGCAACGTGAATCAACGCCAGCAACACCAAGGTGGGCAAGAAAGTGGAGC 311
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QY 701 CACCGTCAGTCTTCTTCTTCCCGGTGTCACACCTTCCCGGTGTCACAGTCTTCCCGGTGTC 760
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QY 761 CTGAGTCAATCGGTGGTGGAGCGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 820
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QY 821 GGTACGTGGACGGGTGGAGTGCATATGTCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 880
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QY 881 ACAGCAGTACCTGGTGGTGGAGCGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 940
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DB 612 AGGAGTACAGTGAAGTGTCCAAACAAAGCCCTTCCAGCCCTTCCAGCAAGCAAGCAAGCA 671
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QY 1121 TGCCTGTGAGTGGAGAGCAATGGCAGCCGAGGAGCAACTACAGACCAAGCCTCCCG 1180
DB 792 TGCCTGTGAGTGGAGAGCAATGGCAGCCGAGGAGCAACTACAGACCAAGCCTCCCG 851
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DB 972 CACAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1006

RESULT 10
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LOCUS
DEFINITION
full-length cDNA clone CS0DE010YH13 of Placenta of Homo sapiens
(human).
ACCESSION
CR595194
VERSION
CR595194.1 GI:50476001
KEYWORDS
HTC; CNSLT_CDNA.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1103)
AUTHORS
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
REMARK
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
Genoscope.
2 (bases 1 to 1103)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CS0DE010YH13"
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ORIGIN
Query Match 73.8%; Score 985.4; DB 3; Length 1103;
Best Local Similarity 99.4%; Pred. No. 1.le-244;
Matches 999; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 341 CAGCCTCCACCAAGGCGCCATCGGTCTTCCCTGGCAGCCCTCTCTCAAGAGCACCTCTG 400
DB 8 CAGCCTCCACCAAGGCGCCATCGGTCTTCCCTGGCAGCCCTCTCTCAAGAGCACCTCTG 67
QY 401 GGGGACAGGGCCCTGGGTGTCACAGTGTACTTCCCGAACCGGTGACGGTGT 460
DB 68 GGGGACAGAGCAGCCCTGGGTGTCACAGTGTACTTCCCGAACCGGTGACGGTGT 127

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Qy 461 CGTGGAACTCAGCGCCCTGACACCGCGGTGACACCTTCCCGGTGTCTTACAGTCT 520
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Qy 521 CAGGACTCTACTCCTCAGCAGCGTGGTACCGTCCCTCAGCAGCTTGGGCAACCCAGA 580
Db 188 CAGGACTCTACTCCTCAGCAGCGTGGTACCGTCCCTCAGCAGCTTGGGCAACCCAGA 247
Qy 581 CCTACATCTGCAAGCTGAATCACAAGCCCGAGCAACACCAAGGTGGCAAGAAAGTGGAGC 640
Db 248 CCTACATCTGCAAGCTGAATCACAAGCCCGAGCAACACCAAGGTGGCAAGAAAGTGGAGC 307
Qy 641 CCAATCTTGTGCAAAACTCACAATGCGCCACCGTCCCGAGCACTGAACTCCCGGGG 700
Db 308 CCAATCTTGTGCAAAACTCACAATGCGCCACCGTCCCGAGCACTGAACTCCCGGGG 367
Qy 701 CACCGTCAGTCTTCTTCTTCCCGCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCC 760
Db 368 GACCGTCAGTCTTCTTCTTCCCGCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCC 427
Qy 761 CTGAGGTCAATGCGTGGTGGAGCGTGAGCCGACGAGACCCCTGAGGTCAAGTTCAACT 820
Db 428 CTGAGGTCAATGCGTGGTGGAGCGTGAGCCGACGAGACCCCTGAGGTCAAGTTCAACT 487
Qy 821 GGTACGTGGACCGGTGGAGTGTCATTAATGCAAGACAAAGCCCGGGAGGAGCAGTACA 880
Db 488 GGTACGTGGACCGGTGGAGTGTCATTAATGCAAGACAAAGCCCGGGAGGAGCAGTACA 547
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DEFINITION full-length cDNA clone CS0D10421G24 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR591904
VERSION CR591904.1 GI:50472711
KEYWORDS HTC; cDNA;
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
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REFERENCE

1 (bases 1 to 1104)
Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1104)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail: seque@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)

REFERENCE

1 (bases 1 to 1104)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail: seque@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of invitrogen.

FEATURES

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1. 1104
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D10421G24"
/tissue_type="Placenta Cot 25-normalized"
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ORIGIN

Query Match 73.8%; Score 985.4; DB 3; Length 1104;
Best Local Similarity 99.4%; Pred. No. 1.1e-244;
Matches 989; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 341 CAGCCTCCACCAAGGGCCCATCGGTCTTCCCTGGCACCCTCTCCAAAGACACCTCTG 400
Db 12 CAGCCTCCACCAAGGGCCCATCGGTCTTCCCTGGCACCCTCTCCAAAGACACCTCTG 71
Qy 401 GGGGCAAGCGGCGCTGGCTGCTGGTCAAGAGCTACTTCCCGAAACCGGTGACGTTG 460
Db 72 GGGGCAAGCGGCGCTGGCTGCTGGTCAAGAGCTACTTCCCGAAACCGGTGACGTTG 131
Qy 461 CGTGGAACTCAGCGGCGCTGACACGAGCGGTGACACCTTCCCGGTGTCTTACAGTCT 520
Db 132 CGTGGAACTCAGCGGCGCTGACACGAGCGGTGACACCTTCCCGGTGTCTTACAGTCT 191
Qy 521 CAGGACTCTACTCCTCAGCAGCGTGTGACCGTCCCTCAGCAGCTTGGGCAACCCAGA 580
Db 192 CAGGACTCTACTCCTCAGCAGCGTGTGACCGTCCCTCAGCAGCTTGGGCAACCCAGA 251
Qy 581 CCTACATCTGCAAGCTGAATCACAAGCCCAAGCAACCAAGGTGGCAAGAAAGTGGAGC 640
Db 252 CCTACATCTGCAAGCTGAATCACAAGCCCAAGCAACCAAGGTGGCAAGAAAGTGGAGC 311
Qy 641 CCAATCTTGTGCAAAACTCACAATGCGCCACCGTCCCGAGCACTGAACTCCCGGGG 700
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Db 372 GACCGTCAGTCTTCTTCTTCCCGCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCC 431
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Best Local Similarity 99.4%; Pred. No. 1.1e-244;
Matches 989; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 12 CAGCCTCCACCAAGGCCCCATCGGTCTTCCCTCGGCACCTCTCTCCAAAGAGCACCTCTG 71

QY 401 GGGGCACAGCGGCCCTGGCTGCTGCTCAAGAGCTACTTCCCGCAACCGGTGACGGTGT 460
DB 72 GGGGCACAGCAGCCCTGGCTGCTGCTCAAGAGCTACTTCCCGCAACCGGTGACGGTGT 131

QY 461 CGTGGAACCTCAGCGCCCTTGACCGCGGTGCACACCTTCCCGGTGTCTTACAGTCT 520
DB 132 CGTGGAACCTCAGCGCCCTTGACCGCGGTGCACACCTTCCCGGTGTCTTACAGTCT 191

QY 521 CAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTGCCTTCCAGCAGCTTGGGCACCCAGA 580
DB 192 CAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTGCCTTCCAGCAGCTTGGGCACCCAGA 251

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DB 372 CACCGTCAGTCTTCTTCCCTCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCC 431

QY 761 CTGAGGTCAATCGTGGTGGAGCTGAGCCAGCAACCAAGGTTGACAAGAAAGTGGAGC 820
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RESULT 15
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DEFINITION
full-length cDNA clone CSODI041Y011 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION
CR614200
VERSION
CR614200.1 GI:50495007
KEYWORDS
HTC; CNSLT_cDNA.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1109)
AUTHORS
Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished
REMARK
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1109)
REFERENCE
Genoscope.
AUTHORS
Direct Submission
TITLE
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL
Bp 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
COMMENT
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
source
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Best Local Similarity 99.4%; Pred. No. 1.1e-244;
Matches 989; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 401 GGGGCACAGCGGCCCTTGCTGCTGCTCAAGAGCTACTTCCCGCAACCGGTGACGGTGT 460
DB 72 GGGGCACAGCAGCCCTTGCTGCTGCTCAAGAGCTACTTCCCGCAACCGGTGACGGTGT 131

QY 461 CGTGGAACCTCAGCGCCCTTGACCGCGGTGCACACCTTCCCGGTGTCTTACAGTCT 520
DB 132 CGTGGAACCTCAGCGCCCTTGACCGCGGTGCACACCTTCCCGGTGTCTTACAGTCT 191

QY 521 CAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTGCCTTCCAGCAGCTTGGGCACCCAGA 580
DB 192 CAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTGCCTTCCAGCAGCTTGGGCACCCAGA 251

QY 581 CCTACATCTGCAACGTAATCAAGCCCAAGCAACCAAGGTGGACAAGAAAGTGGAGC 640
DB 252 CCTACATCTGCAACGTAATCAAGCCCAAGCAACCAAGGTGGACAAGAAAGTGGAGC 311

QY 641 CCAATCTTTGTGACAAAATCTCAACATGCCCAAGTCCCGTCCAGCACTGAACTCGCGGGG 700
DB 312 CCAATCTTTGTGACAAAATCTCAACATGCCCAAGTCCCGTCCAGCACTGAACTCGCGGGG 371

QY 701 CACCGTCAGTCTTCTTCCCTCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCC 760
DB 372 CACCGTCAGTCTTCTTCCCTCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCC 431
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 11:10:40 ; Search time 750.97 Seconds
(without alignments)
10523.523 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 1335

Sequence: 1 gagtgagctgtgtggagtc.....ccctgtctccgggtaataaga 1335

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
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- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	1168	87.5	11590	13	AdS91476 Transposo
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6	1168	87.5	11593	13	AdS91477 Transposo
7	1168	87.5	11593	13	Adt62606 Transposo
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9	1168	87.5	11964	13	Adt62603 Transposo
10	1168	87.5	11967	13	AdS91475 Transposo
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18	1168	87.5	12342	13	AdS91479 Transposo
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20	1158	86.7	1645	13	Adr07256 Full leng

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25	1154.6	86.5	9568	8	AAD53219	Aad53219 BIWA4 ant
26	1149.2	86.1	1442	5	AAC84208	Aac84208 Plasmid G
27	1147.8	86.0	1798	3	AAC98220	Aac98220 Human col
28	1147.2	85.9	1437	2	AAV35487	AAV35487 Macaque p
29	1147.2	85.9	1437	6	AAV35487	AAV35487 DNA sequ
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32	1145	85.8	1416	12	ADH34600	Adh34600 021 heavy
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36	1142.8	85.6	1386	2	AAQ49834	Aaq49834 Anti-HIV-
37	1142.8	85.6	6281	5	AAC84206	Aac84206 Plasmid G
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ALIGNMENTS

RESULT 1

AAZ34748

ID AAZ34748 standard; CDNA; 1335 BP.

XX AAZ34748;

XX AAZ34748;

DT 15-FEB-2000 (first entry)

XX Humanised anti-CD23 MAb C11 heavy chain cDNA.

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XX monoclinal antibody; chimeric antibody; humanised antibody;

KW complementarity determining region; CDR; autoimmune disease;

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;

KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

KW urticaria; nephrotic syndrome; glomerulonephritis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;

KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;

KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;

XX therapy; ds.

XX Homo sapiens.

OS Synthetic.

XX WO9558679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB001434.

XX 09-MAY-1998; 98GB-00009839.

XX (GLAX) GLAXO GROUP LTD.

XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX WPI; 2000-053101/04.

XX P-PSDB; AAV32263.

XX Cell receptor specific antibodies useful for treating e.g. arthritis,

XX diabetes, multiple sclerosis and psoriasis.

XX Claim 17; Fig 4; 81pp; English.

PS

XX CC This DNA sequence encodes the heavy chain of humanised anti-CD23 (IgE
CC receptor, FCER1) monoclonal antibody C11, composed of a human framework
CC (H5IGKV17) and the heavy chain complementarity determining regions (see
CC RAY32256-58) of murine antibody C11. The invention provides altered
CC antibodies, such as chimeric or humanised antibodies, which comprise
CC sufficient of the amino acid sequences of the C11 light and heavy chain
CC complementarity determining regions to render them capable of binding to
CC the CD23 type II molecule expressed on haematopoietic cells. The
CC antibodies are used to block soluble CD23 formation in human therapy, for
CC the treatment of arthritis, lupus erythematosus, Hashimoto's thyroiditis,
CC multiple sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria,
CC nephrotic syndrome, glomerulonephritis, inflammatory bowel disease,
CC ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies,
CC allergic asthma, intrinsic asthma, acute asthmatic exacerbation,
CC rhinitis, eczema, graft-versus-host disease, COPD, insulinitis, bronchitis
CC (particularly chronic bronchitis) or diabetes (particularly type 1
CC diabetes), and B-cell malignancies (claimed). They are also useful for
CC studying interactions between CD23 and various ligands and determining
CC the binding agents

XX SQ Sequence 1335 BP; 321 A; 414 C; 360 G; 240 T; 0 U; 0 Other;

Query Match 100.0%; Score 1335; DB 3; Length 1335;
Best Local Similarity 100.0%; Pred. No. 2.1e-268;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 TCGGTCTTCCCTCGGACCCCTCTCTCAAGAGACCTCTGGGGGACAGGGCCCTGGGC 420
DB 361 TCGGTCTTCCCTCGGACCCCTCTCTCAAGAGACCTCTGGGGGACAGGGCCCTGGGC 420

QY 421 TGCTGTGTCAGGACTACTTCCCGAACCGGTGACCGTGTGCGGAACTCAGCGCCCTG 480
DB 421 TGCTGTGTCAGGACTACTTCCCGAACCGGTGACCGTGTGCGGAACTCAGCGCCCTG 480

QY 481 ACCAGCGGCGTGACACCTTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGC 540
DB 481 ACCAGCGGCGTGACACCTTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGC 540

QY 541 AGCGTGTGACCGTCCCTCAGAGCTTGGGACCCAGACCTACATCTGCACAGTGAAT 600
DB 541 AGCGTGTGACCGTCCCTCAGAGCTTGGGACCCAGACCTACATCTGCACAGTGAAT 600

QY 601 CACAAGCCAGCAACACCAAGGTGGAACAAGAAAGTGGAGCCCAATCTTGTGACAAAAC 660
DB 601 CACAAGCCAGCAACACCAAGGTGGAACAAGAAAGTGGAGCCCAATCTTGTGACAAAAC 660

QY 661 CACACATGCCCACCGTCCCGACCACTTGAATCTCGCGGGGCAACCGTCAGTCTTCTCTTC 720

DB 661 CACACATGCCCACCGTCCCGACCACTGAACTCGCGGGGGACCGTCAGTCTTCTCTTC 720

QY 721 CCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTG 780

DB 721 CCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTG 780

QY 781 GTGGACGTGAGCCACGACAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG 840

DB 781 GTGGACGTGAGCCACGACAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG 840

QY 841 GTGCATAATGCCAAGCAAAAGCCGCGGAGGAGTACAAAGCCAAAGGGCAGCC 1020

DB 841 GTGCATAATGCCAAGCAAAAGCCGCGGAGGAGTACAAAGCCAAAGGGCAGCC 1020

QY 901 AGCGTCTCACCGTCTCTGCAACAGACCTGCGTGAATGCAAGGATCAAGTGCAGGTC 960

DB 901 AGCGTCTCACCGTCTCTGCAACAGACCTGCGTGAATGCAAGGATCAAGTGCAGGTC 960

QY 961 TCCAAACAAAGCCCTCCAGCCCTCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCC 1020

DB 961 TCCAAACAAAGCCCTCCAGCCCTCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCC 1020

QY 1021 CGAGAACCAAGGTGTACACCTGCGCCCATCCCGGATGAGCTGACCAAGAACCGAGTC 1080

DB 1021 CGAGAACCAAGGTGTACACCTGCGCCCATCCCGGATGAGCTGACCAAGAACCGAGTC 1080

QY 1081 AGCCTGACCTGCTGCTCAAGGGCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGC 1140

DB 1081 AGCCTGACCTGCTGCTCAAGGGCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGC 1140

QY 1141 AATGGGACGCGGAGAAACAACTACAAGACACCGCTCCCGTCTGGACTCCGACGGCTCC 1200

DB 1141 AATGGGACGCGGAGAAACAACTACAAGACACCGCTCCCGTCTGGACTCCGACGGCTCC 1200

QY 1201 TTCTTCTCTACAGCAAGCTACCGTGGACAAAGAGAGGTGGCAGAGGGGAAACGTCTTC 1260

DB 1201 TTCTTCTCTACAGCAAGCTACCGTGGACAAAGAGAGGTGGCAGAGGGGAAACGTCTTC 1260

QY 1261 TCATGCTCGGTGATGATGAGGCTCTGCACAAACCTACTACGCAAGAGACCTCTCCCTG 1320

DB 1261 TCATGCTCGGTGATGATGAGGCTCTGCACAAACCTACTACGCAAGAGACCTCTCCCTG 1320

QY 1321 TCTCCGGGTAAATGA 1335

DB 1321 TCTCCGGGTAAATGA 1335

RESULT 2
ACC47231
ID ACC47231 standard; cDNA; 1386 BP.
XX
AC ACC47231;
XX
DT 18-AUG-2003 (first entry)
XX
DE Hu266 N56S heavy chain encoding cDNA.
XX
KW Amyloid-beta; Abeta; antibody 266; nootropic; neuroprotective; CDR;
XX immunostimulant; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1386
FT /*tag= a
FT /product= "heavy chain"
XX
PN WO2003016466-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US021322.
XX

PR 17-AUG-2001; 2001US-0313224P.
 XX (ELIL) LILLY & CO ELI.
 XX Jia AV, Tsurushita N, Vasquez MJ;
 XX WPI; 2003-278557/27.
 DR P-PSDB; ABR39847.
 XX
 XX New antibodies comprising a heavy chain and a light chain complementarity
 PT determining regions from antibody 266, for treating and preventing
 PT conditions associated with the A beta peptide, e.g. Alzheimer's disease
 PT or Down syndrome.
 XX
 XX Disclosure; Fig 6; 82pp; English.
 XX
 XX The invention relates to an anti-Abeta (amyloid-beta peptide) antibody
 CC 266. The antibodies are useful for treating and preventing conditions
 CC associated with the A beta peptide, such as Alzheimer's disease, Down
 CC syndrome, and cerebral amyloid angiopathy; for diagnosing diseases in
 CC humans; for determining whether a human subject will respond to treatment
 CC using humanized antibodies against A beta; for treating, preventing and
 CC reversing cognitive decline in clinical or pre-clinical Alzheimer's
 CC disease, Down's syndrome or cerebral amyloid angiopathy; for inhibiting
 CC formation of amyloid plaques or the effects of toxic soluble A beta
 CC species in humans. Treatment of the patients with antibody will inhibit
 CC or prevent cognitive decline typically associated with disease
 CC progression and reverses it. The present sequence represents a humanised
 CC anti-Abeta antibody 266 N56S heavy chain encoding cDNA
 XX
 XX Sequence 1386 BP; 321 A; 435 C; 368 G; 262 T; 0 U; 0 Other;
 SQ
 Query Match 87.6%; Score 1169; DB 8; Length 1386;
 Best Local Similarity 92.8%; Pred. No. 8e-234;
 Matches 1239; Conservative 0; Mismatches 90; Indels 6; Gaps 1;
 1 GAGGTGAGCTGTGGAGTGTGGGGAGGCTTGGTAAAGCCGGGGGCTCCCTTAGACTC 60
 58 GAAGTGCAGCTGTGGAGTGTGGGGAGGTTTGTAGTGAGCTGGAGGGTCCCTGAGACTC 117
 61 TCCTGTGAGCTAGCGGATTCACCTTCAGTGGCTACTGGATGCTCGGTCCCGCAGGCT 120
 118 TCCTGTGAGCTGTGAGTTCACCTTTAGTAGGTTTCCATGCTTGGGTTCGCGAGGCT 177
 121 CCAGGGAAGGGCTCGAGTGGTGTGTAATAGATGTAATCTGTAATATTGCAACA 180
 178 CCAGGGAAGGGCTGGATTTGGTGCACAAAT-----ATAGTGTGGTAGTAGCACC 231
 181 CATTATCGGAGTGTGGAAGGGGAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
 232 TACTATCCAGACACTGTAAAGGGCGGATTCACCATCTCCAGAGACAATGCCAAGAACACC 291
 241 CTGTATCTGCAATGACAGCTGAAACCGAGGACACAGCCGTGTATTACTGTACAGAT 300
 292 CTGTACTGCAATGAACTCCCTGAGGGCGGAAGACACGCGCGGTGTATTACTGTGCAAGC 351
 301 TTCATAGACTGGGGCCAGGGAACACTAGTCACTGCTCTCTCAGCTCCACCAAGGGGCCA 360
 352 GGAGACTACTGGGGCCAGGACACCTGTGTGACAGTCTCTCAGCTCCACCAAGGGGCCA 411
 361 TCGGTCTTCCCTCCCTGGCACCCTCTCCCAAGAGCACCTCTGGGGGACAGCGGCCCTGGGC 420
 412 TCGGTCTTCCCTCCCTGGCACCCTCTCCCAAGAGCACCTCTGGGGGACAGCGGCCCTGGGC 471
 421 TGCTGTCTCAAGACTACTTCCCGAACCGGTGACGCTGTCTGTGGAACTCAGGGGCCCTG 480
 472 TGCCTGTCTCAAGACTACTTCCCGAACCGGTGACGCTGTCTGTGGAACTCAGGGGCCCTG 531
 481 ACCAGCGCGGTGCACACTTCCCGGCTGTCTCTACAGTCTCTCAGACTCTACTCCCTCAGC 540
 532 ACCAGCGCGGTGCACACTTCCCGGCTGTCTCTACAGTCTCTCAGACTCTACTCCCTCAGC 591
 541 AGCGTGTGACCGTGCCTCCAGCAGCTTGGGCAACCCAGACCTACATCTGCAACAGTGAAT 600

592	AGCGTGTGACCGTGCCTCCAGCAGCTTGGGCAACCCAGACCTACATCTGCAACGTGAAT	651
601	CACAAGCCAGCAACACCAAGGTGGCAAGAAAGTGGAGCCCAAACTCTTGCAAAAAC	660
652	CACAAGCCAGCAACACCAAGGTGGCAAGAAAGTGGAGCCCAAACTCTTGCAAAAAC	711
661	CACACATGCCACCGTGCCTCCAGCAGCTGAACTCGCGGGGACCGTCAGTCTTCTCTTC	720
712	CACACATGCCACCGTGCCTCCAGCAGCTGAACTCTCTGGGGGACCGTCAGTCTTCTCTTC	771
721	CCCCCAAAACCCCAAGACACCTCATGATCTCCGGACCCCTGAGGTCAATGGTGGTGGT	780
772	CCCCCAAAACCCCAAGACACCTCATGATCTCCGGACCCCTGAGGTCAATGGTGGTGGT	831
781	GTGAGCTGAGCCACCAAGACACCTGAGGTCAAGTTCAACTGGTACGTGGAGCGGTGGAG	840
832	GTGAGCTGAGCCACCAAGACACCTGAGGTCAAGTTCAACTGGTACGTGGAGCGGTGGAG	891
841	GTGCATAATGCCAAGACCAAGCCCGGGAGGACAGTACAAAGCAGCTACCGTGTGGTC	900
892	GTGCATAATGCCAAGACCAAGCCCGGGAGGACAGTACAAAGCAGCTACCGTGTGGTC	951
901	AGCGTCTCACCCTCTGTCACCAAGACTGCTGTAATGGCAAGGAGTACAAGTGAAGTTC	960
952	AGCGTCTCACCCTCTGTCACCAAGACTGCTGTAATGGCAAGGAGTACAAGTGAAGTTC	1011
961	TCCAAACAAAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAG	1020
1012	TCCAAACAAAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAG	1071
1021	CGAGAACCCAGCTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCCAGGTC	1080
1072	CGAGAACCCAGCTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCCAGGTC	1131
1081	AGCGTCACTGCTGCTGCTCAAAAGGCTTCTATCCAGCGACATTCGCGCTGGAGTGGAGAGC	1140
1132	AGCGTCACTGCTGCTGCTCAAAAGGCTTCTATCCAGCGACATTCGCGCTGGAGTGGAGAGC	1191
1141	AATGGGCGAGCCGAGAACCACTACAGACCCACGCTCCCGTGTGAGTCCGAGCGCTCC	1200
1192	AATGGGCGAGCCGAGAACCACTACAGACCCACGCTCCCGTGTGAGTCCGAGCGCTCC	1251
1201	TTCTTCTCTTACAGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGAGGGAACGTCTTC	1260
1252	TTCTTCTCTTACAGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGAGGGAACGTCTTC	1311
1261	TCATGTCTCGTGTATGAGGCTCTGCAACCACTACACGCAAGAGGCTCTTCCCTG	1320
1312	TCATGTCTCGTGTATGAGGCTCTGCAACCACTACACGCAAGAGGCTCTTCCCTG	1371
1321	TCCTCCGGTAAATGA 1335	
1372	TCCTCCGGTAAATGA 1386	

RESULT 3

ACC47232
 ID ACC47232 standard; cDNA; 1386 BP.

XX ACC47232;

XX 18-AUG-2003 (first entry)

XX Hu266 N56T heavy chain encoding cDNA.

XX Amyloid-beta; Abeta; antibody 266; nootropic; neuroprotective; CDR;
 XX immunostimulant; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX FT 1. .1386
 XX CDS

Transposon-based vector pTnMCS (CMV-prepro-HCPro-CPA).

ds; multimeric protein; egg-laying; avian; milk producing animal;
transgenic; transposase; cancer; immunotherapy; infectious disease;
pTnMCS; CMV-prepro-HCPro-CPA; cecropia moth; chicken; gene; CMV;
chimeric; RM2 antibody.

Hyalophora cecropia.

Cyomegalovirus.

Gallus gallus.

Synthetic.

Unidentified.

Key Location/Qualifiers

FT misc_feature

1..3715

/*tag= a

/note= "From vector pTnMCS"

3721..5364

/*tag= b

/note= "CMV promoter/enhancer"

5371..5541

/*tag= c

/note= "Capsite/prepro from cecropia moth"

5548..6912

/*tag= d

/note= "Heavy chain gene construct from RM2 antibody"

6913..6924

/*tag= e

/note= "Pro sequence from cecropia moth"

6931..7575

/*tag= f

/note= "Light chain gene construct from RM2 antibody"

7582..7989

/*tag= g

/note= "Chicken conalbumin"

7991..11590

/*tag= h

/note= "This portion of the sequence is from cloning

vector pTnMCS."

XX

PN W02004067706-A2.

XX

PD 12-AUG-2004.

XX

PF 24-DEC-2003; 2003WO-US041261.

XX

PR 21-JAN-2003; 2003US-0441377P.

PR

PR 21-JAN-2003; 2003US-0441381P.

PR

PR 21-JAN-2003; 2003US-0441392P.

PR

PR 21-JAN-2003; 2003US-0441405P.

PR

PR 21-JAN-2003; 2003US-0441447P.

PR

PR 21-JAN-2003; 2003US-0441502P.

PR

PR 26-JUN-2003; 2003US-00609019.

XX

PA (TRAN-) TRANSGENRX INC.

PA (LOU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.

XX

PI Cooper RK, Fioretti WC, Cadd GG;

XX

XX WPI; 2004-580985/56.

XX

XX New isolated polynucleotide having two or more genes of interest and pro

PT nucleotide sequences, for use in pharmaceutical, diagnostic and

PT industrial uses, such as in treating and diagnosing cancer.

XX

PS Example 4; SEQ ID NO 100; 119pp; English.

XX

CC polynucleotide cassette containing genes of interest (for example
CC proinsulin, antibodies, cytokines, etc.). The polynucleotide cassettes
CC are administered to egg-laying or milk producing animals to create the
CC transgenic animals. Several different signal sequences and promoters can
CC be used to achieve the deposition of the multimeric protein in the egg or
CC milk. The transposon based vector has been used for the incorporation of
CC polynucleotide cassettes into the genomic DNA. The polynucleotide
CC cassette may additionally contain multiple pro sequences, prepro
CC sequences, cecropin prepro sequences and cleavage sites. Each gene
CC encodes a polypeptide which forms part of a multimeric protein. The pro
CC portion of the sequences has been used to facilitate appropriate
CC processing, expression and formation of multimeric proteins. These
CC multimeric proteins can be produced much more efficiently and
CC economically by this method than earlier conventional methods. This
CC improved method can produce the multimeric proteins on a large scale. The
CC transposon-based vectors of the invention produce high integration
CC frequencies compared to the earlier vectors. The intratesticular
CC injections with the novel transposon based vector produces 77 % sperm
CC positive rosters (compared to 41% of a previous method). The transposon-
CC based vectors of the invention include a transposase gene linked to a
CC first promoter and a coding sequence of a desired protein linked to a
CC second promoter. The coding sequence for the desired protein and its
CC promoter are flanked by transposase insertion sequences recognised by the
CC transposase. The transposon based vectors also include multiple Kozak
CC sequences (which enhance the expression of the transposase gene),
CC modified multiple codons at the N-terminal end (to facilitate the
CC transcription of the transposase gene), an effective polyA sequence (to
CC further enhance the expression of the transposase gene) and an additional
CC stop codon (to enhance the termination of transposon synthesis). The
CC method of the invention can be used to produce antibodies for cancer
CC immunotherapy, infectious disease and toxic agents. The methods and
CC compositions of producing multimeric proteins are useful in
CC pharmaceutical, diagnostic and industrial uses (treatment and diagnosis
CC of cancer). The polypeptide cassettes also include one or more epitopes
CC or domains for facilitating purification of a desired protein. The
CC presented nucleotide sequence is the transposon-based vector pTnMCS (CMV-
CC prepro-HCPro-CPA).

XX SQ Sequence 11590 BP; 2999 A; 2984 C; 2722 G; 2885 T; 0 U; 0 Other;

Query Match

Best Local Similarity

Matches 1256; Conservative

0; Mismatches 75; Indels 33; Gaps 1;

2 AGGTGAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61

5549 AGGTGAGCTGGAGGAGTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 5608

62 CCTGTGAGCTAGCGGATTACATTTTCAGTGGCTTACTGGATGTCTGGTCCGCGAGGCTC 121

5609 CCTGTGAGCTCTGGATTACATTTTCAGAAAGCCCTGGATGAGTGGTCCGCGAGGCTC 5668

122 CAGGGAAGGGGCTCGAGTGGTGGTCTGAAATTAGATTGAAATCTGATAATTATGCAACAC 181

5669 CAGGGAAGGGGCTCGAGTGGTGGTCTGAAATTAGATTGAAATCTGATAATTATGCAACAC 5728

182 ATTATCGGAGTCTGTGAAGGGGAATTCACCATCTCAGAGATGATTCAAATCTAGAC 241

5729 ACTATCTGCACCCCGGGAAGGCAGATTACCATCTCAGAGATGATTCAAATCTAGAC 5788

242 TGTATCTGAAATGAAACAGCTGAAACCGAGGACACAGCCGTGTTATCTGTAC----- 296

5789 TATATCTGAAATGATAGCTGAAAGCCGAGGACACAGCCGTATATCTGTACACCG 5848

297 -----AGATTTCATAGACTGGGCGCAGGGAACACTAG 328

5849 GGATTATGATAACATTTGGGGGAGTTATCCCTCCCGGAATTGGGGCCAGGGAACCTGG 5908

329 TCACCGTCTCTCAGCTCCACCAAGGGCCCTCGCTCTTCCCGCTGGACCTCTCTCCA 388

5909 TCACCGTCTCTCAGCTCCACCAAGGGCCCTCGCTCTTCCCGCTGGACCTCTCTCCA 5968

389 AGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGGAC 448

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Db 5969 AGAGCACCTCTGGGGCAGACGGCCCTGGGCTGCTGTCAAGACTACTTCCCGGAAC 6028
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Db 6029 CGGTGACGGTGTGCTGGAACCTAGAGCGCCCTGACAGCGCGGTGACACATCTTCCCGGCTG 6088
Qy 509 TCCTACAGTCCCTCAGAGCTACTCTCCTCAGCAGCGTGTGACCGGCTCCACGAGCT 568
Db 6089 TCCTACAGTCCCTCAGAGCTACTCTCCTCAGCAGCGTGTGACCGGCTCCACGAGCT 6148
Qy 569 TGGGCACCCAGACCTACATCTGCAAGCTGTAATCACAAGCCCGACCAACACCAAGGTGGACA 628
Db 6149 TGGGCACCCAGACCTACATCTGCAAGCTGTAATCACAAGCCCGACCAACACCAAGGTGGACA 6208
Qy 629 AGAAGTGGAGCCCAAACTTTGTGACAAACTCACAATGCAATGCGCCCGACGACCTG 688
Db 6209 AGAAGTGGAGCCCAAACTTTGTGACAAACTCACAATGCGCCCGACGACCTG 6268
Qy 689 AACTCGGGGGCAGCTGAGTCTTCTTCTTCCCGCCAAACCCCAAGGACACCTCATGA 748
Db 6269 AACTCTGGGGGACCGTCACTTCTTCTTCCCGCCAAACCCCAAGGACACCTCATGA 6328
Qy 749 TCTCCCGGACCCCTGAGGTCAATGCGTGTGAGCTGAGCCACGAGACCCCTGAGG 808
Db 6329 TCTCCCGGACCCCTGAGGTCAATGCGTGTGAGCTGAGCCACGAGACCCCTGAGG 6388
Qy 809 TCAAGTTCAACTGGTACGTGAGCGGTGAGTGCATTAATGCAAGACCAAGCCCGGG 868
Db 6389 TCAAGTTCAACTGGTACGTGAGCGGTGAGTGCATTAATGCAAGACCAAGCCCGGG 6448
Qy 869 AGAGCAGTACACAGCAGTACCGTGTGCTGAGCGTCTCACCGTCTGCAACGAGCT 928
Db 6449 AGAGCAGTACACAGCAGTACCGTGTGCTGAGCGTCTCACCGTCTGCAACGAGCT 6508
Qy 929 GGCTGAATGCAAGGAGTACAACTGCAAGGTCTTCCAAAGAGCCCTCCAGCCCGCCATCG 988
Db 6509 GGCTGAATGCAAGGAGTACAACTGCAAGGTCTTCCAAAGAGCCCTCCAGCCCGCCATCG 6568
Qy 989 AGAAACCATCTCCAAAGCCAAAGGGAGCGCCCGAGAACACACAGGTGTACACCTGCC 1048
Db 6569 AGAAACCATCTCCAAAGCCAAAGGGAGCGCCCGAGAACACACAGGTGTACACCTGCC 6628
Qy 1049 CATCCCGGATGAGTGCACCAAGAACAGTCAAGCTGACCTGCTGCTGTTCAAGGCTTCT 1108
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Qy 1109 ATCCAGCGCATCGCCGTGGAGTGGAGCAATGGCGAGCGCGAGAACCACTACAAGA 1168
Db 6689 ATCCAGCGCATCGCCGTGGAGTGGAGCAATGGCGAGCGCGAGAACCACTACAAGA 6748
Qy 1169 CACAGCTCCCGTGTGAGTCCGAGCGCTCTTCTTCTTCTTCAAGAGCTCACCGTGG 1228
Db 6749 CACAGCTCCCGTGTGAGTCCGAGCGCTCTTCTTCTTCTTCAAGAGCTCACCGTGG 6808
Qy 1229 ACAAGCAGGTGCGACGAGGGAAGTCTTCTTCTTCTTCTTCTTCAAGAGCTCACCGTGG 1288
Db 6809 ACAAGCAGGTGCGACGAGGGAAGTCTTCTTCTTCTTCTTCTTCAAGAGCTCACCGTGG 6868
Qy 1289 ACAACCACTACACGCGAGAGGCTCTTCCCTGTCTCCGGGTAAA 1332
Db 6869 ACAACCACTACACGCGAGAGGCTCTTCCCTGTCTCCGGGTAAA 6912
```

RESULT 5

ADT62605

XX ID ADT62605 standard; DNA; 11590 BP.

XX AC ADT62605;

XX DT 16-DEC-2004 (first entry)

XX DE Transposon based vector pTnMCS (CMV-prepro-HCPro-CPA).

```
XX Transposon-based vector; transposon; transgenic; vaccine;
KW immune response; anthrax; botulism; brucellosis; glanders; Q fever;
KW plague; shigellosis; small pox; tularemia; viral encephalitis;
KW typhus fever; viral hemorrhagic fever; bird; mammal; egg; milk;
KW antibacterial; anti-viral; antimicrobial; anti-inflammatory;
KW neuroprotective; transposase; pTnMCS; CMV-prepro-HCPro-CPA; ds;
KW cecropia moth.
XX Cytomegalovirus.
OS Hyalophora cecropia.
OS Chimeric.
XX Key Location/Qualifiers
FT promoter 3721..5364
FT /tag= a
FT /note= "CMV promoter/enhancer"
FT misc_feature 5371..5541
FT /tag= b
FT /note= "Capsite prepro sequence"
FT misc_feature 5548..6912
FT /tag= c
FT /note= "Heavy Chain gene construct taken from antibody
FT RM2."
FT misc_feature 6913..6924
FT /tag= d
FT /note= "Pro sequence"
FT misc_feature 6931..7575
FT /tag= e
FT /note= "Light Chain gene construct taken from antibody
FT RM2"
FT polyA_signal 7582..7989
FT /tag= f
FT /note= "Conalbumin polyA sequence"
XX WO2004067743-A1.
XX 12-AUG-2004.
XX 24-DEC-2003; 2003WO-US041269.
XX 21-JAN-2003; 2003US-0441377P.
XX 21-JAN-2003; 2003US-0441381P.
XX 21-JAN-2003; 2003US-0441392P.
XX 21-JAN-2003; 2003US-0441405P.
XX 21-JAN-2003; 2003US-0441447P.
XX 21-JAN-2003; 2003US-0441502P.
XX 26-JUN-2003; 2003US-00609019.
XX (TRAN-) TRANSENX INC.
XX (LOU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
XX Cooper RK, Fioretti WC, Cadd GG;
XX WPI; 2004-581003/56.
XX New polynucleotide (transposon-based vector) cassette comprising gene of
XX interest operably linked to a cecropin prepro sequence, is useful in
XX producing vaccines to protect an individual against infectious diseases.
XX Example 4; SEQ ID NO 100; 155pp; English.
XX The patent discloses novel, effective and efficient method of producing
XX multimeric proteins, antibodies using transposon-based vectors, in
XX transgenic individuals. These proteins can be used as a vaccine.
XX Immunising individuals with such compositions, comprising vaccines is
XX capable of generating an immune response, to prevent or ameliorate the
XX severity of a disease. The invention provides polynucleotide cassettes
XX containing at least one gene of interest and one or more pro
XX polynucleotide sequence, where in each gene of interest are operably-
XX linked to a pro nucleotide sequence of at least one gene of interest. The
XX transposon-based vector comprises the polynucleotide and further
XX comprises a transposase gene operably linked to a first promoter and
```

CC where the first promoter comprises a modified Kozak sequence, two or more
CC genes of interest are each operably-linked to one or more additional
CC promoters, and two or more genes of interest and their operably-linked
CC promoters are flanked by transposase insertion sequences recognized by a
CC transposase encoded by the transposase gene. Many diseases and disease
CC causing organisms can be targets of the vaccine of the present invention.
CC Some of these include, anthrax, botulism, brucellosis, glanders, Q fever,
CC plague, shigellosis, small pox, tularemia, viral encephalitis, typhus
CC fever, viral hemorrhagic fever, etc. The preferred animal for production
CC of protein is a bird or a mammal. The egg or milk of these animals
CC comprises the multimeric protein encoded by the isolated polynucleotide
CC of the invention. Hence, these proteins are endowed with varied
CC properties and are antibacterial, anti viral, antimicrobial, anti-
CC inflammatory, and neuroprotective in nature. The sequence presented here
CC is the transposon based vector pTnMCS (CMV-prepro-HCPro-CPA).
XX
SQ

Sequence 11590 BP; 2999 A; 2984 C; 2722 G; 2885 T; 0 U; 0 Other;
Query Match 87.5%; Score 1168; DB 13; Length 11590;
Best Local Similarity 92.1%; Pred. No. 1.8e-233;
Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;

QY 2 AGGTGACGCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
DB 5549 AGGTGACGCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 5608
QY 62 CCTGTGAGCTAGCGGATTCACCTTTCAGTGGCTACTGATGCTCTGGGTCCGCCAGGCTC 121
DB 5609 CCTGTGAGCTAGCGGATTCACCTTTCAGTGGCTACTGATGCTCTGGGTCCGCCAGGCTC 5668
QY 122 CAGGGAAGGGCTCGAGTGGGTGCTGAAATAGATTGAAATCTGATTAATATGCAACAC 181
DB 5669 CAGGGAAGGGCTCGAGTGGGTGCTGAAATAGATTGAAATCTGATTAATATGCAACAC 5728
QY 182 ATTATGCGAGCTGTGAGGGGAAATTCACCATCTCAAGATGATTCAAAATCTAGAC 241
DB 5729 ACTATGTGACCCGTGAAAGGCGAGATTACCATCTCAAGATGATTCAAAATCTAGAC 5788
QY 242 TGATCTGCAAAATGAAACAGCTGAAACCCGAGGACACAGCGTGTATTACTGTAC----- 296
DB 5789 TATATCTGCAAAATGAAACAGCTGAAACCCGAGGACACAGCGTGTATTACTGTAC----- 5848
QY 297 -----AGATTTTCATAGACTGGGGCCAGGGGAACACTAG 328
DB 5849 GGATTATGATAACATTTGGGGAGTTATCCCTCCCGGAAATTTGGGGCCAGGGAAACCTCG 5908
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DB 5909 TCACCGTCTCTGAGCTTCACCAAGGGCCCATCGCTTCCCTCCCTGGACACCTCTCTCCA 5968
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DB 5969 AGACACCTCTGGGGCACAGCGGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGGAAC 6028
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DB 6029 CGGTGACGGTGTCTGGAACTCAGCGGCCCTGACAGCGGGCTGCACACCTTCCCGGCTG 6088
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QY 569 TGGGCCCCCAGACCTACATCTGCAACCTGAAATCAAGCCCGCAGCAACCAAGGTGGACA 628
DB 6149 TGGGCCCCCAGACCTACATCTGCAACCTGAAATCAAGCCCGCAGCAACCAAGGTGGACA 6208
QY 629 AGAAAGTGGAGCCCAAACTTTGTGACAAAACTCACACATGCCACCGTGGCCAGCACTTG 688
DB 6209 AGAAAGTGGAGCCCAAACTTTGTGACAAAACTCACACATGCCACCGTGGCCAGCACTTG 6268
QY 689 AACTCGGGGGGACCGTCTAGTCTTCTTCTTCCCGCCCAAAACCAAGGACACCGCTCATGA 748
DB 6269 AACTCGGGGGGACCGTCTAGTCTTCTTCTTCTTCCCGCCCAAAACCAAGGACACCGCTCATGA 6328

QY 749 TCTCCCGGACCCCTGAGGTCAATGCGTGTGGTGGACGTGAGCCAGAACCCCTGAGG 808
DB 6329 TCTCCCGGACCCCTGAGGTCAATGCGTGTGGTGGACGTGAGCCAGAACCCCTGAGG 6388
QY 809 TCAAGTTCAACTGGTGTAGTGGACGGGTGGAGTGCATATGTCACAGACAAAGCCGCGG 869
DB 6389 TCAAGTTCAACTGGTGTAGTGGACGGGTGGAGTGCATATGTCACAGACAAAGCCGCGG 6448
QY 869 AGGAGCAGTACCAACAGCAGCTACCGTGTGTGTGAGCGTCTCAGCGTCTCCACAGGACT 928
DB 6449 AGGAGCAGTACCAACAGCAGCTACCGTGTGTGTGAGCGTCTCAGCGTCTCCACAGGACT 6508
QY 929 GGCTGAATGCAAGGAGTACAACTGCAAGGTCTCCAAACAAAGCCCTCCACAGCCCATCG 988
DB 6509 GGCTGAATGCAAGGAGTACAACTGCAAGGTCTCCAAACAAAGCCCTCCACAGCCCATCG 6568
QY 989 AGAAACCATCTCCAAAGCCAAAGGGGAGCCCGAGAGAACACAGGTGTACACCTGCCCC 1048
DB 6569 AGAAACCATCTCCAAAGCCAAAGGGGAGCCCGAGAGAACACAGGTGTACACCTGCCCC 6628
QY 1049 CATCCCGGATGAGCTGACCAAGAACAGGTGAGCTGACCTGCTGCTCAAGGGCTTCT 1108
DB 6629 CATCCCGGATGAGCTGACCAAGAACAGGTGAGCTGACCTGCTGCTCAAGGGCTTCT 6688
QY 1109 ATCCCGAGCAGATCGCGCTGGAGTGGAGAGCAATGGCGAGCCGAGAGAACAACTACAAGA 1168
DB 6689 ATCCCGAGCAGATCGCGCTGGAGTGGAGAGCAATGGCGAGCCGAGAGAACAACTACAAGA 6748
QY 1169 CCAAGGCTCCCGTGTGGACTCCGAGCGGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1228
DB 6749 CCAAGGCTCCCGTGTGGACTCCGAGCGGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 6808
QY 1229 ACAAGAGCAGGTGGCGAGCGGGAAGCTCTTCTCATGCTCCGTCGTCATGAGGCTCTGC 1288
DB 6809 ACAAGAGCAGGTGGCGAGCGGGAAGCTCTTCTCATGCTCCGTCGTCATGAGGCTCTGC 6868
QY 1289 ACAACCACTACACGCAAGAGAGCTCTCCCTGCTCTCCGGGTAAA 1332
DB 6869 ACAACCACTACACGCAAGAGAGCTCTCCCTGCTCTCCGGGTAAA 6912

RESULT 6

ADS91477

ID ADS91477 standard; DNA; 11593 BP.

AC ADS91477;

XX ADS91477;

DT 02-DEC-2004 (first entry)

XX Transposon-based vector pTnMCS (CMV-prepro-HCPro-Lys-CPA).
XX ds, multimeric protein; egg-laying; avian; milk producing animal;
XX transgenic; transposase; cancer; immunotherapy; infectious disease;
XX pTnMCS; CMV-prepro-HCPro-Lys-CPA; cecropia moth; chicken; gene; CMV;
XX chimeric; RM2 antibody.

XX Hyalophora cecropia.
XX Gallus gallus.
XX Cytomegalovirus.
XX Synthetic.
XX Unidentified.

XX Key Location/Qualifiers
XX misc_feature 1..3715
XX /tag= a
XX /note= "From vector pTnMCS"
XX promoter 3721..5364
XX /tag= b
XX /note= "CMV promoter/enhancer"
XX misc_feature 5371..5541
XX /tag= c
XX /note= "Capsite/prepro from cecropia moth"

FT misc_feature 5548. .6912
 FT /tag= d
 FT /note= "Heavy chain gene construct from RM2 antibody"
 FT 6913. .6927
 FT /tag= e
 FT /note= "Pro sequence from cecropia moth"
 FT 6934. .7578
 FT /tag= f
 FT /note= "light chain gene construct from RM2 antibody"
 FT 7585. .7992
 FT /tag= g
 FT /note= "Chicken conalbumin"
 FT 7994. .11593
 FT /tag= h
 FT /note= "this portion of the sequence is from cloning
 FT vector pTnMCS."
 XX
 PN WO2004067706-A2.
 XX
 PD 12-AUG-2004.
 XX
 PF 24-DEC-2003; 2003WO-US041261.
 XX
 PR 21-JAN-2003; 2003US-0441377P.
 PR 21-JAN-2003; 2003US-0441381P.
 PR 21-JAN-2003; 2003US-0441392P.
 PR 21-JAN-2003; 2003US-0441405P.
 PR 21-JAN-2003; 2003US-0441447P.
 PR 21-JAN-2003; 2003US-0441502P.
 PR 26-JUN-2003; 2003US-00609019.
 XX
 PA (TRAN-) TRANSENX INC.
 PA (LOU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
 PA
 PI Cooper RK, Fioretti WC, Cadd GG;
 XX
 DR WPI; 2004-580985/56.
 XX
 XX New isolated polynucleotide having two or more genes of interest and pro
 PT nucleotide sequences, for use in pharmaceutical, diagnostic and
 PT industrial uses, such as in treating and diagnosing cancer.
 XX
 PS Example 4; SEQ ID NO 101; 119pp; English.
 XX
 CC The present invention provides a new, effective and efficient method for
 CC producing multimeric proteins in the egg-laying (avian) or milk producing
 CC animals. The multimeric proteins include associated multimeric proteins
 CC (two or more associated polypeptides) and multivalent multimeric proteins
 CC (a single polypeptide is encoded by multiple genes). The expression and
 CC formation of a multimeric protein is achieved by administering a
 CC polynucleotide cassette containing genes of interest (for example
 CC proinsulin, antibodies, cytokines, etc.). The polynucleotide cassettes
 CC are administered to egg-laying or milk producing animals to create the
 CC transgenic animals. Several different signal sequences and promoters can
 CC be used to achieve the deposition of the multimeric protein in the egg or
 CC milk. The transposon based vector has been used for the incorporation of
 CC polynucleotide cassettes into the genomic DNA. The polynucleotide
 CC cassette may additionally contain multiple pro sequences, prepro
 CC sequences, cecropin prepro sequences and cleavage sites. Each gene
 CC encodes a polypeptide which forms part of a multimeric protein. The pro
 CC portion of the sequences has been used to facilitate appropriate
 CC processing, expression and formation of multimeric proteins. These
 CC multimeric proteins can be produced much more efficiently and
 CC economically by this method than earlier conventional methods. This
 CC improved method can produce the multimeric proteins on a large scale. The
 CC transposon-based vectors of the invention produce high integration
 CC frequencies compared to the earlier vectors. The intratesticular
 CC injections with the novel transposon based vector produces 77 % sperm
 CC positive rosters (compared to 41 % of a previous method). The transposon-
 CC based vectors of the invention include a transposase gene linked to a
 CC first promoter and a coding sequence of a desired protein linked to a
 CC second promoter. The coding sequence for the desired protein and its
 CC promoter are flanked by transposase insertion sequences recognised by the

CC transposase. The transposon based vectors also include multiple Kozak
 CC sequences (which enhance the expression of the transposase gene),
 CC modified multiple codons at the N-terminal end (to facilitate the
 CC transcription of the transposase gene), an effective polyA sequence (to
 CC further enhance the expression of the transposase gene) and an additional
 CC stop codon (to enhance the termination of transposon synthesis). The
 CC method of the invention can be used to produce antibodies for cancer
 CC immunotherapy, infectious disease and toxic agents. The methods and
 CC compositions of producing multimeric proteins are useful in
 CC pharmaceutical, diagnostic and industrial uses (treatment and diagnosis
 CC of cancer). The polypeptide cassettes also include one or more epitopes
 CC or domains for facilitating purification of a desired protein. The
 CC presented nucleotide sequence is the transposon-based vector pTnMCS (CMV-
 CC prepro-NCPro-Lys-CPA).

XX Sequence 11593 BP; 3004 A; 2983 C; 2719 G; 2887 T; 0 U; 0 Other;
 SQ

Query Match 87.5%; Score 1168; DB 13; Length 11593;
 Best Local Similarity 92.1%; Pred. No. 1.8e-233;
 Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;

QY 2 AGGTGACGCTGTGTGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGGTCCCTTAGACTCT 61
 DB 5549 AGGTGACGCTGCAGGAGTCGGGGGAGGCTTGGTAAAGCCCGGGGGGTCCCTTAGACTCT 5608
 QY 62 CCTGTGCAGCTAGCGGATTCACTTTTCAGTGGCTACTTGGATGTCCTGGGTCCGCCAGGCTC 121
 DB 5609 CTTGTGCAGCTCTGGATTCACTTTTCAGAAACGCCCTGGATGAGTGGGTCCGCCAGGCTC 5668
 QY 122 CAGGGAAGGGGCTCGAGTGGGTTCGTAATTTAGATTGAAATCTGATAATTTATGCAACAC 181
 DB 5669 CAGGGAAGGGGCTGGAGTGGGTTCGTAATTTAGATTGAAATTTATGTTGGGACAAACAG 5728
 QY 182 ATTATGCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTTCAAAATCTAGAC 241
 DB 5729 ACTATGCTGCACCCGCTGAAGGCAGATTTCACCATCTCAAGAGATGATTTCAAAACACGT 5788
 QY 242 TGTATCTGCAATGAACAGCCTGAAACCGAGGACACAGCCGTGTATTACTGTAC ---- 296
 DB 5789 TATATCTGCAATGAATAGATGCTGAAACCGAGGACACAGCCGTGTATTACTGTACACCG 5848
 QY 297 -----AGATTTTATAGACTGGGGCCAGGGAACACTAG 328
 DB 5849 GGATATTATGATAACATTTGGGGGAGTTATCCCTCCCGGAATTTGGGGCCAGGGAACCTCG 5908
 QY 329 TCACCGTCTCCTCAGCCTCCACCAAGGGCCATCGGTCTTCCCTCCCTGGCACACCTCTCTCA 388
 DB 5909 TCACCGTCTCCTCAGCCTCCACCAAGGGCCATCGGTCTTCCCTCCCTGGCACACCTCTCTCA 5968
 QY 389 AGAGACACCTCTGGGGGCACAGCGGCCCTGGGTGCTGCTCAAGGACTACTTCCCGGAAC 448
 DB 5969 AGAGACACCTCTGGGGGCACAGCGGCCCTGGGTGCTGCTCAAGGACTACTTCCCGGAAC 6028
 QY 449 CGGTGACGCTGTCTGTGGAATCAGGGCCCTGACAGCGCGGTGACACACTTCCCGGCTG 508
 DB 6029 CGGTGACGCTGTCTGTGGAATCAGGGCCCTGACAGCGCGGTGACACACTTTCGGCTG 6088
 QY 509 TCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTCCCTCCAGCAGCT 568
 DB 6089 TCTTACAGTCTCAGGACTCTACTCCCTTGTAGCAAGCGTGGTACCGTCCCTCCAGCAGCT 6148
 QY 569 TGGGGACCCAGACCTACATCTGCAAGCGTGAATCAAAAGCCCGAGCAACACCAAGGTGGACA 628
 DB 6149 TGGGGACCCAGACCTACATCTGCAAGCGTGAATCAAAAGCCCGAGCAACACCAAGGTGGACA 6208
 QY 629 AGAAGTGAAGCCCAAAATTTGTGCAAAATCTGACATATGCCCCACCGTCCCGACGACCTG 688
 DB 6209 AGAAGTGAAGCCCAAAATTTGTGCAAAATCTGACATATGCCCCACCGTCCCGACGACCTG 6268
 QY 689 AACTCGCGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCCAAGGACACCTCATGA 748
 DB 6269 AACTCTCGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCCAAGGACACCTCATGA 6328

5549 AGTGCAGCTGCAGGAGTGGGGGAGGCTTGGTAAAGCGGGGGGTCCCTTAGAGTCT 5608
62 CTTGTCCAGCTAGCGATTCACTTTCACTGGTGTACTGGAGTCTCTGGGTCCGCCAGGCTC 121
5609 CTTGTCCAGCTCTGGATTCACTTTTCAGAAAACCGCTGGATGAGTGGGTCCGCCAGGCTC 5668
122 CAGGGAAGGGCTCGAGTGGGTGCTGAAATAGATTGAATCTGATTAATATGAACAC 181
5669 CAGGGAAGGGCTCGAGTGGGTGCTGAAATAGATTGAATCTGATTAATATGAACAC 5728
182 ATTATCGGAGTCTGTAAGGGGAAATTCACATCTCAAGAGATGATTCAAAATCTAGAC 241
5729 ACTATGCTGCACCGTGAAGGCAGATTCAACATCTCAAGAGATGATTCAAAACACGT 5788
242 TGTATCTGCAATGAAACAGCTGAAACCCGAGGACACAGCGGTGTAATCTGTAC----- 296
5789 TATATCTGCAATGAAATAGCTGAAAGCGGAGGACACAGCGGTGTAATCTGTACACGG 5848
297 -----AGATTTCATAGACTGGGGCCAGGGAACACTAG 328
5849 GGAATATGATAACATTTGGGGGAGTTATCCCTCCCCCGAATTGGGGCCAGGGAACCCCTGG 5908
329 TCACCGTCTCTCAGAGCTCCACCAAGGGCCATCGGTCTTCCCGCTGGCACCCCTCTCCA 388
5909 TCACCGTCTCTCAGAGCTCCACCAAGGGCCATCGGTCTTCCCGCTGGCACCCCTCTCCA 5968
389 AGAGCACCTCTGGGGGACAGCGCCCTGGGTGCTCTCAAGACTACTTCTCCCGGAAC 448
5969 AGAGCACCTCTGGGGGACAGCGCCCTGGGTGCTCTCAAGACTACTTCTCCCGGAAC 6028
449 CGGTGACGGTGTCTGGAACCTAGCGCCCTGACAGCGCGGTGACACCTTCCCGGCTG 508
6029 CGGTGACGGTGTCTGGAACCTAGCGCCCTGACAGCGCGGTGACACCTTCCCGGCTG 6088
509 TCCTACAGTCTCTCAGAGCTCTACTCTCCTCAGAGCGTGTGAGCGTCCCTCCAGCAGCT 568
6089 TCCTACAGTCTCTCAGAGCTCTACTCTCCTTAGCAACGTGTGACCGTGCCTCCAGCAGCT 6148
569 TGGGCAACCCAGACTTACATCTGCAAGTGAATCACAAGCCAGCAACACCAAGGTGGACA 628
6149 TGGGCAACCCAGACTTACATCTGCAAGTGAATCACAAGCCAGCAACACCAAGGTGGACA 6208
629 AGAAGTGGAGCCCAATCTTGTGACAAACTCACAATGCTGCGTCCAGCACCTG 688
6209 AGAAGTGGAGCCCAATCTTGTGACAAACTCACAATGCTGCGTCCAGCACCTG 6268
689 AACTCGCGGGGACCGTCACTCTCTCTTCCCGCCCAAAACCAAGGACACCTCATGA 748
6269 AACTCTCGGGGACCGTCACTCTCTCTTCCCGCCCAAAACCAAGGACACCTCATGA 6328
749 TCTCCCGGACCCCTGAGGTCAATGCTGCTGTGTGAGCGTGGAGCAGAGACCTTGAGG 808
6329 TCTCCCGGACCCCTGAGGTCAATGCTGCTGTGTGAGCGTGGAGCAGAGACCTTGAGG 6388
809 TCAAGTTCAACTGTAGTGCAGCGGTGAGGTGCAATATGCAAGACAAAGCCCGGG 868
6389 TCAAGTTCAACTGTAGTGCAGCGGTGAGGTGCAATATGCAAGACAAAGCCCGGG 6448
869 AGGAGCAGTACAAAGCAGCAGTACCGTGTGTGCTCAGCGTCTCAGCGTCTGACAGGACT 928
6449 AGGAGCAGTACAAAGCAGCAGTACCGTGTGTGCTCAGCGTCTCAGCGTCTGACAGGACT 6508
929 GCGTGAATGGAGGAGTACAGTGCAGGTCTTCCAAAGCCCTCCAGCGCCCATCG 988
6509 GCGTGAATGGAGGAGTACAGTGCAGGTCTTCCAAAGCCCTCCAGCGCCCATCG 6568
989 AGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCAAGGTTGACACCTTGCCCC 1048
6569 AGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCAAGGTTGACACCTTGCCCC 6628
1049 CATCCCGGGATGAGTGCACCAAGAACAGGTGACCTGACCTGCTGGTCAAAAGGCTTCT 1108
6629 CATCCCGGGATGAGTGCACCAAGAACAGGTGACCTGACCTGCTGGTCAAAAGGCTTCT 6688

RESULT 8

ADS91474

ID ADS91474 standard; DNA; 11964 BP.

XX ADS91474;

XX AC

XX 02-DEC-2004 (first entry)

XX Transposon-based vector pTnMCS (CHOVep-prepro-HCPro-CPA).

XX ds; multimeric protein; egg-laying; avian; milk producing animal;

XX transgenic; transposase; cancer; immunotherapy; infectious disease;

XX pTnMCS; CHOVep-prepro-HCPro-CPA; cecropia moth; chicken; gene; chimeric;

XX RM2 antibody.

XX Hyalophora cecropia.

XX Gallus gallus.

XX Synthetic.

XX Unidentified.

XX Key

XX Location/Qualifiers

XX 1..3715

XX /tag= a

XX /note= "Vector pTnMCS"

XX 3721..4395

XX /tag= b

XX /note= "Chicken ovalbumin enhancer"

XX 4402..5738

XX /tag= c

XX /note= "Chicken ovalbumin promoter"

XX 5745..5915

XX /tag= d

XX /note= "Capsite prepro from cecropia moth"

XX 5922..7286

XX /tag= e

XX /note= "Heavy chain gene construct from antibody RM2"

XX 7287..7298

XX /tag= f

XX /note= "Pro sequence from cecropia moth"

XX 7305..7949

XX /tag= g

XX /note= "Light chain gene construct from antibody RM2"

XX 7956..8363

XX /tag= h

XX /note= "Chicken conalbumin poly A"

XX 8365..11964

XX /tag= i

XX /note= "This portion is from cloning vector pTnMCS."

XX WO2004067706-A2.

XX 12-AUG-2004.

XX 24-DEC-2003; 2003WO-US041261.

XX


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QY 1109 ATCCAGCAGATCGCGTGGAGTGGGAGAGCAATGGGAGCCGAGAACTACAAGA 1168
Db 7063 ATCCAGCAGATCGCGTGGAGTGGGAGAGCAATGGGAGCCGAGAACTACAAGA 7122
QY 1169 CCAGCGCTCCGCTGGAGATCCGAGCGGCTCTTCTCTCTACAGCAAGCTCACCGTGG 1228
Db 7123 CCAGCGCTCCGCTGGAGATCCGAGCGGCTCTTCTCTCTACAGCAAGCTCACCGTGG 7182
QY 1229 ACAGAGCAGGTGGCAGCAGGGAACGCTTCTCTATGCTCCGTCGATGATGAGGCTCTGC 1288
Db 7183 ACAAGAGCAGGTGGCAGCAGGGAACGCTTCTCTATGCTCCGTCGATGATGAGGCTCTGC 7242
QY 1289 ACAACCACTACAGCAGAGAGCTCTCCCTGTCCTCGGGTAAA 1332
Db 7243 ACAACCACTACAGCAGAGAGCTCTCCCTGTCCTCGGGTAAA 7286

RESULT 9
ADT62603
ID ADT62603 standard; DNA; 11964 BP.
AC ADT62603;
XX DT 16-DEC-2004 (first entry)
XX DE Transposon based vector pTnMCS (CHOVep-Prepro-Hcpro-CPA).
XX KW Transposon-based vector; transposon; transgenic; vaccine;
KW immune response; anthrax; botulism; brucellosis; glanders; Q fever;
KW plague; shigellosis; small pox; tularemia; viral encephalitis;
KW typhus fever; viral hemorrhagic fever; bird; mammal; egg; milk;
KW antibacterial; anti viral; antimicrobial; anti-inflammatory;
KW neuroprotective; transposase; pTnMCS; CHOVep-Prepro-Hcpro-CPA; ds;
KW cecropia moth.
XX OS Gallus gallus.
OS Hyalophora cecropia.
OS Chimeric.
XX FH Key Location/Qualifiers
FT enhancer 3721..4395
FT /tag= a
FT /note= "Ovalbumin enhancer. The sequence does not match
FT with the GenBank Id specified (Bos Taurus)"
FT promoter 4402..5738
FT /tag= b
FT /note= "ovalbumin promoter"
FT misc_feature 5745..5915
FT /tag= c
FT /note= "Capsite/Prepro sequence"
FT misc_feature 5922..7286
FT /tag= d
FT /note= "Heavy Chain construct taken from antibody RM2"
FT misc_feature 7287..7298
FT /tag= e
FT /note= "Pro sequence"
FT misc_feature 7305..7949
FT /tag= f
FT /note= "Light Chain gene construct"
FT polyA_signal 7956..8363
FT /tag= g
FT /note= "Conalbumin PolyA"
XX WO2004067743-A1.
XX PD 12-AUG-2004.
XX PF 24-DEC-2003; 2003WO-US041269.
XX PR 21-JAN-2003; 2003US-0441377P.
XX PR 21-JAN-2003; 2003US-0441381P.
XX PR 21-JAN-2003; 2003US-0441392P.

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PR 21-JAN-2003; 2003US-0441405P.
PR 21-JAN-2003; 2003US-0441447P.
PR 21-JAN-2003; 2003US-0441502P.
PR 26-JUN-2003; 2003US-00609019.
XX (TRAN-) TRANSGENEX INC.
PA (LOU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
XX Cooper RK, Fioretti WC, Cadd GG;
XX WPI; 2004-581003/56.
XX New polynucleotide (transposon-based vector) cassette comprising gene of
PT interest operably linked to a cecropin prepro sequence, is useful in
PT producing vaccines to protect an individual against infectious diseases.
XX Example 4; SEQ ID NO 98; 155pp; English.
XX The patent discloses novel, effective and efficient method of producing
CC multimeric proteins, antibodies using transposon-based vectors, in
CC transgenic individuals. These proteins can be used as a vaccine.
CC Immunising individuals with such compositions, comprising vaccines is
CC capable of generating an immune response, to prevent or ameliorate the
CC severity of a disease. The invention provides polynucleotide cassettes
CC containing at least one gene of interest and one or more pro
CC polynucleotide sequence, where in each gene of interest are operably-
CC linked to a pro nucleotide sequence of at least one gene of interest. The
CC transposon-based vector comprises the polynucleotide and further
CC comprises a transposase gene operably linked to a first promoter and
CC where the first promoter comprises a modified kozak sequence, two or more
CC genes of interest are each operably-linked to one or more additional
CC promoters, and two or more genes of interest and their operably-linked
CC promoters are flanked by transposase insertion sequences recognized by a
CC transposase encoded by the transposase gene. Many diseases and disease
CC causing organisms can be targets of the vaccine of the present invention.
CC Some of these include, anthrax, botulism, brucellosis, glanders, Q fever,
CC plague, shigellosis, small pox, tularemia, viral encephalitis, typhus
CC fever, viral hemorrhagic fever, etc. The preferred animal for production
CC of protein is a bird or a mammal. The egg or milk of these animals
CC comprises the multimeric protein encoded by the isolated polynucleotide
CC of the invention. Hence, these proteins are endowed with varied
CC properties and are antibacterial, anti viral, antimicrobial, anti-
CC inflammatory, and neuroprotective in nature. The sequence presented here
CC is the transposon based vector pTnMCS (CHOVep-Prepro-Hcpro-CPA).
XX SQ Sequence 11964 BP; 3260 A; 2975 C; 2686 G; 3043 T; 0 U; 0 Other;
Query Match 87.5%; Score 1168; DB 13; Length 11964;
Best Local Similarity 92.1%; Pred. No. 1.8e-233;
Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;
QY 2 AGGTGACAGTGTGAGTCTGGGGAGGCTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
Db 5923 AGGTGACAGTGTGAGTCTGGGGAGGCTGGTAAAGCCCGGGGGTCCCTTAGACTCT 5982
QY 62 CCGTGTGACAGTGTGAGTCTGGGGAGGCTGGTAAAGCCCGGGGGTCCCTTAGACTCT 121
Db 5983 CCGTGTGACAGTGTGAGTCTGGGGAGGCTGGTAAAGCCCGGGGGTCCCTTAGACTCT 6042
QY 122 CAGGGAAGGGGCTCGAGTGGGTGCTGAAATTTAGATTTGAAATTTGATTAATTCGAACAC 181
Db 6043 CAGGGAAGGGGCTCGAGTGGGTGCTGAAATTTAGATTTGAAATTTGATTTGATTCGAACAC 6102
QY 182 ATTATGCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAATCTAGAC 241
Db 6103 ACTATGCTGCACCCGCTGAAGGCAATTCACCATCTCAAGAGATGATTCAAATCTAGAC 6162
QY 242 TGTATCTGCAATGAACAGCCCTGAAAACCGAGGACACAGCCGCTGATTACTCTAC 296
Db 6163 TATATCTGCAATGAATGATGAGCTGAAAACCGAGGACACAGCCGCTGATTACTCTAC 6222
QY 297 -----AGATTTCATAGCTGGGGCCAGGGAACTAG 328

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Example 4; SEQ ID NO 99; 119pp; English.

PS The present invention provides a new, effective and efficient method for
 XX producing multimeric proteins in the egg-laying (avian) or milk producing
 CC animals. The multimeric proteins include associated multimeric proteins
 CC (two or more associated polypeptides) and multivalent multimeric proteins
 CC (a single polypeptide is encoded by multiple genes). The expression and
 CC formation of a multimeric protein is achieved by administering a
 CC polynucleotide cassette containing genes of interest (for example
 CC proinsulin, antibodies, cytokines, etc.). The polynucleotide cassettes
 CC are administered to egg-laying or milk producing animals to create the
 CC transgenic animals. Several different signal sequences and promoters can
 CC be used to achieve the deposition of the multimeric protein in the egg or
 CC milk. The transposon based vector has been used for the incorporation of
 CC polynucleotide cassettes into the genomic DNA. The polynucleotide
 CC cassette may additionally contain multiple pro sequences, prepro
 CC sequences, cecropin prepro sequences and cleavage sites. Each gene
 CC encodes a polypeptide which forms part of a multimeric protein. The pro
 CC portion of the sequences has been used to facilitate appropriate
 CC processing, expression and formation of multimeric proteins. These
 CC multimeric proteins can be produced much more efficiently and
 CC economically by this method than earlier conventional methods. This
 CC improved method can produce the multimeric proteins on a large scale. The
 CC transposon-based vectors of the invention produce high integration
 CC frequencies compared to the earlier vectors. The intratesticular
 CC injections with the novel transposon based vector produces 77 % sperm
 CC positive roosters (compared to 41% of a previous method). The transposon-
 CC based vectors of the invention include a transposase gene linked to a
 CC first promoter and a coding sequence of a desired protein linked to a
 CC second promoter. The coding sequence of the desired protein and its
 CC promoter are flanked by transposase insertion sequences recognised by the
 CC transposase. The transposon based vectors also include multiple Kozak
 CC sequences (which enhance the expression of the transposase gene),
 CC modified multiple codons at the N-terminal end (to facilitate the
 CC transcription of the transposase gene), an effective polyA sequence (to
 CC further enhance the expression of the transposase gene) and an additional
 CC stop codon (to enhance the termination of transposon synthesis). The
 CC method of the invention can be used to produce antibodies for cancer
 CC immunotherapy, infectious disease and toxic agents. The methods and
 CC compositions of producing multimeric proteins are useful in
 CC pharmaceutical, diagnostic and industrial uses (treatment and diagnosis
 CC of cancer). The polypeptide cassettes also include one or more epitopes
 CC or domains for facilitating purification of a desired protein. The
 CC presented nucleotide sequence is the transposon-based vector pTnMS
 CC (CHOVep-prepro-HCPro-Lys-CPA).

XX SQ Sequence 11967 BP; 3263 A; 2975 C; 2686 G; 3043 T; 0 U; 0 Other;

Query Match 87.5%; Score 1168; DB 13; Length 11967;
 Best Local Similarity 92.1%; Pred. No. 1.8e-233;
 Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;
 QY 2 AGTGCAGCTGTGGAGCTCGGGGGAGCTTGTAAAGCCCGGGGGTCCCTTAGACTCT 61
 DB 5923 AGTGCAGCTGTGGAGCTCGGGGGAGCTTGTAAAGCCCGGGGGTCCCTTAGACTCT 5982
 QY 62 CCTGTCAGCTAGCGGATTCACCTTTCAGTGGCTACTGGATGCTCTGGGTCGCGCAGGCTC 121
 DB 5983 CCTGTCAGCTAGCGGATTCACCTTTCAGTGGCTACTGGATGCTCTGGGTCGCGCAGGCTC 6042
 QY 122 CAGGGAAGGGGCTCGAGTGGGTGCTGAAATAGATTGAAATCTGATTAATTATGCAACAC 181
 DB 6043 CAGGGAAGGGGCTCGAGTGGGTGCTGAAATAGATTGAAATCTGATTAATTATGCAACAC 6102
 QY 182 ATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTTAGAC 241
 DB 6103 ACTATGCTGCACCGGTGAAGGGGAGATTCACCATCTCAAGAGATGATTCAAAATCTTAGAC 6162
 QY 242 TGTATCTGCAATGAAACAGCTGAAACCGGAGACACCGCGTATTACTGTAC----- 296
 DB 6163 TATATCTGCAATGAAATAGCTGAAACCGGAGACACCGCGTATTACTGTACACCGG 6222
 QY 297 -----AGATTTCATAGACTGGGGCCAGGGAACACTAG 328

DB 6223 GGATTATGATAACATTTGGGGGAGTTATCCCTCCCCGGAATTTGGGGCCAGGGAACCTCTGG 6282
 QY 329 TCACCGTCTCTCCTCAGCTCCACCAAGGGGCCATCGGTTCTTCCCTTGGCAGCCCTCTCTCCA 388
 DB 6283 TCACCGTCTCTCCTCAGCTCCACCAAGGGGCCATCGGTTCTTCCCTTGGCAGCCCTCTCTCCA 6342
 QY 389 AGAGCACCTCTGGGGGACACAGGGGCCCTGGGCTGCTCGTCAAGACTACTTCCCGGAC 448
 DB 6343 AGAGCACCTCTGGGGGACACAGGGGCCCTGGGCTGCTCGTCAAGACTACTTCCCGGAC 6402
 QY 449 CGGTCAAGCTGTCTGGGAACTCAGGCGGCTCACCAGGGGGCTGCACACCTTCCCGGGCTG 508
 DB 6403 CGGTCAAGCTGTCTGGGAACTCAGGCGGCTCACCAGGGGGCTGCACACCTTCCCGGGCTG 6462
 QY 509 TCTCTACAGTCTCAGGACTCTACTCTCTCAGAGGCTGTGACCTGCTGCCCTCAGAGCT 568
 DB 6463 TCTCTACAGTCTCAGGACTCTACTCTCTTAGCAAGCTGTGACCTGCTGCCCTCAGAGCT 6522
 QY 569 TGGGCAACCCAGACCTACATCTGCAACGTGAATCAAGCCCAAGCAACCAAGGTTGGACA 628
 DB 6523 TGGGCAACCCAGACCTACATCTGCAACGTGAATCAAGCCCAAGCAACCAAGGTTGGACA 6582
 QY 629 AGAAGTGGAGGCCCAATCTTGTGACAAAATCTCACACATGCCCCACCGTCCCGCAGACCTG 688
 DB 6583 AGAAGTGGAGGCCCAATCTTGTGACAAAATCTCACACATGCCCCACCGTCCCGCAGACCTG 6642
 QY 689 AACTCGGGGGGACCGTCACTCTCTTCCCTCCCAAAACCCCAAGGACACCTCATGA 748
 DB 6643 AACTCTCGGGGGGACCGTCACTCTCTTCCCTCCCAAAACCCCAAGGACACCTCATGA 6702
 QY 749 TCTCCGGGACCCCTCAGGTCAATCGGTGTGGAGCTGAGCCACCAAGACCTCTGAGG 808
 DB 6703 TCTCCGGGACCCCTCAGGTCAATCGGTGTGGAGCTGAGCCACCAAGACCTCTGAGG 6762
 QY 809 TCAAGTTCAACTGTGACGTGACGCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG 868
 DB 6763 TCAAGTTCAACTGTGACGTGACGCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG 6822
 QY 869 AGGAGAGTAAACAGACGTACCTGTGTGTGAGCTCTTCACTCTCTGACCAAGGACT 928
 DB 6823 AGGAGAGTAAACAGACGTACCTGTGTGTGAGCTCTTCACTCTCTGACCAAGGACT 6882
 QY 929 GGTCTGAATGGCAAGGAGTACAAAGTCAAGTCTCCAAACAAAGCCCTCCAGCCCCCATCG 988
 DB 6883 GGTCTGAATGGCAAGGAGTACAAAGTCAAGTCTCCAAACAAAGCCCTCCAGCCCCCATCG 6942
 QY 989 AGAAACCATCTCTCCAAAGCCAAAGGGGACGCCCCGAGAACCAAGGTGTACACCTGCCCC 1048
 DB 6943 AGAAACCATCTCTCCAAAGCCAAAGGGGACGCCCCGAGAACCAAGGTGTACACCTGCCCC 7002
 QY 1049 CATCCCGGGATGAGCTGACCAAGAACAGGTGAGCTGACCTGCTGTGTTCAAGGCTTCT 1108
 DB 7003 CATCCCGGGATGAGCTGACCAAGAACAGGTGAGCTGACCTGCTGTGTTCAAGGCTTCT 7062
 QY 1109 ATCCCAAGGACATCCCGGTGGAGTGGAGAGCAATGGGAGCCGAGAACCAACTACAAGA 1168
 DB 7063 ATCCCAAGGACATCCCGGTGGAGTGGAGAGCAATGGGAGCCGAGAACCAACTACAAGA 7122
 QY 1169 CCACGCTCCCGTGTGAGCTCCGACGGCTCTTCTTCTCTTACAGCAAGCTCAGCGTGG 1228
 DB 7123 CCACGCTCCCGTGTGAGCTCCGACGGCTCTTCTTCTCTTACAGCAAGCTCAGCGTGG 7182
 QY 1229 ACAAGAGAGGTGGGAGAGAGGAGAGCTTCTTCTATGCTCCGTGATGATGAGGCTCTGC 1288
 DB 7183 ACAAGAGAGGTGGGAGAGAGGAGAGCTTCTTCTATGCTCCGTGATGATGAGGCTCTGC 7242
 QY 1289 ACAACCACTTACACGAGAGAGGAGCTCTCCCTGCTCTCCGGTAAA 1332
 DB 7243 ACAACCACTTACACGAGAGAGGAGCTCTCCCTGCTCTCCGGTAAA 7286

RESULT 11

ADT62604
 ID ADT62604 standard; DNA; 11967 BP.
 AC ADT62604;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Transposon based vector pTnMCS (CMV-prepro-HCPro-Lys-CPA).
 XX
 KW Transposon-based vector; transposon; transgenic; vaccine;
 KW immune response; anthrax; botulism; brucellosis; glanders; Q fever;
 KW plague; shigellosis; small pox; tularemia; viral encephalitis;
 KW typhus fever; viral hemorrhagic fever; bird; mammal; egg; milk;
 KW antibacterial; anti viral; antimicrobial; anti-inflammatory;
 KW neuroprotective; transposase; pTnMCS; CMV-prepro-HCPro-Lys-CPA; ds;
 KW cecropia moth.
 XX
 OS Gallus gallus.
 OS Hyalophora cecropia.
 OS Chimeric.
 XX
 PH Key Location/Qualifiers
 FT enhancer 3721..4395
 FT /*tag= a
 FT /note= "Ovalbumin enhancer. This region of the sequence is
 FT not identical to the GenBank sequence (Bos taurus) as
 FT mentioned in the specification."
 FT 4402..5738
 FT promoter /*tag= b
 FT /note= "Ovalbumin promoter"
 FT 5745..5915
 FT /*tag= c
 FT /note= "Capsite pre pro sequence"
 FT 5922..7286
 FT misc_feature /*tag= d
 FT /note= "Heavy chain gene construct taken from antibody
 FT RM2"
 FT 7287..7301
 FT misc_feature /*tag= e
 FT /note= "Pro sequence"
 FT 7308..7952
 FT misc_feature /*tag= f
 FT /note= "Light chain gene construct"
 FT 7959..8366
 FT polyA_signal /*tag= g
 FT /note= "Conalbumin PolyA sequence"
 XX
 PN WO2004067743-A1.
 XX
 PD 12-AUG-2004.
 XX
 PP 24-DEC-2003; 2003WO-US041269.
 XX
 PR 21-JAN-2003; 2003US-0441377P.
 PR 21-JAN-2003; 2003US-0441381P.
 PR 21-JAN-2003; 2003US-0441392P.
 PR 21-JAN-2003; 2003US-0441405P.
 PR 21-JAN-2003; 2003US-0441447P.
 PR 21-JAN-2003; 2003US-0441502P.
 PR 26-JUN-2003; 2003US-00609019.
 XX
 (TRAN-) TRANSGENRX INC.
 PA (LOU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
 XX
 PI Cooper RK, Fioretti WC, Cadd GG;
 XX
 DR WPI; 2004-581003/56.
 XX
 PT New polynucleotide (transposon-based vector) cassette comprising gene of
 PT interest operably linked to a cecropin prepro sequence, is useful in
 PT producing vaccines to protect an individual against infectious diseases.
 XX
 PS Example 4; SEQ ID NO 99; 155pp; English.

XX The patent discloses novel, effective and efficient method of producing
 CC multimeric proteins, antibodies using transposon-based vectors, in
 CC transgenic individuals. These proteins can be used as a vaccine.
 CC Immunising individuals with such compositions, comprising vaccines is
 CC capable of generating an immune response, to prevent or ameliorate the
 CC severity of a disease. The invention provides polynucleotide cassettes
 CC containing at least one gene of interest and one or more pro
 CC polynucleotide sequence, where in each gene of interest are operably-
 CC linked to a pro nucleotide sequence of at least one gene of interest. The
 CC transposon-based vector comprises the polynucleotide and further
 CC comprises a transposase gene operably linked to a first promoter and
 CC where the first promoter comprises a modified kozak sequence, two or more
 CC genes of interest are each operably-linked to one or more additional
 CC promoters, and two or more genes of interest and their operably-linked
 CC promoters are flanked by transposase insertion sequences recognized by a
 CC transposase encoded by the transposase gene. Many diseases and disease
 CC causing organisms can be targets of the vaccine of the present invention.
 CC Some of these include, anthrax, botulism, brucellosis, glanders, Q fever,
 CC plague, shigellosis, small pox, tularemia, viral encephalitis, typhus
 CC fever, viral hemorrhagic fever, etc. The preferred animal for production
 CC of protein is a bird or a mammal. The egg or milk of these animals
 CC comprises the multimeric protein encoded by the isolated polynucleotide
 CC of the invention. Hence, these proteins are endowed with varied
 CC properties and are antibacterial, anti viral, antimicrobial, anti-
 CC inflammatory, and neuroprotective in nature. The sequence presented here
 CC is the transposon based vector pTnMCS (CMV-prepro-HCPro-Lys-CPA).
 XX
 SQ Sequence 11967 BP; 3263 A; 2975 C; 2686 G; 3043 T; 0 U; 0 Other;
 Query Match 87.5%; Score 1168; DB 13; Length 11967;
 Best Local Similarity 92.1%; Pred. No. 1.8e-233;
 Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;
 QY 2 AGGTGACGTGGTGGAGTCTGGGGAGGCTTGTTAAAGCCCGGGGGTCCCTTAGACTCT 61
 DB 5923 AGGTGACGTGGAGGAGTGGGGAGGCTTGTTAAAGCCCGGGGGTCCCTTAGAGTCT 5982
 QY 62 CCTGTGACGTACGCGATTCACTTTTCAGTGGGTCTCTGGGTCCGCGAGGCTC 121
 DB 5983 CCTGTGACGCTCTGGATTCACTTTTCAGAAACGCTGGATGAGTGGTCCGCGAGGCTC 6042
 QY 122 CAGGGAAGGGGCTCGAGTGGTGGTGAATAATTAGATTGAAATCTGATAATATTGCAACAC 181
 DB 6043 CAGGGAAGGGGCTGGAGTGGTGGTGAATAATTAAAGCAAAATTTGATGGTGGCAACAG 6102
 QY 182 ATTATCGGAGTCTGTGAAGGGAATTCACCATCTCAGAGATGATTCAAATCTAGAC 241
 DB 6103 ACTATGCTGACCCGCTGAAAGGCAGATTCAACCATCTCAAGAGATGATTCAAAAACACGT 6162
 QY 242 TGTATCTGCAATGAACAGCTGAAAACCGAGGACACAGCCGTGATTACTGTAC----- 296
 DB 6163 TATATCTGCAATGAATAGCTGAAAGCCGAGGACACAGCCGTATATTACTGTACCACGG 6222
 QY 297 -----AGATTTATAGACTGGGCGCAGGGAACTAG 328
 DB 6223 GGATTATGATAACATTTGGGGAGATTATCCCTCCCGGAATTTGGGCGCAGGAAACCTTGG 6282
 QY 329 TCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGACCTCTCTCCA 388
 DB 6283 TCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGACCTCTCTCCA 6342
 QY 389 AGAGCACCTCTGGGGGCACAGCGGCCCTGGGTGCTGGTCAAGGACTACTTCCCGGAAC 448
 DB 6343 AGAGCACCTCTGGGGGCACAGCGGCCCTGGGTGCTGGTCAAGGACTACTTCCCGGAAC 6402
 QY 449 CGGTGACGCTGTGCTGGAACCTCAGGGCCCTTGACACGCGCGTGCACACCTTCCCGGCTG 508
 DB 6403 CGGTGACGCTGTGCTGGAACCTCAGGGCCCTTGACACGCGCGTGCACACCTTCCCGGCTG 6462
 QY 509 TCCTACAGTCTCAGGACTCTACTCCCTGACGAGCGTGTGACCGTCCCTCAGGAGCT 568
 DB 6463 TCCTACAGTCTCAGGACTCTACTCCCTGACGAGCGTGTGACCGTCCCTCAGGAGCT 6522

CC processing, expression and formation of multimeric proteins. These
 CC multimeric proteins can be produced much more efficiently and
 CC economically by this method than earlier conventional methods. This
 CC improved method can produce the multimeric proteins on a large scale. The
 CC transposon-based vectors of the invention produce high integration
 CC frequencies compared to the earlier vectors. The intratesticular
 CC injections with the novel transposon based vector produces 77 % sperm
 CC positive rosters (compared to 41% of a previous method). The transposon-
 CC based vectors of the invention include a transposase gene linked to a
 CC first promoter and a coding sequence of a desired protein linked to a
 CC second promoter. The coding sequence for the desired protein and its
 CC promoter are flanked by transposase insertion sequences recognised by the
 CC transposase. The transposon based vectors also include multiple kozak
 CC sequences (which enhance the expression of the transposase gene),
 CC modified multiple codons at the N-terminal end (to facilitate the
 CC transcription of the transposase gene), an effective polyA sequence (to
 CC further enhance the expression of the transposase gene) and an additional
 CC stop codon (to enhance the termination of transposon synthesis). The
 CC method of the invention can be used to produce antibodies for cancer
 CC immunotherapy, infectious disease and toxic agents. The methods and
 CC compositions of producing multimeric proteins are useful in
 CC pharmaceutical, diagnostic and industrial uses (treatment and diagnosis
 CC of cancer). The polypeptide cassettes also include one or more epitopes
 CC or domains for facilitating purification of a desired protein. The
 CC presented nucleotide sequence is the transposon-based vector pTnMod (CMV-
 CC prepro-HCPro-CPA).

XX Sequence 11970 BP; 3060 A; 3088 C; 2807 G; 3015 T; 0 U; 0 Other;

Query Match 87.5%; Score 1168; DB 13; Length 11970;
 Best Local Similarity 92.1%; Pred. No. 1.8e-233;
 Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;

QY 2 AGGTGACAGTGGTGGGAGGCTTGGTAAAGCCGGGGGTCCCTTAGACTCT 61
 DB 5924 AGGTGACAGTGGGAGGCTTGGTAAAGCCGGGGGTCCCTTAGACTCT 5983
 QY 62 CCTGTGACGTAGCGGATTCACTTTCAGTGGTACTCGGATGTCTGGGTCCGCCAGGCTC 121
 DB 5984 CCTGTGACGCTCTGGATTCACTTTCAGAAAGCGCTGGATGAGCTGGGTCCGCCAGGCTC 6043
 QY 122 CAGGGAAGGGGCTGAGTGGGTGCTGAAATAGATTGAATCTGATAATTATGCAACAC 181
 DB 6044 CAGGGAAGGGGCTGAGTGGGTGCTGAAATAGATTGAATCTGATAATTATGCAACAC 6103
 QY 182 ATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241
 DB 6104 ACTATGCTGACCGGTGAAGGCGAGATTACCATCTCAAGAGATGATTCAAAATCTAGAC 6163
 QY 242 TGTATCTGCAAAATGAACAGCTGTGAAACCGAGGACACAGCCGTTGATTACTGTAC----- 296
 DB 6164 TATATCTGCAAAATGAATAGCTGTGAAACCGAGGACACAGCCGTTGATTACTGTACACGG 6223
 QY 297 -----AGATTTCATAGACTGGGGCCAGGGAACTAG 328
 DB 6224 GGATTATGATAAATTTGGGGAGTATTATCCCTCCCGGAAATTTGGGGCCAGGGAACTAG 6283
 QY 329 TCACCGTCTCTCAGCTCCACCAAGGGCCATCGGTCTTCCCGCTGGCACCCTCTCTCCA 388
 DB 6284 TCACCGTCTCTCAGCTCTCACCAGGGCCATCGGTCTTCCCGCTGGCACCCTCTCTCCA 6343
 QY 389 AGAGCACCCTCTGGGGGACACAGCGCCCTGGGCTGCTCGTCAAGGACTACTTCCCGGAAC 448
 DB 6344 AGAGCACCCTCTGGGGGACACAGCGCCCTGGGCTGCTCGTCAAGGACTACTTCCCGGAAC 6403
 QY 449 CGGTGACGGTGTCTGTGAATCTAGCGCCCTGACAGCGGGGTGCAACCTTCCCGGCTG 508
 DB 6404 CGGTGACGGTGTCTGTGAATCTAGCGCCCTGACAGCGGGGTGCAACCTTCCCGGCTG 6463
 QY 509 TCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGACCGTCCCTCCAGGAGCT 568
 DB 6464 TCCTACAGTCTCAGGACTCTACTCCCTTAGCAACAGTGGTGACCGTCCCTCCAGGAGCT 6523

QY 569 TGGGCAACCCAGACCTATCTGCAAGCGTGAATCAACAGCCACAGCAACACCAAGGTGACA 628
 DB 6524 TGGGCAACCCAGACCTATCTGCAAGCGTGAATCAACAGCCACAGCAACACCAAGGTGACA 6583
 QY 629 AGAAGTGGAGCCCAATCTTGTGACAAACTCAGACATGCCACCGTGCACGACCTG 688
 DB 6584 AGAAGTGGAGCCCAATCTTGTGACAAACTCAGACATGCCACCGTGCACGACCTG 6643
 QY 689 AACTCCGGGGGACCGTCACTCTTCTTCCCCCAAAACCAAGGACACCTCATGA 748
 DB 6644 AACTCTGGGGGACCGTCACTCTTCTTCCCCCAAAACCAAGGACACCTCATGA 6703
 QY 749 TCTCCCGGACCCCTGAGGTCAATGCGTGGTGTGAGCGAGCCAGAAAGCCCTGAGG 808
 DB 6704 TCTCCCGGACCCCTGAGGTCAATGCGTGGTGTGAGCGAGCCAGAAAGCCCTGAGG 6763
 QY 809 TCAAGTTCAACTGGTGGAGCGGTGGAGTGCATATGCAAGAAAGCCCGGG 868
 DB 6764 TCAAGTTCAACTGGTGGAGCGGTGGAGTGCATATGCAAGAAAGCCCGGG 6823
 QY 869 AGGAGCAGTACAAACAGCAGTACCGTGTGTGAGCGTCTCAGCGTCTGTCACACGAGCT 928
 DB 6824 AGGAGCAGTACAAACAGCAGTACCGTGTGTGAGCGTCTCAGCGTCTGTCACACGAGCT 6883
 QY 929 GGCTGAATGGCAAGGAGTCAAGTGCAGGTCTTCCAAAGCCCTCCAGCCCCCATCG 988
 DB 6884 GGCTGAATGGCAAGGAGTCAAGTGCAGGTCTTCCAAAGCCCTCCAGCCCCCATCG 6943
 QY 989 AGAAACCATCTCCAAAGCCNAAGGCGCCCGGAAACCAAGGTGTACACCTGCCCC 1048
 DB 6944 AGAAACCATCTCCAAAGCCNAAGGCGCCCGGAAACCAAGGTGTACACCTGCCCC 7003
 QY 1049 CATCCCGGATGAGCTGACCAAGAACAGGTCAAGCTCAGCTCCTCGCTGCTCAAGGCTTCT 1108
 DB 7004 CATCCCGGATGAGCTGACCAAGAACAGGTCAAGCTCAGCTCCTCGCTGCTCAAGGCTTCT 7063
 QY 1109 ATCCAGCAGCATCGCCGTGGAGTGGAGAGCAATGGGAGCGGAGAAACAATACAAGA 1168
 DB 7064 ATCCAGCAGCATCGCCGTGGAGTGGAGAGCAATGGGAGCGGAGAAACAATACAAGA 7123
 QY 1169 CACGCGCTCCGCTGCTGAGCTCCGAGCGCTCTTCTTCTTCTACACAGCTCACCGTGG 1228
 DB 7124 CACGCGCTCCGCTGCTGAGCTCCGAGCGCTCTTCTTCTTCTACAGAGCTCACCGTGG 7183
 QY 1229 ACAAGAGCAGGTGGCAGCAGGGGAAAGCTCTTCTCATGTCCGTGATGATGAGGCTCTGC 1288
 DB 7184 ACAAGAGCAGGTGGCAGCAGGGGAAAGCTCTTCTCATGTCCGTGATGATGAGGCTCTGC 7243
 QY 1289 ACAACCACTACACGCAAGAGAGCTCTCCCTGTCTCCGGGTAAA 1332
 DB 7244 ACAACCACTACACGCAAGAGAGCTCTCCCTGTCTCCGGGTAAA 7287

RESULT 13

ADT62609

ID ADT62609 standard; DNA; 11970 BP.

XX AC ADT62609;

XX DT 16-DEC-2004 (first entry)

XX Transposon based vector pTnMod (CMV-prepro-HCPro-CPA).

XX Transposon-based vector; transposon; transgenic; vaccine;
 KW immune response; anthrax; botulism; brucellosis; glanders; Q fever;
 KW plague; shigellosis; small pox; tularemia; viral encephalitis;
 KW typhus fever; viral hemorrhagic fever; bird; mammal; egg; milk;
 KW antibacterial; anti viral; antimicrobial; anti-inflammatory;
 KW neuroprotective; transposase; pTnMod; CMV-prepro-HCPro-CPA; ds;
 KW cecropia moth.

XX Cytomegalovirus.

OS Hyalophora cecropia.


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Db 6824 AGGAGCAGTACAAACAGCACGTACCGTGTGGTCTGAGCGTCTCACCGTCTCTCACCAGGACT 6883
Qy 929 GGCTGAATGCAAGAGGTACAAAGTCAAGTGTCCCAAAAGCCCTCCAGCCCCCATCG 988
Db 6884 GGCTGAATGCAAGAGGTACAAAGTCAAGTGTCCCAAAAGCCCTCCAGCCCCCATCG 6943
Qy 989 AGAAACCATCTTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTTGCCTCC 1048
Db 6944 AGAAACCATCTTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTTGCCTCC 7003
Qy 1049 CATCCCGGATGAGCTACCAAGAACACAGGTACGCTGACCTGCTGCTCAAGGCTTCT 1108
Db 7004 CATCCCGGATGAGCTACCAAGAACACAGGTACGCTGACCTGCTGCTCAAGGCTTCT 7063
Qy 1109 ATCCCGGATGAGCTACCAAGAACACAGGTACGCTGACCTGCTGCTCAAGGCTTCT 1168
Db 7064 ATCCCGGATGAGCTACCAAGAACACAGGTACGCTGACCTGCTGCTCAAGGCTTCT 7123
Qy 1169 CCAGCCTCCCGTGTGAGTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGG 1228
Db 7124 CCAGCCTCCCGTGTGAGTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGG 7183
Qy 1229 ACAAGAGAGGTGCGACGAGGGAACGCTTCTCATGCTCCGTCGATGAGCTTCTGCTGC 1288
Db 7184 ACAAGAGAGGTGCGACGAGGGAACGCTTCTCATGCTCCGTCGATGAGCTTCTGCTGC 7243
Qy 1289 ACACCACTACACGACGAGGCTCTCCCTGCTCCGGGTAA 1332
Db 7244 ACACCACTACACGACGAGGCTCTCCCTGCTCCGGGTAA 7287

RESULT 14
ADS91473
ID ADS91473 standard; DNA; 11973 BP.
AC ADS91473;
XX
DT 02-DEC-2004 (first entry)
XX
DE Transposon-based vector pTnMod (CMV-prepro-HCPro-Lys-CPA).
XX
KW ds; multimeric protein; egg-laying; avian; milk producing animal;
KW transgenic; transposase; cancer; immunotherapy; infectious disease;
KW pTnMod; CMV-prepro-HCPro-Lys-CPA; cecropia moth; CMV; chicken; gene;
KW chimeric; RM2 antibody.
XX
OS Hyalophora cecropia.
OS Cytomegalovirus.
OS Gallus gallus.
OS Synthetic.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_feature 1..4090
FT /tag= a
FT /note= "From vector pTnMod"
FT promoter 4096..5739
FT /tag= b
FT /note= "CMV promoter/enhancer"
FT misc_feature 5746..5916
FT /tag= c
FT /note= "Capsite/prepro from cecropia moth"
FT misc_feature 5925..7287
FT /tag= d
FT /note= "Heavy chain gene construct from RM2 antibody"
FT misc_feature 7288..7302
FT /tag= e
FT /note= "Pro sequence from cecropia moth"
FT misc_feature 7309..7953
FT /tag= f
FT /note= "Light chain gene construct from RM2 antibody"
FT polyA_site 7960..8372
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FT /note= "Chicken conalbumin"
FT misc_feature 8374..11973
FT /tag= h
FT /note= "This portion of the sequence is from cloning
FT vector pTnMod"
XX
PN WO2004067706-A2.
XX
PD 12-AUG-2004.
XX
XX 24-DEC-2003; 2003WO-US041261.
XX
XX 21-JAN-2003; 2003US-0441377P.
XX 21-JAN-2003; 2003US-0441381P.
PR 21-JAN-2003; 2003US-0441392P.
PR 21-JAN-2003; 2003US-0441405P.
PR 21-JAN-2003; 2003US-0441447P.
PR 21-JAN-2003; 2003US-0441502P.
PR 26-JUN-2003; 2003US-0609019.
XX
XX (TRAN-) TRANSGENIX INC.
XX (LOU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
PA
PA Cooper RK, Fioretti WC, Cadd GG;
XX
XX WPI; 2004-580985/56.
XX
XX New isolated polynucleotide having two or more genes of interest and pro
FT nucleotide sequences, for use in pharmaceutical, diagnostic and
FT industrial uses, such as in treating and diagnosing cancer.
XX
XX Example 3; SEQ ID NO 97; 119pp; English.
XX
CC The present invention provides a new, effective and efficient method for
CC producing multimeric proteins in the egg-laying (avian) or milk producing
CC animals. The multimeric proteins include associated multimeric proteins
CC (two or more associated polypeptides) and multivalent multimeric proteins
CC (a single polypeptide is encoded by multiple genes). The expression and
CC formation of a multimeric protein is achieved by administering a
CC polynucleotide cassette containing genes of interest (for example
CC proinsulin, antibodies, cytokines, etc.). The polynucleotide cassettes
CC are administered to egg-laying or milk producing animals to create the
CC transgenic animals. Several different signal sequences and promoters can
CC be used to achieve the deposition of the multimeric protein in the egg or
CC milk. The transposon based vector has been used for the incorporation of
CC polynucleotide cassettes into the genomic DNA. The polynucleotide
CC cassette may additionally contain multiple pro sequences, prepro
CC sequences, cecropin prepro sequences and cleavage sites. Each gene
CC encodes a polypeptide which forms part of a multimeric protein. The pro
CC portion of the sequences has been used to facilitate appropriate
CC processing, expression and formation of multimeric proteins. These
CC multimeric proteins can be produced much more efficiently and
CC economically by this method than earlier conventional methods. This
CC improved method can produce the multimeric proteins on a large scale. The
CC transposon-based vectors of the invention produce high integration
CC frequencies compared to the earlier vectors. The intratesticular
CC injections with the novel transposon based vector produces 77 % sperm
CC positive roosters (compared to 41% of a previous method). The transposon-
CC based vectors of the invention include a transposase gene linked to a
CC first promoter and a coding sequence of a desired protein linked to a
CC second promoter. The coding sequence for the desired protein and its
CC promoter are flanked by transposase insertion sequences recognised by the
CC transposase. The transposon based vectors also include multiple Kozak
CC sequences (which enhance the expression of the transposase gene),
CC modified multiple codons at the N-terminal end (to facilitate the
CC transcription of the transposase gene), an effective polyA sequence (to
CC further enhance the expression of the transposase gene) and an additional
CC stop codon (to enhance the termination of transposon synthesis). The
CC method of the invention can be used to produce antibodies for cancer
CC immunotherapy, infectious disease and toxic agents. The methods and
CC compositions of producing multimeric proteins are useful in
CC pharmaceutical, diagnostic and industrial uses (treatment and diagnosis
```

CC of cancer). The polypeptide cassettes also include one or more epitopes
 CC or domains for facilitating purification of a desired protein. The
 CC presented nucleotide sequence is the transposon-based vector pTnMod (CMV-
 XX prepro-HCPro-Lys-CPA).

Sequence 11973 BP; 3063 A; 3088 C; 2807 G; 3015 T; 0 U; 0 Other;
 Query Match 87.58; Score 1168; DB 13; Length 11973;
 Best Local Similarity 92.14; Pred. No. 1.8e-233;
 Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;
 2 AGGTGACGCTGGTGGAGCTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
 Db 5924 AGGTGACGCTGGAGAGTCCGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGAGTCT 5983
 Qy 62 CCTGTGACGTAGCGGATTCATTTTCAGTGGCTACTGTGATGTCTCTGGTCCGACAGCTC 121
 Db 5984 CCTGTGACGCTCTGGATTCATTTTCAGAAACGCTGGATGAGTGGGTCCGACAGCTC 6043
 Qy 122 CAGGAGGGGCTCGAGTGGTTCGTAATTTAGATTGAATCTGATATATTATGCAACAC 181
 Db 6044 CAGGAGGGGCTCGAGTGGTTCGCGGTATTTAAAGCAAAATTTGATGGTGGACAAACAG 6103
 Qy 182 ATTATGCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241
 Db 6104 ACTATGCTGCACCGTGAAGGCGAGATTCACCATCTCAAGAGATGATTCAAAACACAGT 6163
 Qy 242 TGTATCTGCAAAATGAACAGCTGAAACCGAGACACAGCCGCTGATATTCTGTAC----- 296
 Db 6164 TATATCTGCAAAATGAATAGCTGAAAGCCGAGACACAGCCGCTATATTCTGTACCAACG 6223
 Qy 297 -----AGATTTCTAGACTGGGCGGCGGGAACACTAG 328
 Db 6224 GGATTTATGATAAATTTGGGGAGTATTCCTCCCGGAAATTTGGGGCGAGGAAACCTGG 6283
 Qy 329 TCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACACCTCTCTCCA 388
 Db 6284 TCACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACACCTCTCTCCA 6343
 Qy 389 AGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCTGTGTCAGAGACTACTTCCCGGAAC 6403
 Db 6344 AGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCTGTGTCAGAGACTACTTCCCGGAAC 6403
 Qy 449 CGGTGACGGTGTCTGGAATCTAGGCGCCCTGACACAGCGCGTGCACACTTCCCGGCTG 508
 Db 6404 CGGTGACGGTGTCTGGAATCTAGGCGCCCTGACACAGCGCGTGCACACTTTCGCGCTG 5463
 Qy 509 TCCTACAGTCTCTCAGGACTACTCTCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCT 568
 Db 6464 TCCTACAGTCTCTCAGGACTACTCTCCTTAGCAACGTGTGACCGTCCCTCCAGCAGCT 6523
 Qy 569 TGGGACCCAGACCTATCTGCAACGTAATCAAGCCCGACCAACCAAGAGTGGACA 628
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 Qy 689 AACTCGGGGGACCGTCACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 748
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RESULT 15
 ADT62602
 ID ADT62602 standard; DNA; 11973 BP.
 XX
 AC ADT62602;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Transposon based vector pTnMod (CMV-prepro-HCPro-Lys-CPA).
 KW Transposon-based vector; transposon; transgenic; vaccine;
 KW immune response; anthrax; botulism; brucellosis; glanders; Q fever;
 KW plague; shigellosis; small pox; tularemia; viral encephalitis;
 KW typhus fever; viral hemorrhagic fever; bird; mammal; egg; milk;
 KW antibacterial; viral; antimicrobial; anti-inflammatory;
 KW neuroprotective; transposase; pTnMod; CMV-prepro-HCPro-Lys-CPA; ds;
 KW cecropia moth.
 XX
 OS Cytomegalovirus.
 OS Hyalophora cecropia.
 OS Gallus gallus.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
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 FT /tag= a
 FT /note= "CMV promoter enhancer taken from vector pGWiZ."
 FT misc_feature 5746..5916
 FT /tag= b
 FT /note= "Capsite/prepro sequence"
 FT misc_feature 5923..7287
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 FT /note= "Heavy chain gene construct taken from antibody
 RM2."
 FT misc_feature 7288..7302
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 FT /note= "pro sequence"
 FT misc_feature 7309..7953
 FT /tag= e
 FT /note= "Light chain construct taken from antibody RM2."
 FT polyA_signal 7960..8372
 FT /tag= f

/note= "Conalbumin polyA sequence"

PT XX WO2004067743-A1.
 XX PN
 XX PD
 XX PF 12-AUG-2004.
 XX PR 24-DEC-2003; 2003WO-US041369.
 XX PR 21-JAN-2003; 2003US-0441377P.
 XX PR 21-JAN-2003; 2003US-0441381P.
 XX PR 21-JAN-2003; 2003US-0441392P.
 XX PR 21-JAN-2003; 2003US-0441405P.
 XX PR 21-JAN-2003; 2003US-0441447P.
 XX PR 21-JAN-2003; 2003US-0441502P.
 XX PR 26-JUN-2003; 2003US-00609019.
 XX PA (TRAN-) TRANSENEX INC.
 XX PA (LOU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
 XX PI Cooper RK, Fioretti WC, Cadd GG;
 XX DR WPI; 2004-581003/56.
 XX PT New polynucleotide (transposon-based vector) cassette comprising gene of
 PT interest operably linked to a cecropin prepro sequence, is useful in
 PT producing vaccines to protect an individual against infectious diseases.
 XX PS Example 3; SEQ ID NO 97; 155pp; English.
 XX CC The patent discloses novel, effective and efficient method of producing
 CC multimeric proteins, antibodies using transposon-based vectors, in
 CC transgenic individuals. These proteins can be used as a vaccine.
 CC Immunising individuals with such compositions, comprising vaccines is
 CC capable of generating an immune response, to prevent or ameliorate the
 CC severity of a disease. The invention provides polynucleotide cassettes
 CC containing at least one gene of interest and one or more pro
 CC polynucleotide sequence, where in each gene of interest are operably-
 CC linked to a pro nucleotide sequence of at least one gene of interest. The
 CC transposon-based vector comprises the polynucleotide and further
 CC comprises a transposase gene operably linked to a first promoter and
 CC where the first promoter comprises a modified Kozak sequence, two or more
 CC genes of interest are each operably-linked to one or more additional
 CC promoters, and two or more genes of interest and their operably-linked
 CC promoters are flanked by transposase insertion sequences recognized by a
 CC transposase encoded by the transposase gene. Many diseases and disease
 CC causing organisms can be targets of the vaccine of the present invention.
 CC Some of these include, anthrax, botulism, brucellosis, glanders, Q fever,
 CC plague, shigellosis, small pox, tularemia, viral encephalitis, typhus
 CC fever, viral hemorrhagic fever, etc. The preferred animal for production
 CC of protein is a bird or a mammal. The egg or milk of these animals
 CC comprises the multimeric protein encoded by the isolated polynucleotide
 CC of the invention. Hence, these proteins are endowed with varied
 CC properties and are antibacterial, anti viral, antimicrobial, anti-
 CC inflammatory, and neuroprotective in nature. The sequence presented here
 CC is the transposon based vector pTnMod (CMV-prepro-HCPro-Lys-CPA).
 XX SQ Sequence 11973 BP; 3063 A; 3088 C; 2807 G; 3015 T; 0 U; 0 Other;
 Query Match 87.5%; Score 1168; DB 13; Length 11973;
 Best Local Similarity 92.1%; Pred. No. 1.8e-233;
 Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;
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 QY 62 CCTGTGACGTAGCGGATTCACTTTCAGTGGCTACTCGGATGTCTCTGGGTCCGCGAGCTC 121
 DB 5984 CCTGTGACGCTCTGGATTCACTTTCAGAAAGCGCTGGATGAGCTGGTCCGCGAGGCTC 6043
 QY 122 CAGGGAAGGGGCTGAGTGGGTGCTGAAATTAGATTGAATCTGAAATTATGCAACAC 181
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 182 ATTATCGGAGTCTGTGAAGGGGAAATTCACCAATCTCAAGAGATGATTCAAAATCTAGAC 241
 DB 6104 ACTATGCTGCACCCGTGAAGGCGAGATTCAACCATCTCAAGAGATGATTCAAAACACAGT 6163
 QY 242 TGTATCTGCAATGAACAGCCTGAAAACCGAGAGACACAGCCGTGTATTACTGTAC 296
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Job time : 759.97 secs

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OM nucleic - nucleic search, using sw model

Run on: April 18, 2005, 14:42:49 ; Search time 3634.25 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1174.2	88.0	1395	19	US-10-938-353-101
2	1168	87.5	11590	18	US-10-746-943-100
3	1168	87.5	11593	18	US-10-746-943-101
4	1168	87.5	11964	18	US-10-746-943-98
5	1168	87.5	11967	18	US-10-746-943-99
6	1168	87.5	11970	18	US-10-746-943-104
7	1168	87.5	11973	18	US-10-746-943-97
8	1168	87.5	12339	18	US-10-746-943-102
9	1168	87.5	12342	18	US-10-746-943-103
10	1158.8	86.8	1413	19	US-10-938-353-97
11	1154.6	86.5	1392	15	US-10-150-475A-7
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					Sequence 100, Appl
					Sequence 101, Appl
					Sequence 98, Appl
					Sequence 99, Appl
					Sequence 104, Appl
					Sequence 97, Appl
					Sequence 102, Appl
					Sequence 103, Appl
					Sequence 97, Appl
					Sequence 7, Appl

12	1154.6	86.5	1392	18	US-10-704-523-7	Sequence 7, Appl
13	1154.6	86.5	1392	18	US-10-645-215-7	Sequence 7, Appl
14	1147.8	86.0	1798	9	US-09-925-299-230	Sequence 230, App
15	1147.8	86.0	1798	10	US-09-925-299-230	Sequence 230, App
16	1147.2	85.9	1437	9	US-09-758-173-7	Sequence 7, Appl
17	1147.2	85.9	1437	9	US-09-948-429B-7	Sequence 7, Appl
18	1147.2	85.9	1437	13	US-10-124-905-7	Sequence 7, Appl
19	1147.2	85.9	1437	13	US-10-073-138-4	Sequence 4, Appl
20	1147.2	85.9	1437	16	US-10-124-807-7	Sequence 7, Appl
21	1147.2	85.9	1437	16	US-10-291-532-7	Sequence 7, Appl
22	1145	85.8	1616	9	US-09-822-830A-572	Sequence 572, App
23	1142.2	85.6	1427	17	US-10-656-769-25	Sequence 25, Appl
24	1141.8	85.5	1427	13	US-10-066-895-25	Sequence 25, Appl
25	1141.8	85.5	1427	13	US-10-066-895-25	Sequence 27, Appl
26	1141.8	85.5	1427	19	US-10-887-954-25	Sequence 25, Appl
27	1141.8	85.5	1427	19	US-10-887-954-27	Sequence 27, Appl
28	1141.2	85.5	19040	18	US-10-817-950-3	Sequence 3, Appl
29	1140.6	85.4	1356	18	US-10-731-984-33	Sequence 33, Appl
30	1140.2	85.4	1427	13	US-10-066-895-20	Sequence 20, Appl
31	1140.2	85.4	1427	19	US-10-887-954-20	Sequence 20, Appl
32	1139	85.3	1407	17	US-10-656-769-19	Sequence 19, Appl
33	1137.2	85.2	1413	17	US-10-408-901-37	Sequence 37, Appl
34	1136.6	85.1	1617	9	US-09-822-830A-571	Sequence 571, App
35	1136	85.1	1425	17	US-10-461-148-11	Sequence 11, Appl
36	1136	85.1	1430	10	US-09-848-832-1	Sequence 1, Appl
37	1136	85.1	1430	16	US-10-225-108A-1	Sequence 1, Appl
38	1135.4	85.0	1410	17	US-10-408-901-41	Sequence 41, Appl
39	1135	85.0	1347	9	US-09-736-371B-20	Sequence 20, Appl
40	1135	85.0	1347	17	US-10-463-442-20	Sequence 20, Appl
41	1134	84.9	1413	17	US-10-408-901-45	Sequence 45, Appl
42	1132	84.8	1409	17	US-10-408-901-67	Sequence 67, Appl
43	1132	84.8	1409	17	US-10-656-769-51	Sequence 51, Appl
44	1131	84.7	1356	9	US-09-822-698A-27	Sequence 27, Appl
45	1129.2	84.6	2197	18	US-10-858-186-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-10-938-353-101
; Sequence 101, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAR-FRENDSCHO, MARY
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PF4
; CURRENT APPLICATION NUMBER: US/10/938,353
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 101
; LENGTH: 1395
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-938-353-101

Query Match 88.0%; Score 1174.2; DB 19; Length 1395;
Best Local Similarity 93.4%; Pred. No. 2.9e-312;
Matches 1253; Conservative 0; Mismatches 73; Indels 15; Gaps 2;
Qy 2 AGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTCT 61
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QY 242 TGTATCTGCAATGAACAGAGCTGAAACCGAGGACACAGCCGTGATTACTGTACAGATT 301
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QY 1313 TCTCCCTGTCTCCGGGTAAT 1333
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RESULT 2
US-10-746-943-100
; Sequence 100, Application US/10746943
; Publication No. US20040235011A1
; GENERAL INFORMATION:
; APPLICANT: Cooper, Richard K.
; APPLICANT: Fioretti, William C.
; APPLICANT: Cadd, Gary G.
; TITLE OF INVENTION: Production of Multimeric Proteins
; FILE REFERENCE: 51687-0230 (51687-294924)
; CURRENT APPLICATION NUMBER: US/10746,943
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/392,415
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/441,381
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,447
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,405
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,502
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,377
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,392
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 10/609,019
; PRIOR FILING DATE: 2003-06-26
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 100
; LENGTH: 11590
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-746-943-100

Query Match 87.5%; Score 1168; DB 18; Length 11590;
Best Local Similarity 92.1%; Pred. No. 2,5e-310;
Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;
QY 2 AGGTGAGCTGTGTGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
DB 5549 AGGTGAGCTGTGAGGAGTGGGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGAGTCT 5608
QY 62 CCGTGTGAGCTAGCGGATTCACCTTTCAGTGGCTACTGATGTCCTGGGTCCGCCAGGCTC 121
DB 5609 CCGTGTGAGCTCTCTGATTCACCTTTCAGAAACCGCTGATGAGCTGGGGTCCGCCAGGCTC 5668
QY 122 CAGGGAAGGGCTCGAGTGGGTGCTGAAATTTAGATTGAAATCTGATTAATTTATGCAACAC 181
DB 5669 CAGGGAAGGGCTCGAGTGGGTGCTGAAATTTAGATTGAAATTTATGCGGACACAG 5728
QY 182 ATTATGCGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAATCTAGAC 241
DB 5729 ACTATGCTGCACCCCGTGAAGGACAGATTCAACATCTCAAGAGATGATTCAAAAAACAGT 5788

Db 5909 TCACCGCTCTCTCAGCCCTCCACCAAGGGCCCATCGGTCTTCCCTCGGCACCCCTCTCTCCA 5968
QY 389 AGAGCACTTGGGGGACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCGAAC 448
Db 5969 AGAGCACTTGGGGGACAGCGCCCTGGCTGCTGCTCAAGGACTACTTCCCGAAC 6028
QY 449 CGGTGACGCTGCTGGAACCTCAGGCGCCCTGACCAAGCGGCTGCAACCTTCCCGCTG 508
Db 6029 CGGTGACGCTGCTGGAACCTCAGGCGCCCTGACCAAGCGGCTGCAACCTTCCCGCTG 6088
QY 509 TCCTACAGTCTCAGGACTACTCTCTCAGCAGCGTGTGACCGTGCCTCCAGAGCT 568
Db 6089 TCCTACAGTCTCAGGACTACTCTCTCAGCAGCGTGTGACCGTGCCTCCAGAGCT 6148
QY 569 TGGGCAACCCAGACTTACATCTGCAACGCTGAATCACAAGCCCGACCAACCAAGGCTGACA 628
Db 6149 TGGGCAACCCAGACTTACATCTGCAACGCTGAATCACAAGCCCGACCAACCAAGGCTGACA 6208
QY 629 AGAAGTGGAGCCCAATCTTGTGACAAACTCACAATGCCACCGTGCCTCAGCACCTG 688
Db 6209 AGAAGTGGAGCCCAATCTTGTGACAAACTCACAATGCCACCGTGCCTCAGCACCTG 6268
QY 689 AACTCGCGGGGACCGTCACTCTCTCTTCCCGGCAAAACCAAGGACACCTCATGA 748
Db 6269 AACTCTCGGGGACCGTCACTCTCTCTTCCCGGCAAAACCAAGGACACCTCATGA 6328
QY 749 TCTCCCGGACCCCTGAGGTCACATGCTGTGTGTGACGCTGACGCGCAGAGACCTGAGG 808
Db 6329 TCTCCCGGACCCCTGAGGTCACATGCTGTGTGTGACGCTGACGCGCAGAGACCTGAGG 6388
QY 809 TCAAGTTCAACTGTGAGCGGCTGAGGTGCAATATGCAAGACCAAGGACCGCGGG 868
Db 6389 TCAAGTTCAACTGTGAGCGGCTGAGGTGCAATATGCAAGACCAAGGACCGCGGG 6448
QY 869 AGAGCAGTACAAAGCAGTACCGTGTGTGTGCTGAGCGTCTCACCGTCTGCAACGAGCT 928
Db 6449 AGAGCAGTACAAAGCAGTACCGTGTGTGTGCTGAGCGTCTCACCGTCTGCAACGAGCT 6508
QY 929 GCGTGAATGCAAGGAGTACAAGTGCAGGCTCTCAACAAAGGCTCTCCAGCGCCCTATCG 988
Db 6509 GCGTGAATGCAAGGAGTACAAGTGCAGGCTCTCAACAAAGGCTCTCCAGCGCCCTATCG 6568
QY 989 AGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGGCTGACACCTGCCCC 1048
Db 6569 AGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGGCTGACACCTGCCCC 6628
QY 1049 CATCCCGGATGAGCTGACCAAGAACCAAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1108
Db 6629 CATCCCGGATGAGCTGACCAAGAACCAAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 6688
QY 1109 ATCCAGCGATCGCGTGGAGTGGAGAGCAATGGGCGAGCGGAGAACCACTACAAGA 1168
Db 6689 ATCCAGCGATCGCGTGGAGTGGAGAGCAATGGGCGAGCGGAGAACCACTACAAGA 6748
QY 1169 CCAGCGCTCCCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1228
Db 6749 CCAGCGCTCCCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6808
QY 1229 ACAAGAGCGGTGGAGCAGGGGAAACGCTCTTCTCATGCTCCGCTGATGATGAGGCTCTGC 1288
Db 6809 ACAAGAGCGGTGGAGCAGGGGAAACGCTCTTCTCATGCTCCGCTGATGATGAGGCTCTGC 6868
QY 1289 ACAACCACTACAGCAGAGGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1332
Db 6869 ACAACCACTACAGCAGAGGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6912

RESULT 4

US-10-746-943-98
; Sequence 98, Application US/10746943
; Publication No. US20040235011A1
; GENERAL INFORMATION:
; APPLICANT: Cooper, Richard K.

; APPLICANT: Fioretti, William C.
; APPLICANT: Cadd, Gary G.
; TITLE OF INVENTION: Production of Multimeric Proteins
; FILE REFERENCE: 51687-0230 (51687-294924)
; CURRENT APPLICATION NUMBER: US/10/746,943
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/392,415
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/441,381
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,447
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,405
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,502
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,377
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,392
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 10/609,019
; PRIOR FILING DATE: 2003-06-26
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 98
; LENGTH: 11964
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-746-943-98

Query Match 87.5%; Score 1168; DB 18; Length 11964;

Best Local Similarity 92.1%; Pred. No. 2.5e-310;
Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;

QY 2 AGGTGACGCTGCTGAGTCTGGGCGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
Db 5923 AGGTGACGCTGCTGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 5982
QY 62 CTGTGACGCTAGCGGATTCATTTTCAGTGGCTACTGATGCTCTGGGTCCGCCAGGCTC 121
Db 5983 CTGTGACGCTCTGGATTCATTTTCAGAAAGCCCTGGATGAGTGGGTCCGCCAGGCTC 6042
QY 122 CAGGGAAGGGCTCCAGTGGGTGCTGAAATAGATTGAAATCTGATAATATGCAACAC 181
Db 6043 CAGGGAAGGGCTGGAGTGGGTGCGCGGTATTTAAAGCAAAATGATGGTGGGACACAG 6102
QY 182 ATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241
Db 6103 ACTATGCTGCACCGGTGAAAGGACAGATTACCATCTCAAGAGATGATTCAAAACACCT 6162
QY 242 TGTATCTGAAATGAACGCTTGAAACCGAGGACACAGCGCTGTATTACTGTAC----- 296
Db 6163 TATATCTGAAATGAATAGCTTGAAGCGAGGACACAGCGCTATATATTACTGTACCGG 6222
QY 297 -----AGATTTATAGACTGGGGCCAGGGAACACTAG 328
Db 6223 GAATATGATAACATTTGGGGAGTTATCCCTCCCGGAGTTGGGGCCAGGGAACCTCG 6282
QY 329 TCACCGTCTCTCAGCTCCACCAAGGGGCCATCGGTCTTCCCGCTGGCACCTCTCTCCA 388
Db 6283 TCACCGTCTCTCAGCTCCACCAAGGGGCCATCGGTCTTCCCGCTGGCACCTCTCTCCA 6342
QY 389 AGACACCTCTCTGGGGCACAGCGGCTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 448
Db 6343 AGACACCTCTCTGGGGCACAGCGGCTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6402
QY 449 CGGTGACGCTGCTGGGAACTCAGCGGCTCAGCGGCTGACACCTCTTCCCGGCTG 508
Db 6403 CGGTGACGCTGCTGGGAACTCAGCGGCTTGGGAACTCAGCGGCTGACACCTCTTCCCGGCTG 6462
QY 509 TCCTACGCTCTCAGGACTCTACTCTCCTCAGAGCGGTGGTGGCGCTCCAGCAGCT 568

Db 7498 CCAGCCTCCGCTGGAGTCCAGCGCTCTTCTTCTCTACAGCAAGCTCACCGTGG 7557
Qy 1229 ACAAGAGCAGGTGGCAGCGGGAAAGCTTCTCTCATGCTCGTGATCATGAGGCTCTGC 1388
Db 7558 ACAAGAGCAGGTGGCAGCGGGAAAGCTTCTCTCATGCTCGTGATCATGAGGCTCTGC 7617
Qy 1289 ACAACCACTACACGACGAGAGCTCTCCCTGTCTCCGGGTAAA 1332
Db 7618 ACAACCACTACACGACGAGAGCTCTCCCTGTCTCCGGGTAAA 7661

RESULT 9
US-10-746-943-103
; Sequence 103, Application US/10746943
; Publication No. US20040235011A1
; GENERAL INFORMATION:
; APPLICANT: Cooper, Richard K.
; APPLICANT: Fioretti, William C.
; APPLICANT: Cadd, Gary G.
; TITLE OF INVENTION: Production of Multimeric Proteins
; FILE REFERENCE: 51687-0230 (51687-294924)
; CURRENT APPLICATION NUMBER: US/10746,943
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/392,415
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/441,381
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,447
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,405
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,502
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,377
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/441,392
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 10/609,019
; PRIOR FILING DATE: 2003-06-26
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
; LENGTH: 12342
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-746-943-103

Query Match 87.5%; Score 1168; DB 18; Length 12342;
Best Local Similarity 92.1%; Pred. No. 2.5e-310;
Matches 1256; Conservative 0; Mismatches 75; Indels 33; Gaps 1;

Qy 2 AGGTGACGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
Db 6298 AGGTGACGCTGACGAGTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 6357
Qy 62 CCTGTGACGTAGCGGATTCATCTTTCAGTGGCTACTGATGTCCTGGTCCGCCAGGCTC 121
Db 6358 CCTGTGACGCTCTGGGATTCATCTTTCAGAAACCGCTGGATGAGTGGGTCGCCAGGCTC 6417
Qy 122 CAGGGAAGGGCTCGAGTGGGTTCTGAAATAGATTGAAATCTGATAATTATGCACAC 181
Db 6418 CAGGGAAGGGCTCGAGTGGGTTCTGCGCGTATTTAAAGCAAAATGATGGTGGGACACAG 6477
Qy 182 ATATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241
Db 6478 ACTATGCTGCACCCGTGAAGGCGAGATTCACCATCTCAAGAGATGATTCAAAACACGT 6537
Qy 242 TGTATCTGCAAAATGAACAGCTTGAACCCGAGGACACAGCGGTGATTAATCTAGTAC----- 296
Db 6538 TATATCTGCAAAATGAATAGCTTGAAGCCGAGGACACAGCGGTATATTAATCTAGTACACGG 6597

Qy 297 -----AGATTTCATAGACTGGGCGCAGGGAACTAG 328
Db 6598 GGATTATGATAACATTTTGGGGAGTTATCCCTCCCGGAATTGGGGCCAGGGAAACCCCTGG 6657
Qy 329 TCACCGTCTCTCAGAGCTTCACCAAGGGCCATCGGTCTTCCCTCCGACCCCTCTCTCCA 388
Db 6658 TCACCGTCTCTCAGAGCTTCACCAAGGGCCATCGGTCTTCCCTCCGACCCCTCTCTCCA 6717
Qy 389 AGAGCACCTCTGGGGCAGACGCGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGGAAC 448
Db 6718 AGAGCACCTCTGGGGCAGACGCGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGGAAC 6777
Qy 449 CGGTGACGCTGCTGGAACTCAGGGCCCTGACACGCGCGTGCACACCTTCCCGGCTG 508
Db 6778 CGGTGACGCTGCTGGAACTCAGGGCCCTGACACGCGCGTGCACACCTTCCCGGCTG 6837
Qy 509 TCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTCCCTCAGCAGCT 568
Db 6838 TCCTACAGTCTCAGGACTCTACTCCCTTAGCAACCGTGGTACCGTCCCTCAGCAGCT 6897
Qy 569 TGGGCAACCCAGACCTACTCTCAAGCTGAATCAAGCCCGACCAACCAAGTGGACA 628
Db 6898 TGGGCAACCCAGACCTACTCTCAAGCTGAATCAAGCCCGACCAACCAAGTGGACA 6957
Qy 629 AGAAGTGGAGGCCAAATCTTGTGACAAAACCTCACACATGCCCCACCGTCCCGACCTG 688
Db 6958 AGAAGTGGAGGCCAAATCTTGTGACAAAACCTCACACATGCCCCACCGTCCCGACCTG 7017
Qy 689 AACTCGGGGGGACCGTCAAGTCTTCTTCCCGCAAAACCAAGGACACCTCATGA 748
Db 7018 AACTCGGGGGGACCGTCAAGTCTTCTTCCCGCAAAACCAAGGACACCTCATGA 7077
Qy 749 TCTCCCGGACCCCTGAGGTCAACATGCTGGTGGACGCTGAGCCAGAGACCTGAGG 808
Db 7078 TCTCCCGGACCCCTGAGGTCAACATGCTGGTGGACGCTGAGCCAGAGACCTGAGG 7137
Qy 809 TCAAGTTCAACTGCTAGTGGAGCGGCTGGAGTGCATATATGCAAGACAAAGCCCGGG 868
Db 7138 TCAAGTTCAACTGCTAGTGGAGCGGCTGGAGTGCATATATGCAAGACAAAGCCCGGG 7197
Qy 869 AGGAGCAGTACAAACAGCAGTACCGTGTGCTAGCGTCTCAGCGTCTGCAACAGACT 928
Db 7198 AGGAGCAGTACAAACAGCAGTACCGTGTGCTAGCGTCTCAGCGTCTGCAACAGACT 7257
Qy 929 GCCTGAATGCAAGGAGTACAGTCAAGTCTCCAAAGAGCCCTCCAGCCCATCG 988
Db 7258 GCCTGAATGCAAGGAGTACAGTCAAGTCTCCAAAGAGCCCTCCAGCCCATCG 7317
Qy 989 AGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAACAGGTGTACACCTTGCCCC 1048
Db 7318 AGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAACAGGTGTACACCTTGCCCC 7377
Qy 1049 CATCCCGGATGAGTGAACAGAACACAGGTCAAGCTGACCTGCTGGTCAAAAGGTTCT 1108
Db 7378 CATCCCGGATGAGTGAACAGAACACAGGTCAAGCTGACCTGCTGGTCAAAAGGTTCT 7437
Qy 1109 ATCCAGCAGCATCGCCGTGGAGTGGAGAGCAATGGGCGAGCCGGAGACAACTACAGA 1168
Db 7438 ATCCAGCAGCATCGCCGTGGAGTGGAGAGCAATGGGCGAGCCGGAGACAACTACAGA 7497
Qy 1169 CCACGCTCCCGTGTGGACTCCGAGCGGTCTTCTTCTTCTACAGCAAGCTCAACCGTGG 1228
Db 7498 CCACGCTCCCGTGTGGACTCCGAGCGGTCTTCTTCTTCTACAGCAAGCTCAACCGTGG 7557
Qy 1229 ACAAGAGCAGTGGCAGCGGGAAAGCTTCTTCATGCTCCGCTGATGATGAGCTCTGC 1288
Db 7558 ACAAGAGCAGTGGCAGCGGGAAAGCTTCTTCATGCTCCGCTGATGATGAGCTCTGC 7617
Qy 1289 AGAACCACTACAGCAGAGAGGCTCTCCCTGTCTCGGGTAAA 1332
Db 7618 ACAACCACTACAGCAGAGAGGCTCTCCCTGTCTCGGGTAAA 7661

RESULT 10
US-10-938-353-97
; Sequence 97, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAK-FRENSCH, MARY
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PF4
; CURRENT APPLICATION NUMBER: US/10/938,353
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 97
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-938-353-97

Query Match 86.8%; Score 1158.8; DB 19; Length 1413;
Best Local Similarity 92.3%; Pred. No. 4.9e-308;
Matches 1255; Conservative 0; Mismatches 72; Indels 33; Gaps 2;

QY 1 GAGGTGAGCTGTGGAGTCTGGGGAGGCTTGGTAAAGCCGGGGGCTCCCTTAGACTC 60
DB 58 GAGGTGAGCTGTGGAGTCTGGGGAGGCTTGGTAAAGCCGGGGGCTCCCTTAGACTC 117
QY 61 TCCTGTGACGTAGCGGATTCACCTTTCAGTGGTACTGGATGTCCTGGGTCCGCCAGGCT 120
DB 118 TCCTGTGACGCTCTGGATTCACCTTTCAGTGGTACTGGATGTCCTGGGTCCGCCAGGCT 177
QY 121 CCAGGAGAGGCTCGATGGTGTCTGAAATAGATGAAATCTGAAATATGCAACA 180
DB 178 CCAGGAGAGGCTCGATGGTGTCTGAAATAGATGAAATCTGAAATATGCAACA 231
QY 181 CATTATGCGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCATAAATCTAGA 240
DB 232 TCCTAGCGACCTCTGTGAAGGGGCGATTCACCATCTCCAGAGCAATGCGCAAGACTCA 291
QY 241 CTGTATCTGCAATGAACAGCCTCGAAACCGAGGACACAGCGCTGTATTACTG- 293
DB 292 CTGTATCTGCAATGAACAGCCTCGAGAGCGAGGACACAGCGCTGTATTACTGCGAGA 351
QY 294 -----TACAGATTTTCATAGCTGGGCGCAGGGAACACTAGTCACC 333
DB 352 GATCTCTTTCTAGCGGAGCTACCTTTCTTTGACTACTTGGGGCCAGGGAACCTTGGTCACC 411
QY 334 GTCTCTCAGCTCCACCAAGGCGCATCGGTCTTCCCTCGGACCTCTCCCAAGAGC 393
DB 412 GTCTCTCAGCTCCACCAAGGCGCATCGGTCTTCCCTCGGACCTCTCCCAAGAGC 471
QY 394 ACCTCTGGGGGCAAGCGGCTCTGGGTGCTGGTCAAGGACTACTTCCCGCAACCGGTG 453
DB 472 ACCTCTGGGGGCAAGCGGCTCTGGGTGCTGGTCAAGGACTACTTCCCGCAACCGGTG 531
QY 454 ACAGTCTGCGGAACTCAGCGGCTCTGACAGGCGGTGACACCTTCCCGGTGCTCTTA 513
DB 532 ACAGTCTGCGGAACTCAGCGGCTCTGACAGGCGGTGACACCTTCCCGGTGCTCTTA 591
QY 514 CAGTCTCTCAGACTCTACTCTCCCTCAGCAGCGGTGACCGTCTCCAGCAGCTTGGGC 573
DB 592 CAGTCTCTCAGACTCTACTCTCCCTCAGCAGCGGTGACCGTCTCCAGCAGCTTGGGC 651
QY 574 ACCCAGACCTTACTGCAACGCTGAATCAAGACCCAGCAACCAAGGTGGCAAGAAA 633

RESULT 11

US-10-150-475A-7
; Sequence 7, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/10/150,475A
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 7
US-10-150-475A-7

652 ACCCAGACCTACATCTGCAACCGTGAATCACAAAGCCAGCAACACCAAGGTGGACAAGAA 711
QY 634 GTGGAGCCCAAAATCTTGTGACAAAATCACAATGCCACCGTCCCGACGACCTGAATC 693
DB 712 GTTGAGCCCAAAATCTTGTGACAAAATCACAATGCCACCGTCCCGACGACCTGAATC 771
QY 694 GCGGGGCGACCGTCAAGTCTTCTTCCCGCAAAACCAAGGACACCCCTCATGATCTCC 753
DB 772 GTGGGGGACCGTCAAGTCTTCTTCCCGCAAAACCAAGGACACCCCTCATGATCTCC 831
QY 754 CGGACCCCTGAGGTCAATGCGTGTGTGGAGCGTGGAGCCAGAAAGACCCCTGAGGTCAAG 813
DB 832 CGGACCCCTGAGGTCAATGCGTGTGTGGAGCGTGGAGCCAGAAAGACCCCTGAGGTCAAG 891
QY 814 TTCAACTGTGTAGTGGAGCGGTGGAGTGCATATGCCAAGCAAAAGCCCGGGAGGAG 873
DB 892 TTCAACTGTGTAGTGGAGCGGTGGAGTGCATATGCCAAGCAAAAGCCCGGGAGGAG 951
QY 874 CAGTACAACAGCACGCTACCGTGTGTGAGCGTCTCACCGTCTCTGACCAAGGACTGGCTG 933
DB 952 CAGTACAACAGCACGCTACCGTGTGTGAGCGTCTCACCGTCTCTGACCAAGGACTGGCTG 1011
QY 934 AATGCAAGGAGTACAAGTGCAGGTCTCCAAAGAGCCCTCCAGCCCGCCCATCGAGAAA 993
DB 1012 AATGCAAGGAGTACAAGTGCAGGTCTCCAAAGAGCCCTCCAGCCCGCCCATCGAGAAA 1071
QY 994 ACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTGCCCCATCC 1053
DB 1072 ACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTACACCTGCCCCATCC 1131
QY 1054 CGGGATGAGTCAACCAAGAACACAGGTCTGAGCTGCTGCTGCTCAAGGCTTCTATCC 1113
DB 1132 CGGGATGAGTCAACCAAGAACACAGGTCTGAGCTGCTGCTGCTCAAGGCTTCTATCC 1191
QY 1114 AGCGACATGCGGTGAGTGGAGAGCAATGGGAGCGGAGAAACAACTACAAGACCAAG 1173
DB 1192 AGCGACATGCGGTGAGTGGAGAGCAATGGGAGCGGAGAAACAACTACAAGACCAAG 1251
QY 1174 CCTCCGCTGCTGAGTCCGAGCGGCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAG 1233
DB 1252 CCTCCGCTGCTGAGTCCGAGCGGCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAG 1311
QY 1234 AGCAGTGGCAGCAGCGGGAACGCTCTTCTCATGCTCCGTGATCATGAGGCTCTGCACAC 1293
DB 1312 AGCAGTGGCAGCAGCGGGAACGCTCTTCTCATGCTCCGTGATCATGAGGCTCTGCACAC 1371
QY 1294 CACTACAGCAGAGAGGCTCTTCCCTGTCTCCGGTAAAT 1333
DB 1372 CACTACAGCAGAGAGGCTCTTCCCTGTCTCCGGTAAAT 1411

Query Match 86.5%; Score 1154.6; DB 15; Length 1392;
Best Local Similarity 92.5%; Pred. No. 7e-307;
Matches 1240; Conservative 0; Mismatches 89; Indels 12; Gaps 2;

QY 1 GAGGTGAGCTGGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTC 60
DB 58 GAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTC 117
QY 61 TCCTGTGAGCTAGCGGATTCATTTTCAGTGGCTTACTGATGTCCTGGGTCCCGCAGGCT 120
DB 118 TCCTGTGAGCTAGCGGATTCATTTTCAGTGGCTTACTGATGTCCTGGGTCCCGCAGGCT 177
QY 121 CCAGGGAAGGGGCTCGAGTGGTGTGAAATTTAGATTGAAATCTGATAATTTATGCAACA 180
DB 178 CCGGGGAAGGGGCTCGAGTGGTGTGAAATTTAGATTGAAATCTGATAATTTATGCAACA 231
QY 181 CATTATCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCATAATCTAGA 240
DB 232 TACTATCTAGACAGTATAAAGGGCCGATTCACCATCTCCAGACAAATGCCAAGACTCC 291
QY 241 CTGTATCTGAAATGAACAGCTGAAACCGAGGACACAGCGGTGTATTACTGTACA--- 297
DB 292 CTGTACTGAAATGAACAGTCTGAGGGCTGAGGACACGGCCGTGTATTACTGTGACAGA 351
QY 298 ---GATTTCTATAGACTGGGGCCAGGGAACACTAGTACCGTCTCTCAGCGCTCCACCAAG 354
DB 352 CAGGGTGTGACTACTGGGTGAGGAACCTTAGTACCGGTCTCTCAGCTAGCACCAAG 411
QY 355 GGCCCATCGGTCTTCCCGCTGGACCTCTCTCAAGAGACACTCTGGGGGCAAGCGGCC 414
DB 412 GGCCCATCGGTCTTCCCGCTGGACCTCTCTCAAGAGACACTCTGGGGGCAAGCGGCC 471
QY 415 CTGGGCTGCTGGTCAAGGACTACTCTCCCGAACCGGTGACGGTGTCTGCGAACTCAGGC 474
DB 472 CTGGGCTGCTGGTCAAGGACTACTCTCCCGAACCGGTGACGGTGTCTGCGAACTCAGGC 531
QY 475 GCCCTGACAGCGCGTGCACACCTTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCC 534
DB 532 GCCCTGACAGCGCGTGCACACCTTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCC 591
QY 535 CTGACAGCGTGTGACCGTGCCTCAGCAGCTTGGGGCCACAGACCTACATCTGCAAC 594
DB 592 CTCAGCAGCGTGTGACCGTGCCTCAGCAGCTTGGGGCCACAGACCTACATCTGCAAC 651
QY 595 GTGAATCACAGCCCAACACCAAGTGGACAAAGTGGAGGCCAAATCTTGTGAC 654
DB 652 GTGAATCACAGCCCAACACCAAGTGGACAAAGTGGAGGCCAAATCTTGTGAC 711
QY 655 AAAACTCACATGCCCACTGCGCCAGCACCTGAACTCGCGGGGCAACCGTCACTCTTC 714
DB 712 AAAACTCACATGCCCACTGCGCCAGCACCTGAACTCTCGGGGACCGTCACTCTTC 771
QY 715 CTCCTTCCCGCAAAACCAAGGACACCTCATGATCTCCGGACCCCTGAGGTCAATGC 774
DB 772 CTCCTTCCCGCAAAACCAAGGACACCTCATGATCTCCGGACCCCTGAGGTCAATGC 831
QY 775 GTGGTGTGACGTCGACCGAGACCTTGAGTCAAGTTCACTGGTACGTGGAGCGC 834
DB 832 GTGGTGTGACGTCGACCGAGACCTTGAGTCAAGTTCACTGGTACGTGGAGCGC 891
QY 835 GTGGAGTGCATATGCAAGACAAAGCCGGGAGGACAGTACACACAGCATCCGT 894
DB 892 GTGGAGTGCATATGCAAGACAAAGCCGGGAGGACAGTACACACAGCATCCGT 951
QY 895 GTGGTACGCGTCTCAGCGCTCTGCACAGGACTGGCTGAATGGCAAGGAGTCAAGTGC 954
DB 952 GTGGTACGCGTCTCAGCGCTCTGCACAGGACTGGCTGAATGGCAAGGAGTCAAGTGC 1011
QY 955 AAGGTCTCCAAAGCCCTCCAGCGCCCATTCAGAGAAACCATCTCCAAAGCCAAAGG 1014
DB 1012 AAGGTCTCCAAAGCCCTCCAGCGCCCATTCAGAGAAACCATCTCCAAAGCCAAAGG 1071

QY 1015 CAGCCCCGAGAACCAACAGAGTGTACACCTGCCCCCATCCGGGATGAGCTGACCAAGAAC 1074
DB 1072 CAGCCCCGAGAACCAACAGAGTGTACACCTGCCCCCATCCGGGATGAGCTGACCAAGAAC 1131
QY 1075 CAGGTGAGCTGACCTGACCTGGTCAAAAGGCTTCTATCCAGGACATCGCCGTGGAGTGG 1134
DB 1132 CAGGTGAGCTGACCTGACCTGGTCAAAAGGCTTCTATCCAGGACATCGCCGTGGAGTGG 1191
QY 1135 GAGAGCAATGGGAGCCGGAGAACAACTACAAGACCAACGCTCCCGTGTGGACTCCGAC 1194
DB 1192 GAGAGCAATGGGAGCCGGAGAACAACTACAAGACCAACGCTCCCGTGTGGACTCCGAC 1251
QY 1195 GGTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAAGAGCGGTGGCAGCAGGGGAAC 1254
DB 1252 GGTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAAGAGCGGTGGCAGCAGGGGAAC 1311
QY 1255 GTCTTCTCATGCTCCCGTGTATGATGAGTCTGTGCAACCACTACACGCAAGAGCCCTC 1314
DB 1312 GTCTTCTCATGCTCCCGTGTATGATGAGTCTGTGCAACCACTACACGCAAGAGCCCTC 1371
QY 1315 TCCTGTCTCCGGGTAATGA 1335
DB 1372 TCCTGTCTCCGGGTAATGA 1392

RESULT 12
US-10-704-522-7
; Sequence 7, Application US/10704522
; Publication No. US20040120949A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Gunther
; APPLICANT: Baumann, Michael
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and methods for treating cancer using
; TITLE OF INVENTION: cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1414
; CURRENT APPLICATION NUMBER: US/10/704,522
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/429,516
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: EP 02024881
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-10-704-522-7

Query Match 86.5%; Score 1154.6; DB 18; Length 1392;
Best Local Similarity 92.5%; Pred. No. 7e-307;
Matches 1240; Conservative 0; Mismatches 89; Indels 12; Gaps 2;

QY 1 GAGGTGAGCTGGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTC 60
DB 58 GAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTC 117
QY 61 TCCTGTGAGCTAGCGGATTCATTTTCAGTGGCTTACTGATGTCCTGGGTCCCGCAGGCT 120
DB 118 TCCTGTGAGCTAGCGGATTCATTTTCAGTGGCTTACTGATGTCCTGGGTCCCGCAGGCT 177
QY 121 CCAGGGAAGGGGCTCGAGTGGTGTGAAATTTAGATTGAAATCTGATAATTTATGCAACA 180
DB 178 CCGGGGAAGGGGCTCGAGTGGTGTGAAATTTAGATTGAAATCTGATAATTTATGCAACA 231
QY 181 CATTATCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCATAATCTAGA 240
DB 232 TACTATCTAGACAGTATAAAGGGCCGATTCACCATCTCCAGACAAATGCCAAGACTCC 291
QY 241 CTGTATCTGAAATGAACAGCTGAAACCGAGGACACAGCGGTGTATTACTGTACA--- 297

Db 592 CTCAGCAGCGTGTGACCGTGCCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAAC 651
Qy 595 GTGAATCACAGCCAGCAACACCAAGGTGACAAAGAGTGGAGCCCAAAATCTTTGTGAC 654
Db 652 GTGAATCACAGCCAGCAACACCAAGGTGACAAAGAGTGGAGCCCAAAATCTTTGTGAC 711
Qy 655 AAAACTCACATGCCACCGTGGCCAGCAGCTGAACTCGGGGGGACCGTCACTTTC 714
Db 712 AAAACTCACATGCCACCGTGGCCAGCAGCTGAACTCGGGGGGACCGTCACTTTC 771
Qy 715 CTCCTCCCCCAAAACCAAGCACCTCATGATCTCCCGGACCCCTGAGGTACACATGC 774
Db 772 CTCCTCCCCCAAAACCAAGCACCTCATGATCTCCCGGACCCCTGAGGTACACATGC 831
Qy 775 GTGGTGTGAGCGTGGAGCAGCAAGACCCCTGAGTCAAGTTCAACTGGTACGTGAGCGC 834
Db 832 GTGGTGTGAGCGTGGAGCAGCAAGACCCCTGAGTCAAGTTCAACTGGTACGTGAGCGC 891
Qy 835 GTGGAGGTGCATATGCCAAGCAAAAGCCGGGAGGAGCGATCAACAGCACGTACCGT 894
Db 892 GTGGAGGTGCATATGCCAAGCAAAAGCCGGGAGGAGCGATCAACAGCACGTACCGT 951
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Qy 1015 CAGCCCGAGAACCAAGGTGTACACCTGCCCCCATCCCGGAGTACGACCAAGAAC 1074
Db 1072 CAGCCCGAGAACCAAGGTGTACACCTGCCCCCATCCCGGAGTACGACCAAGAAC 1131
Qy 1075 CAGGTGTGAGCGTGGTGTGAGGCTTCTATCCAGCAGCATCGCGTGGAGTGG 1134
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Qy 1255 GTCTTCTCATGCTCGGTGATGATGAGGCTCTGACACACCACTACAGCAGAGAGCCTC 1314
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Qy 1315 TCCCTGTCTCGGTTAAATGA 1335
Db 1372 TCCCTGTCTCGGTTAAATGA 1392

RESULT 14

US-09-925-299-230
; Sequence 230. Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 230
; LENGTH: 1798

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (15)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (24)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (31)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (501)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1798)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-230

Query Match 86.0%; Score 1147.8; DB 9; Length 1798;
Best Local Similarity 91.0%; Pred. No. 5.5e-305;
Matches 1245; Conservative 10; Mismatches 73; Indels 40; Gaps 2;

Qy 2 AGGTGACGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGTCCCTTAGACTCT 61
Db 206 AGGTGACGCTGGTGGAGTCTGGGGAGGCGTGTCCAGCTGGAGGTCCCTGAGACTCT 265
Qy 62 CCTGTGAGCTAGCGATTCACTTTTCAGTGGCTACTGGATGTCTGGTCCGCCAGGCTC 121
Db 266 CCTGTGAGCTAGCGATTCACTTTTCAGTGGCTACTGGATGTCTGGTCCGCCAGGCTC 325
Qy 122 CAGGGAAGGGCTCGAGTGGTGTCTGAAATTTAGATTGAAATCTGATTAATTGCAACAC 181
Db 326 CAGGGAAGGGCTCGAGTGGTGTCTGAAATTTAGATTGAAATCTGATTAATTGCAACAC 379
Qy 182 ATTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241
Db 380 ACTATCGAGACTCCGTGAAGGGCCGATTCAACATCTCCAGAGACAATTCAGAAACACGC 439
Qy 242 TGTATCTGAAAATGAACAGCTGAAACCGAGGACACAGCCGTGTATTTACTGTACAGATT 301
Db 440 TGTATCTGAAAATGAACAGCTGAGAGCTGAGGACACGCGTGTATTTACTGTGCGARAG 499
Qy 302 TCAT-----AGACTGGGGCCAGGAAACACTA 327
Db 500 ANGTACTATGTTTCGAAAGCATCTACTACTTTTGACTCTGGGGCCAGGGAACMCTG 559
Qy 328 GTCACCGTCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCTCGGCACCCCTCCTCC 387
Db 560 GTCACCGTCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCTCGGCACCCCTCCTCC 619
Qy 388 AAGAGCACCTCTGGGGGACAGCGGCCCTGGCTGTCTGTCTCAAGGACTACTTCCCGGAA 447
Db 620 AAGAGCACCTCTGGGGGACAGCGGCCCTGGCTGTCTGTCTCAAGGACTACTTCCCGGAA 679
Qy 448 CCGGTGACGGTGTGTGGAACTCAGCGGCCCTGACCAAGGGCGGTGACACCTTCCCGGCT 507
Db 680 CCGGTGACGGTGTGTGGAACTCAGCGGCCCTGACCAAGGGCGGTGACACCTTCCCGGCT 739
Qy 508 GTCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGC 567
Db 740 GTCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGC 799
Qy 568 TTGGGACCCAGACCTACATCTGCAAGCGTGAATCAAGCCAGCAACCAAGGTTGAC 627
Db 800 TTGGGACCCAGACCTACATCTGCAAGCGTGAATCAAGCCAGCAACCAAGGTTGAC 859
Qy 628 AAGAAAGTGGAGCCCAAAATCTTGTGACAAATCTCAACATGCCCAACCGTCCAGCACT 687

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Db 860 AAGARAGTTGACGCCAAATCTTGACAAAACTACACATGCCACCGTGCCCGACACCT 919
Qy 688 GAACCTCCGGGGGACCGTGAGTCTTCTCTTCCCGCCAAAACCCAAAGGACACCTCATG 747
Db 920 GAACCTCTGGGGGACCGTGAGTCTTCTCTTCCCGCCAAAACCCAAAGGACACCTCATG 979
Qy 748 ATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCGTGAGCCACGAAGACCCCTGAG 807
Db 980 ATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCGTGAGCCACGAAGACCCCTGAG 1039
Qy 808 GTCAAGTTCAACTGTGACGCGGCGGTGGAGGTGCATTAATGCCAAGACAAAGCCGCG 867
Db 1040 GTCAAGTTCAACTGTGACGCGGCGGTGGAGGTGCATTAATGCCAAGACAAAGCCGCG 1099
Qy 868 GAGGAGCAGTACAAACAGCAGTACCGTGTGGTCAAGTCTTCAAGTCTTCAAGGAC 927
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Qy 928 TGGCTGAATGGCAAGGAGTACAAAGTCAAGGTCTTCAACAAAGCCCTCCAGGCCCCATC 987
Db 1160 TGGCTGAATGGCAAGGAGTACAAAGTCAAGGTCTTCAACAAAGCCCTCCAGGCCCCATC 1219
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Db 1520 CACAACCACTACAGCAGAGAGCGCTCTCCCTGTCTCCGGGTAAATGA 1567
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RESULT 15

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US-09-925-299-230
; Sequence 230, Application US/0925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 230
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (15)
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; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (24)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (31)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (501)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1798)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-230
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Query Match 86.0%; Score 1147.8; DB 10; Length 1798;
Best Local Similarity 91.0%; Pred. No. 5.5e-305;
Matches 1245; Conservative 10; Mismatches 73; Indels 40; Gaps 2;
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Qy 2 AGGTGAGCTGTGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
Db 206 AGGTGAGCTGTGAGTCTGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 265
Qy 62 CCGTGTGAGCTAGCGGATTCACCTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCTC 121
Db 266 CCGTGTGAGCTAGCGGATTCACCTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCTC 325
Qy 122 CAGGAAAGGGGTCGAGTGGGTGCTGAAATTTAGATTGAAATTCGATTAATTAATGAACAC 181
Db 326 CAGGAAAGGGGTCGAGTGGGTGCTGAAATTTAGATTGAAATTTAGATTGAAATTAATTAAT 379
Qy 182 ATTATGCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGATGATTTCAAAATCTAGAC 241
Db 380 ACTATGCGAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAAATTTCCAAAGAACACGC 439
Qy 242 TGTATCTGCAAAATGAACAGCTTGAACACCGAGGACACAGCGCTGTATTACTGTACAGATT 301
Db 440 TGTATCTGCAAAATGAACAGCTTGAACACCGAGCTGAGGACACCGCTGTATTACTGTGCGARAG 499
Qy 302 TCAT-----AGACTGGGGCCAGGAAACACTA 327
Db 500 ANGTACTACTATGTTCCGAAAGCATCTACTACTTGTACTCTGGGGCCAGGAAACMCTG 559
Qy 328 GTCACGCTCTCTCAGCCTCCACCAAGGGCCCATCGCTTCCCGCTGGCACCCTCCCTCC 387
Db 560 GTCACGCTCTCTCAGCCTCCACCAAGGGCCCATCGCTTCCCGCTGGCACCCTCCCTCC 619
Qy 388 AAGAGCACCTCTGGGGGACACAGCGCCCTTGGGCTGCCTGGTCAAGGACTACTTCCCGGAA 447
Db 620 AAGAGCACCTCTGGGGGACACAGCGCCCTTGGGCTGCCTGGTCAAGGACTACTTCCCGGAA 679
Qy 448 CCGGTGACGGTGTCTGGAACTCAGCGGCGCTTGACAGGGGCTGCACACTTCCCGGCT 507
Db 680 CCGGTGACGGTGTCTGGAACTCAGCGGCGCTTGACAGGGGCTGCACACTTCCCGGCT 739
Qy 508 GTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGGTACCGTCCCTCCAGCAGC 567
Db 740 GTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGGTACCGTCCCTCCAGCAGC 799
Qy 568 TTGGGACCCAGACCTTACATCTGCAACCGTGAATCAAGCCCGAGCAACCAAGGTGGAC 627
Db 800 TTGGGACCCAGACCTTACATCTGCAACCGTGAATCAAGCCCGAGCAACCAAGGTGGAC 859
Qy 628 AAGAAAGTGGAGCCCAAAATCTTGTGACAAAATCTACATGCCACCGTGCCAGACCT 687
Db 860 AAGAAAGTGGAGCCCAAAATCTTGTGACAAAATCTACATGCCACCGTGCCAGACCT 919
Qy 688 GAACCTCGGGGGGACCGTCAAGTCTTCTTCCCGCCAAAACCCAAAGGACACCTCATG 747
Db 920 GAACCTCGGGGGGACCGTCAAGTCTTCTTCCCGCCAAAACCCAAAGGACACCTCATG 979
Qy 748 ATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGAGCGTGTGAGCCACGAAGACCCCTGAG 807
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Db 1040 GTCAAGTTCAACTGCTGACGTGGACGGCGTGGAGGTGCATTAATGCCAAGACAAAGCCGCGG 1099
Qy 868 GAGGAGCAGTACAAACACACAGCTACCGTGTGGTCAAGCTCTCACCGTCTCTGCAACAGGAC 927
Db 1100 GAGGAGCAGTACAAACACACAGCTACCGTGTGGTCAAGCTCTCACCGTCTCTGCAACAGGAC 1159
Qy 928 TGGCTGAATGGCAAGGAGTCAAGTCAAGTCTCCAAAGCCCTCCAGAGCCCTCCAGAGCCCTCCATC 987
Db 1160 TGGCTGAATGGCAAGGAGTCAAGTCAAGTCTCCAAAGCCCTCCAGAGCCCTCCAGAGCCCTCCATC 1219
Qy 988 GAGAAACCATCTCTCAAAGCCAAAGGCGAGCCCGAGAACCCACAGGTGTACACCCCTGCCCC 1047
Db 1220 GAGAAACCATCTCTCAAAGCCAAAGGCGAGCCCGAGAACCCACAGGTGTACACCCCTGCCCC 1279
Qy 1048 CCATCCCGGATGAGCTGACGAGAACAGGTCAAGCTGACCTGCTGCTGCTCAAGGCTTC 1107
Db 1280 CCATCCCGGAGAGAGTGAACAGAACAGGTCAAGCTGACCTGCTGCTGCTCAAGGCTTC 1339
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Qy 1168 ACCACGCTCCCGTGTGGACTCCGACGGCTCTCTTCTTCTCTACAGCAAGCTCACCGTG 1227
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Qy 1228 GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCCCGTGTGATGCATGAGGCTCTG 1287
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1147.2	85.9	1437	4	US-09-383-916-7
4	1143.6	85.7	1576	1	US-08-157-101A-6
5	1141.2	85.5	19040	3	US-09-343-485A-3
6	1140.6	85.4	1350	1	US-08-157-101A-9
7	1082.6	81.1	8120	3	US-09-027-449-68
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12	1066.4	79.9	1655	3	US-09-049-672A-21
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ALIGNMENTS

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; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; NUMBER OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1437 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1437
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1437
US-08-487-550-7

Query Match 85.9%; Score 1147.2; DB 3; Length 1437;

Best Local Similarity 90.7%; Pred. No. 4.6e-262;
Matches 1252; Conservative 0; Mismatches 83; Indels 45; Gaps 1;

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QY 1 GAGGTGAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 58 GAGGTGCACTGGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGCGGTCCCTGAGAGTC 117
QY 61 TCCTGTGACGTAGCGGATTCATTTTCAGTGGCTACTTGGATGTCCTGGGTCCGCGAGGCT 120
Db 118 TCCTGTGACGTCTCTGATTCACCTTCAGTGACACATCAATGATTTGGTTCCGCCAGGCT 177
QY 121 CCAGGGAAGGGGCTCGAGTGGGTGCTGAAATTAGATTGAAATCTGATTAATTATGCAACA 180
Db 178 CCAGGGAAGGGGCGGAATGGTGGTTCATTTAGAAACAAACCGAACGGTGGGCAACA 237
QY 181 CATTATGCGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAMAACTAGA 240
Db 238 GAATAGCGCGCTGTGTGAAGAGACAGATTCCACATCTCCAGAGATGATTTCCAAAGCATC 297
QY 241 CTGTATCTGCAAAATGAACGCTGAAACCGAGGACACAGCGCTGTATTACTGTAC- --- 296
Db 298 GCCTAICTGCAATAGCAGCCTGAAATTCGAGGACACGGCGCTATTACTGTACTACA 357
QY 297 -----AGATTTTCATAGACTGGGC 315
Db 358 TCCTACATTTACATTTGCGGGTGGTGTCTGCTATGAGGTTTACTTCGAAATTTCTGGGC 417
QY 316 CAGGGAACACTAGTACCCTCTCTGAGCTCTCACCAAGGGGCCCATCGTCTTCCCGCTG 375
Db 418 CAGGGGCGCTGTGCTACCGCTCTCTCAGCTAGCACCAAGGGGCCCATCGTCTTCCCGCTG 477
QY 376 GCACCTCTCTCCAAAGAGCACTCTGGGGGACAGCGCCCTGGGCTGCTGGTCAAGGAC 435
Db 478 GCACCTCTCTCCAAAGAGCACTCTGGGGGACAGCGCCCTGGGCTGCTGGTCAAGGAC 537
QY 436 TACTTCCCCGAACCGGTGACGGTGTCTGGAATCTAGGGCCCTGACGAGCGCGTGCAC 495
Db 538 TACTTCCCCGAACCGGTGACGGTGTCTGGAATCTAGGGCCCTGACGAGCGCGTGCAC 597
QY 496 ACCTTCCCGCTGTCTAGTCTCTCAGGACTCTACTCTCAGAGCGTGTGACCGTG 555
Db 598 ACCTTCCCGCTGTCTAGTCTCTCAGGACTCTACTCTCAGAGCGTGTGACCGTG 657
QY 556 CCCTCCAGAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCACAAAGCCCAACAAC 615
Db 658 CCCTCCAGAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCACAAAGCCCAACAAC 717
QY 616 ACCAAGTGGAACAAGAGTGGAGCCCAATCTTGTGACAAAACTCACATATGCCACCG 675
Db 718 ACCAAGTGGAACAAGAGTGGAGCCCAATCTTGTGACAAAACTCACATATGCCACCG 777
QY 766 TGCCGACGACCTGAACCTCGGGGGGACCGTACGTCTTCTTCCCGCCCAAAACCAAG 735
Db 778 TGCCGACGACCTGAACCTCTGGGGGACCGTACGTCTTCTTCCCGCCCAAAACCAAG 837
QY 736 GACACCTCATGATCTCCCGGACCCCTGAGGTACATGCTGTGTGGAGCGTGAGCCAC 795
Db 838 GACACCTCATGATCTCCCGGACCCCTGAGGTACATGCTGTGTGGAGCGTGAGCCAC 897
QY 796 GAAGACCTCAGGTCAAGTTCAACTGCTAGTGGAGCGGTGGAGGTGCAATATGCCAAG 855
Db 898 GAAGACCTCAGGTCAAGTTCAACTGCTAGTGGAGCGGTGGAGGTGCAATATGCCAAG 957
QY 856 ACAAGCGCGGAGGAGGAGTACACAGACGATGCTGTGTGTGAGCTCTCACCGTC 915
Db 958 ACAAGCGCGGAGGAGGAGTACACAGACGATGCTGTGTGTGAGCTCTCACCGTC 1017
QY 916 CTCACGAGACTGGCTGAATGCAAGAGTACAAGTCAAGTCTTCCAAAGCCCTC 975
Db 1018 CTCACGAGACTGGCTGAATGCAAGAGTACAAGTCAAGTCTTCCAAAGCCCTC 1077
QY 976 CCAGCGCCCATCGAGAAAAACCATCTCCAAAGCAAGGGCAGCGCCCGAGAACACAGGTG 1035
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Db 1078 CCAGCGCCCATCGAGAAAAACCATCTCCAAAGCAAGGCGAGCCCGAGAACACACAGGTG 1137
QY 1036 TACACCTGCCCGCATCCCGGATGAGCTGACCAAGAACCAAGTCCAGCTGACCTGACCTG 1095
Db 1138 TACACCTGCCCGCATCCCGGATGAGCTGACCAAGAACCAAGTCCAGCTGACCTGACCTG 1197
QY 1096 GTCAAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGCAATGGGAGCGCGAG 1155
Db 1198 GTCAAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGCAATGGGAGCGCGAG 1257
QY 1156 AACAATACAAGACCAACCGCTCCCGTGGAGTCCGAGCGCTCTTCTTCTTCTTACAGC 1215
Db 1258 AACAATACAAGACCAACCGCTCCCGTGGAGTCCGAGCGCTCTTCTTCTTCTTACAGC 1317
QY 1216 AGCTCACCGTGGACAAGAGAGGTGGCAGAGGGGAAAGCTTCTCATGCTCCGTGATG 1275
Db 1318 AGCTCACCGTGGACAAGAGAGGTGGCAGAGGGGAAAGCTTCTCATGCTCCGTGATG 1377
QY 1276 CATGAGGCTCTGCACAACCACTACACGAGAGAGCTCTCCCTGTCTCCGGTAAATGA 1335
Db 1378 CATGAGGCTCTGCACAACCACTACACGAGAGAGCTCTCCCTGTCTCCGGTAAATGA 1437
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RESULT 2

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US-09-526-098-7
; Sequence 7, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/526,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1437 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1437
; FEATURE:
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NAME/KEY: mat peptide
LOCATION: 1..1437
US-09-526-098-7

Query Match 85.9%; Score 1147.2; DB 4; Length 1437;
Best Local Similarity 90.7%; Pred. No. 4.6e-262;
Matches 1252; Conservative 0; Mismatches 83; Indels 45; Gaps 1;

Qy	1	GAGTGCAGCTGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGCTCCCTTAGACTC	60
Db	58	GAGGTCAACTGTGTGAGTCTGGGGAGGCTTGTCCAGCTGGCGGCTCCCTGAGAGTC	117
Qy	61	TCCTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT	120
Db	118	TCCTGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT	177
Qy	121	CCAGGAAAGGGGCTGAGTGGTGTGTAATAGATTGAAATCTGTAATATTATGCAACA	180
Db	178	CCAGGAAAGGGGCTGAGTGGTGTGTAATAGATTGAAATCTGTAATATTATGCAACA	237
Qy	181	CATTATCGGAGTCTGTGAAGGGAATTCACCATCTCAAGAGATGATTCATAATCTAGA	240
Db	238	GAATACCGCGCTGTGTGAAGACAGATTTCACCATCTCCAGAGATGATTCATAAGCATC	297
Qy	241	CTGTATCTGCAATGAACAGCTGAAACCGAGGACACAGCGGTGTTACTGTAC	296
Db	298	GCCTATCTGCAATGAGCGCTGAAATCGAGGACACGGCGCTCTATTACTGTACTACA	357
Qy	297	-----AGATTTTCATAGACTGGGC	315
Db	358	TCCTACATTTACATTTGCGGGTGTGTCTGTATGGAGTTACTTCGAATTTCTGGGC	417
Qy	316	CAGGGAACACTAGTACCGTCTCTCAGCCCTCCACCAAGGGCCCATCGTCTTCCCGCTG	375
Db	418	CAGGCGCCCTGTGTACCGTCTCTCAGTACGACCAAGGGCCCATCGTCTTCCCGCTG	477
Qy	376	GCACCTCTCCAAAGACACTCTGGGGGACACAGCGCCCTGGCTGCTGTCAGGAC	435
Db	478	GCACCTCTCCAAAGACACTCTGGGGGACACAGCGCCCTGGCTGCTGTCAGGAC	537
Qy	436	TACTTCCCGCAACCGGTGAGTGTCTGGAATCTCAGCGCCCTGACACGGCGTGCAC	495
Db	538	TACTTCCCGCAACCGGTGAGTGTCTGGAATCTCAGCGCCCTGACACGGCGTGCAC	597
Qy	496	ACCTTCCCGGTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTG	555
Db	598	ACCTTCCCGGTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTG	657
Qy	556	CCCTCCAGAGCTTTGGGACCCAGACCTCATCTGCAACGTGTAATCAAGCCCAAGAAC	615
Db	658	CCCTCCAGAGCTTTGGGACCCAGACCTCATCTGCAACGTGTAATCAAGCCCAAGAAC	717
Qy	616	ACCAAGGTGACAGAAAGTGGGCCCAATCTGTGACAAATCTACATGCCCCACCG	675
Db	718	ACCAAGGTGACAGAAAGTGGGCCCAATCTGTGACAAATCTACATGCCCCACCG	777
Qy	676	TGCCACGACCTGAACTCGGGGGGACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT	735
Db	778	TGCCACGACCTGAACTCTGGGGGGACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT	837
Qy	736	GACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGTGTGTGTGTGTGTGTGTGT	795
Db	838	GACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGTGTGTGTGTGTGTGTGTGT	897
Qy	796	GAAGACCTGAGGTCAATGCTGTAAGTGTGACGCGCTGAGGTGCAATATGCCAAG	855
Db	898	GAAGACCTGAGGTCAATGCTGTAAGTGTGACGCGCTGAGGTGCAATATGCCAAG	957
Qy	856	ACAAAGCGGGGAGGAGTACAAAGCAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	915
Db	958	ACAAAGCGGGGAGGAGTACAAAGCAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1017
Qy	916	CTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAAAGAGCCCTC	975

RESULT 3

US-09-383-916-7
; Sequence 7, Application US/09383916
; Patent No. 6709654
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/383,916
; FILING DATE: 26-AUG-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teekin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1437 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:

; NAME/KEY: CDS
; LOCATION: 1..1437
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1437
; US-09-383-916-7

Query Match 85.9%; Score 1147.2; DB 4; Length 1437;
Best Local Similarity 90.7%; Pred. No. 4.6e-262;
Matches 1252; Conservative 0; Mismatches 83; Indels 45; Gaps 1;

QY 1 GAGGTGACGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTTAGACTC 60
DB 58 GAGGTGCAACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTTGAGATC 117
QY 61 TCCTGTGACGTAGCGGATTCATTTTCAGTGGCTACTGATGATGTCCTGGGTCCGCCAGGCT 120
DB 118 TCCTGTGACGTCTCTGGATTCATTTTCAGTGGCTACTGATGATGTCCTGGGTCCGCCAGGCT 177
QY 121 CCAGGGAAGGGGCTCCAGTGGTGTCTGAAATAGATTGAATCTGATAATTATGCAACA 180
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QY 181 CATTATGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
DB 238 GAATACGCCGCTGTGAAAGACAGATTCCACCATCTCCAGAGATGATTCCTCAAAAGCATC 297
QY 241 CTGTATCTGAATGAACAGCCCTGAAACCGAGGACACAGCGGTGTATTACTGTAC---- 296
DB 298 GCCTATCTGCAATGAGCAGCTGAAATCGAGGACACGCGCGCTTATTACTGTACTACA 357
QY 297 -----AGATTTTCATAGACTGGGC 315
DB 358 TCCTACATTTTCATTTGCGGGTGTGTCTGATATGGAGTTACTTGGAAATTTCTGGGC 417
QY 316 CAGGGAACACTAGTACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTG 375
DB 418 CAGGGCGCCTGTGTACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTG 477
QY 376 GCACCTCTCCAAAGACACTCTGGGGGACAGCGCCCTGGGCTGGCTGTGTCAGGAC 435
DB 478 GCACCTCTCCAAAGACACTCTGGGGGACAGCGCCCTGGGCTGGCTGTGTCAGGAC 537
QY 436 TACTTCCCCAAACCGGTGACGGTGTGTGAACTCAGGCGCCCTGACACGCGCGTGCAC 495
DB 538 TACTTCCCCAAACCGGTGACGGTGTGTGAACTCAGGCGCCCTGACACGCGCGTGCAC 597
QY 496 ACCTTCCCGCTGTCTTACAGTCTCTCAGGACTCTACTTCCCTCAGCAGCGTGTGACCGTG 555
DB 598 ACCTTCCCGCTGTCTTACAGTCTCTCAGGACTCTACTTCCCTCAGCAGCGTGTGACCGTG 657
QY 556 CCCTCCAGCAGCTGGGACCCAGACTATCTGCAAGTGAATCAGAGCCAGCAAC 615
DB 658 CCCTCCAGCAGCTGGGACCCAGACTATCTGCAAGTGAATCAGAGCCAGCAAC 717
QY 616 ACCAAGTGACAAAGAAAGTGGAGCCCAATCTTGTGACAAAACCTCACAATGCCCAACG 675
DB 718 ACCAAGTGACAAAGAAAGTGGAGCCCAATCTTGTGACAAAACCTCACAATGCCCAACG 777
QY 676 TGCCCAAGCCTGAACTTCGCGGGGACCGTCACTTCTTCTTCCCCCAAAACCAAG 735
DB 778 TGCCCAAGCCTGAACTTCGCGGGGACCGTCACTTCTTCTTCCCCCAAAACCAAG 837
QY 736 GACACCTCATGATCTCCCGGACCCCTGAGTTCACATGGTGGTGGTGGAGCGGAC 795
DB 838 GACACCTCATGATCTCCCGGACCCCTGAGTTCACATGGTGGTGGTGGAGCGGAC 897
QY 796 GAAGACCTGAGTCAAGTTCAACTGTCAGTGGAGCGGCTGGAGTGTGATATGCAAG 855
DB 898 GAAGACCTGAGTCAAGTTCAACTGTCAGTGGAGCGGCTGGAGTGTGATATGCAAG 957
QY 856 ACAAAGCCGGGAGGAGAGTGAACAAGACCATGACGCTGTGTGTGCTCAGCGTCTCAGCGTC 915

DB 958 ACAAAGCCGGGAGGAGCAGTACAAACAGCACCTACCGTGTGGTCAAGCGTCTCACCCTC 1017
QY 916 CTGCAACCAAGTCTGCTGATGCGAAGGATCAAGTCAAGTCTCAAGCAAGCCCTC 975
DB 1018 CTGCAACCAAGTCTGCTGATGCGAAGGATCAAGTCAAGTCTCAAGCAAGCCCTC 1077
QY 976 CCAGCCCGCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGGTG 1035
DB 1078 CCAGCCCGCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGGTG 1137
QY 1036 TACACCTGCCCCATCCCGGATGAGTGAACCAAGAACCAAGTCAAGTCTCAGCTGCTGCTG 1095
DB 1138 TACACCTGCCCCATCCCGGATGAGTGAACCAAGAACCAAGTCAAGTCTCAGCTGCTGCTG 1197
QY 1096 GTCAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGAGCAATGGGCGAGCGGAG 1155
DB 1198 GTCAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGAGCAATGGGCGAGCGGAG 1257
QY 1156 AACAACCTACAGAACCAAGCCTCCCGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1215
DB 1258 AACAACCTACAGAACCAAGCCTCCCGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1317
QY 1216 AAGCTCACCGTGGACCAAGAGCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1275
DB 1318 AAGCTCACCGTGGACCAAGAGCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1377
QY 1276 CATGAGGCTTCACAAACCACTACAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1335
DB 1378 CATGAGGCTTCGCAACCACTACAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1437

RESULT 4

US-08-157-101A-6
; Sequence 6, Application US/08157101A
; Patent No. 580832
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1576 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear		
; MOLECULE TYPE: DNA (genomic)		
; US-08-157-101A-6		
Query Match 85.78; Score 1143.6; DB 1; Length 1576;		
Best Local Similarity 91.61; Pred. No. 3.4e-261;		
Matches 1244; Conservative 0; Mismatches 84; Indels 30; Gaps 2;		
Qy	2	AGGTGACAGCTGGTGGAGCTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
Db	43	AGGTGACAGCTGGTGGAGCTCTGGGGAGGCTGGTCCAGCCTGGGAGCTCCTGAGACTCT 102
Qy	62	CTGTGACAGTACGGGATTCACATTTAGTGGCTACTGGATGTCTGGTCCGCGCAGCTC 121
Db	103	CTGTGACAGCTCTGGATTCACCTTCAGTAGCAATTCATGCACTGGTCCGCGCAGCTC 162
Qy	122	CAGGAGGGGCTCAGTGGTGTCTGAAATAGATTGAATCTGTAATTTATGCAACAC 181
Db	163	CAGGCAAGGGGTTGGAGTGGGTGGCAGTTA-----TATTATATGATGGAATTCATAAAT 216
Qy	182	ATTATGCGGAGTCTGTGAAGGGGAAATTCACCAATCTCAAGAGATGATTCAAAATCTAGAC 241
Db	217	TCTAGCAGACTCGCTGAAGGGCGATTCCACATTTCCAGAGCAATTCCAAGAACACAC 276
Qy	242	TGTATCTGCAAAATGAACAGCTGAAACCAGAGGACACAGCGGTGTATTACTGTACA---- 297
Db	277	TGTATCTGGAAGTGAAGAGCTGCAAACTGAGGACACGGGTGTCTATTACTGTATAAGAG 336
Qy	298	-----GATTTATAGACTGGGGCCAGGGAACACTAGTACCGTCT 337
Db	337	ATCAAACTTACGGAGTCCACAGATTTGACTCTCTGGGGCCAGGGAACCTGGTCAACCGTCT 396
Qy	338	CCTCAGCTCTCACCAGGGCCATCGGTCTTCCCTCGGCACCTCTCTCCAAAGAGCACCT 397
Db	397	CCTCAGCTCTCACCAGGGCCATCGGTCTTCCCTCGGCACCTCTCTCCAAAGAGCACCT 456
Qy	398	CTGGGGGCACAGCGGCCCTGGGTCTCGTCTCAAGGACTACTTCCCCGGAACCCGGTGACGG 457
Db	457	CTGGGGGCACAGCGGCCCTGGGTCTCGTCTCAAGGACTACTTCCCCGGAACCCGGTGACGG 516
Qy	458	TGTCGTGGAACCTAGGGCCCTGACAGCGCGGTGACACCTTCCCGGCTGTCTTACAGT 517
Db	517	TGTCGTGGAACCTAGGGCCCTGACAGCGCGGTGACACCTTCCCGGCTGTCTTACAGT 576
Qy	518	CCTCAGACTCTACTCTCTCAGCAGCGTGTGACCGTCCCTCAGCAGCTTGGGGACCC 577
Db	577	CCTCAGACTCTACTCTCTCAGCAGCGTGTGACCGTCCCTCAGCAGCTTGGGGACCC 636
Qy	578	AGACCTACATCTGCAAGTGAATCAAGGCCACAGCAACCAAGGTGGACAAGAAAGTGG 637
Db	637	AGACCTACATCTGCAAGTGAATCAAGGCCACAGCAACCAAGGTGGACAAGAAAGTGG 696
Qy	638	AGCCCAAACTTTGTGACAAAACCTCACATGCCCCACCGTGCACGACCTGAACTCGCGG 697
Db	697	AGCCCAAACTTTGTGACAAAACCTCACATGCCCCACCGTGCACGACCTGAACTCTCTGG 756
Qy	698	GGGCACCGTCACTCTCTCTTCCCCCAAAACCCAGGACACCTCATGATCTCCCGGA 757
Db	757	GGGCACCGTCACTCTCTCTTCCCCCAAAACCCAGGACACCTCATGATCTCCCGGA 816
Qy	758	CCCCGTGAGGTCAATGCGTGTGGACGTGAGCCACGAAGACCTTGAGGTCAAGTTCA-817
Db	817	CCCCGTGAGGTCAATGCGTGTGGACGTGAGCCACGAAGACCTTGAGGTCAAGTTCA 876
Qy	818	ACTGGTACGTGACCGGTGGAGTGCATTAATGCAAGACAAAGCCCGGGAGGAGCAGT 877
Db	877	ACTGGTACGTGACCGGTGGAGTGCATTAATGCAAGACAAAGCCCGGGAGGAGCAGT 936
Qy	878	ACAACAGCAGTACCGTGTGTGACGCTCTCAGCGTCTCGACCGACGAGTGGCTGAATG 937
Db	937	ACAACAGCAGTACCGGTGTGTGACGCTCTCAGCGTCTCGACCGACGAGTGGCTGAATG 996
Qy	938	GCAAGGAGTACAAGTGAAGGTCTCTCCAAAGAAAGCCCTCCCGAGCCCATCGAGAAAACCA 997

Db	997	GCAAGGAGTACAAGTGAAGGTCTCTCCAAAGAAAGCCCTCCCGAGCCCATCGAGAAAACCA 1056
Qy	998	TCTTCCAAAGCCAAAGGGCAGCCCGAGAACACACAGGTGTACACCTGCCCCCATCCCGGG 1057
Db	1057	TCTTCCAAAGCCAAAGGGCAGCCCGAGAACACACAGGTGTACACCTGCCCCCATCCCGGG 1116
Qy	1058	ATGAGCTGACCAAGAACACAGGTGAGCTGACCTGCTGCTCAAGAGCTTCTATCCAGCG 1117
Db	1117	ATGAGCTGACCAAGAACACAGGTGAGCTGACCTGCTGCTCAAGAGCTTCTATCCAGCG 1176
Qy	1118	ACATCCCGCTGAGTGGGAGAGCAATGGCAGCCGAGAACCAACTACAGACACACGCTC 1177
Db	1177	ACATCCCGCTGAGTGGGAGAGCAATGGCAGCCGAGAACCAACTACAGACACACGCTC 1236
Qy	1178	CGTGTCTGACTCCGACGGCTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGACGA 1237
Db	1237	CGTGTCTGACTCCGACGGCTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGACGA 1296
Qy	1238	GGTGGCAGCAGGGGAACGTCTTCTCTCTCTGATGATGATGATGATGATGATGATGATGAT 1297
Db	1297	GGTGGCAGCAGGGGAACGTCTTCTCTCTCTGATGATGATGATGATGATGATGATGATGAT 1356
Qy	1298	ACACGCAAGAGACCTCTCCCTGCTCTCCGGGTAATGA 1335
Db	1357	ACACGCAAGAGACCTCTCCCTGCTCTCCGGGTAATGA 1394

RESULT 5

US-09-343-485A-3

Sequence 3, Application US/09343485A

Patent No. 6413777

GENERAL INFORMATION:

APPLICANT: REFF, MITCHELL R.

APPLICANT: BARNETT, RICHARD S.

APPLICANT: MCLACHLAN, KAREN R.

TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND

TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME

FILE REFERENCE: 037003-0275807

CURRENT APPLICATION NUMBER: US/09/343,485A

CURRENT FILING DATE: 1999-06-30

PRIOR APPLICATION NUMBER: 09/023,715

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: 08/819,866

PRIOR FILING DATE: 1997-03-14

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 3

LENGTH: 19040

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA

OTHER INFORMATION: referred to as "Mandy"

US-09-343-485A-3

Query Match 85.51; Score 1141.2; DB 3; Length 19040;

Best Local Similarity 92.01; Pred. No. 2.7e-260;

Matches 1246; Conservative 0; Mismatches 83; Indels 25; Gaps 3;

Qy 1 | GAGGTGACAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60 || Db | 9493 | GAGGTGACAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 9552 |
Qy	61	TCTGTGACAGTAGCG-----GATTCACTTTTCAGTGGCTACTGGAATGCTCTGGGTCCGC 114
Db	9553	TCTGTGACAGCTTCCGGGTTTCAGGTTTCACTTCAATAAATACTACTACATGAGTGGGTCCGC 9612
Qy	115	CAGGCTTCCAGGAGGAGGCTCGAGTGGTGTGCTGAAATAGATTGAAATCTGATTAATAT 174
Db	9613	CAGGCTTCCAGGAGGAGGCTCGAGTGGTGTGCTGAAATAGATTGAAATCTGATTAATAT 9666

QY 241 CTGTATCTCAAAATGAACAGCCTGAAACCGAGGACACAGCCGTGTATTACTGTACA--- 297
Db 1597 GCATACCTGCAGATGAACAGCCTGCGTGTGAGACACTGCGGTCTATTACTGTCAAGA 1656
QY 298 -----GATTTTCATAGACTGGGGCCAGGGAACACTAGTTC 330
Db 1657 GGGGATTATCGCTACAATGGTGACTGGTTCTTCGACGTCTGGGGTCAAGGAACCTTGGTC 1716
QY 331 ACCGTCTCTCAGCTCCACAAAGGGCCCATCGGTCTTCCCTCGGACCCCTCTCCAAG 390
Db 1717 ACCGTCTCTCGGCTCCACAAAGGGCCCATCGGTCTTCCCTCGGACCCCTCTCCAAG 1776
QY 391 AGCACCTCTGGGGGACAGGGCCCTGGGTCTGCTCAAGACTACTTCCCGGAACCG 450
Db 1777 AGCACCTCTGGGGGACAGGGCCCTGGGTCTGCTCAAGACTACTTCCCGGAACCG 1836
QY 451 GTGACGGTGTGTGGAACTCAGCGGCCCTGACAGGGGGGTGCACACCTTCCCGGCTGTC 510
Db 1837 GTGACGGTGTGTGGAACTCAGCGGCCCTGACAGGGGGGTGCACACCTTCCCGGCTGTC 1896
QY 511 CTACAGTCTCAGGACTCTACTCCCTCAGCAGGGTGTGACCGTCCCTCCAGCAGCTTG 570
Db 1897 CTACAGTCTCAGGACTCTACTCCCTCAGCAGGGTGTGACCGTCCCTCCAGCAGCTTG 1956
QY 571 GGCACCCAGACCTACATCTGCAACGTGAATCAAGCCAGCAACCAAGGTGGACAAG 630
Db 1957 GGCACCCAGACCTACATCTGCAACGTGAATCAAGCCAGCAACCAAGGTGGACAAG 2016
QY 631 AAAGTGGAGCCCAAACTTTGTGCAAAACTCACACATGCCACCGTCCCGCAGCACCTGAA 690
Db 2017 AAAGTGGAGCCCAAACTTTGTGCAAAACTCACACATGCCACCGTCCCGCAGCACCTGAA 2076
QY 691 CTCGGGGGACCGTCACTTCTTCTTCCCGCCCAAAACCAAGACACCTCTATGATC 750
Db 2077 CTCCTGGGGGACCGTCACTTCTTCTTCCCGCCCAAAACCAAGACACCTCTATGATC 2136
QY 751 TCCCGGACCCCTCAGGTCACTCGTGGTGGAGTGTGAGCCACCAAGACCTCTAGGTC 810
Db 2137 TCCCGGACCCCTCAGGTCACTCGTGGTGGAGTGTGAGCCACCAAGACCTCTAGGTC 2196
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Db 2197 AAGTTCAACTGTGTACGTGGACGGGTGAGGTGCATAATGCCAAGCAAAAGCCGCGGAG 2256
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Db 2257 GACAGTACAACAGCAGTACCGTGTGGTGTGAGGTGTCTCACCGTCTGACACAGGACTGG 2316
QY 931 CTGAATGGCAAGGAGTACAGGTCAAGGTCTCAACAAAGCCCTCCAGCCCGCCATCGAG 990
Db 2317 CTGAATGGCAAGGAGTACAGGTCAAGGTCTCAACAAAGCCCTCCAGCCCGCCATCGAG 2376
QY 991 AAACCATCTCCAAAGCCAAAGGGACCGCCGAGAACCAAGGTGTACACCTTCCCGCCCA 1050
Db 2377 AAACCATCTCCAAAGCCAAAGGGACCGCCGAGAACCAAGGTGTACACCTTCCCGCCCA 2436
QY 1051 TCCCGGGATGAGTGTACCAAGAACAGGTGTGAGGTGTGAGGTGTGAGGTGTGAGGTGTGAG 1110
Db 2437 TCCCGGGATGAGTGTACCAAGAACAGGTGTGAGGTGTGAGGTGTGAGGTGTGAGGTGTGAG 2496
QY 1111 CCCAGGACATCCCGTGTGAGTGGGAGAGCAATGGGCGAGCAACCTACAGAGCC 1170
Db 2497 CCCAGGACATCCCGTGTGAGTGGGAGAGCAATGGGCGAGCAACCTACAGAGCC 2556
QY 1171 ACCGCTCCCGTGTGAGTCCCGAGCGCTCTTCTTCTTACAGCAAGTCTACCGTGGAC 1230
Db 2557 ACCGCTCCCGTGTGAGTCCCGAGCGCTCTTCTTCTTACAGCAAGTCTACCGTGGAC 2616
QY 1231 AAGAGCAGTGGCAGCAGGGGACGCTTCTCATGCTCCGTGTGATGATGAGGCTCTGCAC 1290
Db 2617 AAGAGCAGTGGCAGCAGGGGACGCTTCTCATGCTCCGTGTGATGATGAGGCTCTGCAC 2676
QY 1291 AACCACTACACGCAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1335

Db 2677 AACCACTACACGCAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 2721
RESULT 8
US-09-026-985-68
; Sequence 68, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8120 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-09-026-985-68
Query Match 81.1%; Score 1082.6; DB 3; Length 8120;
Best Local Similarity 88.6%; Pred. No. 1.6e-246;
Matches 1210; Conservative 0; Mismatches 119; Indels 36; Gaps 2;
QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 1363 GAAGTTCAGCTAGTGCAGTCTGGCGGTGGCTGTGCGAGCCAGGGGGCTCACTCCGTTTG 1422
QY 61 TCCTGTGCAGCTAGCGGATTCACCTTTCAGTGGCTACTGATGCTCTGGTCCGCCAGGCT 120
Db 1423 TCCTGTGCAGCTCTGGCTACTCCCTTTCAGTGTACTATATGACTGGTCCGTCAGGCC 1482
QY 121 CCAGGGAAGGGGCTCGAGTGGGTTCGAAATTAGATTGAATCTGATAATTTATGCAACA 180
Db 1483 CCGGTAAGGGCTCGAATGGGTGGATATTT-----GATCCTTCCAATGGTGAACCT 1536
QY 181 CATTTATGGAGTCTGTAGAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
Db 1537 ACGTATAATAAAGTTCAAGGGCCGTTTCACTTTTATTCGCGCAACTCCAAAAACACA 1596
QY 241 CTGTATCTGCAAAATCAACAGCCTGAAACCCGAGGACACAGCGGTGATTACTGTACA--- 297
Db 1597 GCATACCTGCAGATGAACAGCCTGGTGTGAGGACACTGCGGTCTATTACTGTCAAGA 1656
QY 298 -----GATTTTCATAGACTGGGGCCAGGGAACACTAGTTC 330
Db 1657 GGGGATTATCGCTACAATGGTGACTGGTTCTTCGACGTCTGGGGTCAAGGAACCTTGGTC 1716

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QY 331 ACCGTCCTCAGCCTCACAAGAGGCGCCATCGGTCTTCCCTCCCTGGCACCCCTCCTCCAAG 390
Db 1717 ACCGTCCTCCTGGGCTCCACCAAGGCGCCATCGGTCTTCCCTCCCTGGCACCCCTCCTCCAAG 1776
QY 391 AGCACCTCTGGGGCAGACAGCGCCCTGGGCTGCTGCTCAAGACTACTTCCCGGACCG 450
Db 1777 AGCACCTCTGGGGCAGACAGCGCCCTGGGCTGCTGCTCAAGACTACTTCCCGGACCG 1836
QY 451 GTACGGTGTCTGGAACCTCAGGCGCCTGACACAGCGCGTGACACCTTCCCGGCTGTC 510
Db 1837 GTACGGTGTCTGGAACCTCAGGCGCCTGACACAGCGCGTGACACCTTCCCGGCTGTC 1896
QY 511 CTACAGTCTCAGACTCTACTCTCCTCAGCAGCGTGTGACCGGTCCCTCCAGCAGCTTG 570
Db 1897 CTACAGTCTCAGACTCTACTCTCCTCAGCAGCGTGTGACCGGTCCCTCCAGCAGCTTG 1956
QY 571 GGCACCCAGACCTACATCTGCAAGTGAATCAGACGCGCCAGCAACCAAGGTGGACAAG 630
Db 1957 GGCACCCAGACCTACATCTGCAAGTGAATCAGACGCGCCAGCAACCAAGGTGGACAAG 2016
QY 631 AAGTGAGAGCCCAATCTGTGACAAACTCACAATGCCCGTCCCGCAGCACCTGAA 690
Db 2017 AAGTTGAGCCCAATCTGTGACAAACTCACAATGCCCGTCCCGCAGCACCTGAA 2076
QY 691 CTCGCGGGGCGACCGTCAAGTCTTCTCTTCCCGCCAAACCCAGGACACCCCTCATGTC 750
Db 2077 CTCGCGGGGCGACCGTCAAGTCTTCTCTTCCCGCCAAACCCAGGACACCCCTCATGTC 2136
QY 751 TCCCGGACCCCTGAGGTCAATGCTGTGTGTGAGTGCAGCAGCAAGACCTTGAGTTC 810
Db 2137 TCCCGGACCCCTGAGGTCAATGCTGTGTGTGAGTGCAGCAGCAAGACCTTGAGTTC 2196
QY 811 AAGTTCAACTGTTAGTGGAGCGGTGAGGTGATTAATGCCAGCAAGACCGCGGAG 870
Db 2197 AAGTTCAACTGTTAGTGGAGCGGTGAGGTGATTAATGCCAGCAAGACCGCGGAG 2256
QY 871 GAGCAGTACAAACAGCAGTACCGTGTGTGAGTGTCTCAGCGTCTCTGACACGAGACTGG 930
Db 2257 GAGCAGTACAAACAGCAGTACCGTGTGTGAGTGTCTCAGCGTCTCTGACACGAGACTGG 2316
QY 931 CTGAATGGCAAGAGTCAAGTCAAGGTCTTCCAAAGCCCTTCCAGCCCCCATCGAG 990
Db 2317 CTGAATGGCAAGAGTCAAGTCAAGGTCTTCCAAAGCCCTTCCAGCCCCCATCGAG 2376
QY 991 AAAACCATCTCCAAAGCCAAAGGCGAGCGCGGAGAACCAAGTGTACACCTTGCCTCCA 1050
Db 2377 AAAACCATCTCCAAAGCCAAAGGCGAGCGCGGAGAACCAAGTGTGTACACCTTGCCTCCA 2436
QY 1051 TCCCGGATGAGTGCACCAAGAACCGGTGAGTGTGAGTGTCTCAGCGTCTCTGACAGGCTTCTAT 1110
Db 2437 TCCCGGAGAGATGACCAAGAACCGGTGAGTGTGAGTGTCTCAGCGTCTCTGACAGGCTTCTAT 2496
QY 1111 CCCAGCAGATCGCGTGGAGTGGAGCAATGGGAGCGCGGAGCAACTCAAGACC 1170
Db 2497 CCCAGCAGATCGCGTGGAGTGGAGCAATGGGAGCGCGGAGCAACTCAAGACC 2556
QY 1171 ACGCTCCGCTGTGAGTCCGAGCGCTCTTCTCTTCTACAGCAAGTCTACCGTGGAC 1230
Db 2557 ACGCTCCGCTGTGAGTCCGAGCGCTCTTCTCTTCTACAGCAAGTCTACCGTGGAC 2616
QY 1231 AAGAGCAGGTGGAGCAGGCGGAGCGTCTTCTATGCTCCGTGATGATGAGGCTTCTGCAC 1290
Db 2617 AAGAGCAGGTGGAGCAGGCGGAGCGTCTTCTATGCTCCGTGATGATGAGGCTTCTGCAC 2676
QY 1291 AACCACTACAGCAGAGAGCGCTCTCCCTGTCTCCCGGGTAAATGA 1335
Db 2677 AACCACTACAGCAGAGAGCGCTCTCCCTGTCTCCCGGGTAAATGA 2721
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RESULT 9

US-09-121-952A-68

; Sequence 68, Application US/09121952A

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; Patent No. 6458355
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952A
; FILING DATE: 24-Jul-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8120 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-09-121-952A-68
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Query Match 81.1%; Score 1082.6; DB 3; Length 8120;
Best Local Similarity 88.6%; Pred. No. 1.6e-246;
Matches 1210; Conservative 0; Mismatches 119; Indels 36; Gaps 2;

QY 1 GAGGTCAGCTGGTGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 1363 GAAGTTTCAGTAGTCAGTCTGGCGGTGGCTGGTGACGACGAGGGGCTCACTCCGTTG 1422
QY 61 TCCTGTGACAGTAGCGGATTCATTTCAGTGGCTACTGATGTCTCGGTCCGCCAGGCT 120
Db 1423 TCCTGTGACAGTCTCTGGCTACTCTCTTCGAGTCACTATATGCACTGGGTCGAGGCC 1482
QY 121 CCAGGGAAGGGGCTCCAGTGGGTTCGAAATAGATTGAAATCTGATTAATTATGCAACA 180
Db 1483 CCGGTAAGGCGCTGGAATGGGTGGATATATT-----GATCCTTCAATGTGAAACT 1536
QY 181 CATTTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
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QY 241 CTGTATCTGGAATGAACAGCCTGAAAAACGAGGACACAGCCGTGTATTACTGTAC--- 297
Db 1597 GCATACCTCGAGATGAACAGCCTGCGTGTGAGGACACTGCCGCTCTATTACTGTGCAAGA 1656
QY 298 -----GATTTTCATAGACTGGGGCCCGAGGAAACACTAGTC 330
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Db 1657 GGGATTATCGCTACAAATGGTGAAGTGGTCTTCGACGCTCTGGGGTCAAGGAACCCCTGGTC 1716
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Db 1717 ACCGTCTCTCGGCTCCACCAAGGGCCCATCGGTCTTCCCTCTGGGACCCCTCTCTCAAG 1776
QY 391 AGCACCTCTGGGGGACAGGGGCCCTGGGTCTGGTCAAGGACTACTTCCCGGAACCG 450
Db 1777 AGCACCTCTGGGGGACAGGGGCCCTGGGTCTGGTCAAGGACTACTTCCCGGAACCG 1836
QY 451 GTACGCTGTCTGTGAAGTCAAGGGCCCTGACAGGGGGTGTACACCTTCCCGGCTGTC 510
Db 1837 GTACGCTGTCTGTGAAGTCAAGGGCCCTGACAGGGGGTGTACACCTTCCCGGCTGTC 1896
QY 511 CTACAGTCTCTCAGGACTCTATCTCCCTCAGAGGGTGTGACCGTCCCTCCAGCAGCTTG 570
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Db 1957 GGCACCCAGACCTACATCTGACAGTGAATCAAGCCGAGCAACCAACCAAGTGGACAG 2016
QY 631 AAAGTGGAGCCCAAAATCTTGTGACAAAATCTCACATGCCCCACCGTCCCGAGCACCTGAA 690
Db 2017 AAAGTGGAGCCCAAAATCTTGTGACAAAATCTCACATGCCCCACCGTCCCGAGCACCTGAA 2076
QY 691 CTCGGGGGGGACCGTCAAGTCTTCTCTTCCCCCAAAACCCCAAGACACCCCTCATGATC 750
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QY 751 TCCCGGACCCCTGAGCTACATCGTGGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 810
Db 2137 TCCCGGACCCCTGAGTCAATCGTGGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 2196
QY 811 AAGTTCAACTGGTACGTTGAGCGGCTGGAGTGCATAATGCCAAGCAAAAGCCCGGGAG 870
Db 2197 AAGTTCAACTGGTACGTTGAGCGGCTGGAGTGCATAATGCCAAGCAAAAGCCCGGGAG 2256
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QY 931 CTGAATGGCAAGAGTACAGTGCAGAGTCTCAACAAAGCCCTCCAGCCGCCATCGAG 990
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Db 2377 AAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCAAGGTGTACACCCCTGCCCCCA 2436
QY 1051 TCCCGGATGAGTGAACCAAGAACAGGTCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCT 1110
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QY 1111 CCAGAGCATCCCGTGGAGTGGGAGCAATGGGCGCCGAGACCAACTACAGACC 1170
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QY 1231 AAGAGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1290
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QY 1291 AACCATCTACAGCAGAGAGCTCTCCCTGCTCCGGGTAATGA 1335
Db 2677 AACCATCTACAGCAGAGAGCTCTCCCTGCTCCGGGTAATGA 2721
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RESULT 10

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US-09-234-340A-68
; Sequence 68, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,340A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952
; FILING DATE: 24-Jul-1998
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8120 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-09-234-340A-68

Query Match 81.1%; Score 1082.6; DB 3; Length 8120;
Best Local Similarity 88.6%; Pred. No. 1.6e-246;
Matches 1210; Conservative 0; Mismatches 119; Indels 36; Gaps 2;

QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 1363 GAAGTTACGTAGTCAGTCTGGCGGTGGCTGGTGCAGCCAGGGGGCTCACTCGGTTTG 1422
QY 61 TCCTGTGACGTAGCGGATTCTCACTTTCAGTGGCTACTGGATGCTCTGGGTCGCGCCAGGCT 120
Db 1423 TCCTGTGACGTCTTGGTACTCTCTTCGAGTCACTATATGCACTGGTCCGTGAGGCC 1482
QY 121 CCAGGGAAGGGGCTCGAGTGGTGTCTGAAATAGATTGAAATCTGATTAATATGCAACA 180
Db 1483 CCGGGTAAGGGCTGGAATGGGTGGATATTT-----GATCCTTCCCAATGGTGAACCT 1536
QY 181 CATTATGCGGAGTCTGTGAGGGGAAATTCACCACTCAAGAGATGATTCAAATCTAGA 240
Db 1537 ACGTATATCAAAAGTTCAAGGGGCGGTTTCACTTTTATCTCGCGACAACTCCAAAACACA 1596
QY 241 CTGTATCTGCAAAATGAACAGCCTGAAACCCGAGGACACAGCGGTGTATTACTGTACA --- 297
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QY 298 -----GATTTCATAGACTGGGGCCAGGGAACACTAGTCCACGCTCTCT 340
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QY 341 CAGCCTCCACAAAGGGCCCATCGCTTTCCCTTGGCACCTCTCTCCAAAGACCTCTG 400
Db 454 CAGCCTCCACAAAGGGCCCATCGCTTTCCCTTGGCACCTCTCTCCAAAGACCTCTG 513
QY 401 GGGGCACAGCGGCGCTGGCTGGCTGGTCAAGACTACTTCCCGAACCGGTGACGGT 460
Db 514 GGGGCACAGCGGCGCTGGCTGGCTGGTCAAGACTACTTCCCGAACCGGTGACGGT 573
QY 461 CGTGGAACTCAGGCGCCTCAGCAGGGCTGACACACTTCCCGGTGCTCTACAGTCT 520
Db 574 CGTGGAACTCAGGCGCCTCAGCAGGGCTGACACACTTCCCGGTGCTCTACAGTCT 633
QY 521 CAGGACTCTACTCCCTCAGCAGCGTGGTGAACCTGCTCCCTCAGCAGCTTGGGCACCCAGA 580
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QY 581 CTTACATCTGCAAGCTGAATCACAAGCCAGCAACACCAAGGTGGACAGAAAGTGGAGC 640
Db 694 CTTACATCTGCAAGCTGAATCACAAGCCAGCAACACCAAGGTGGACAGAAAGTGGAGC 753
QY 641 CCAAACTTTGTGACAAAACCTCACACATGCCACCGTCCAGCACCTGAACCTCGCGGGG 700
Db 754 CCAAACTTTGTGACAAAACCTCACACATGCCACCGTCCAGCACCTGAACCTCGCGGGG 813
QY 701 CACCGTCAGTCTTCTCTTCCCTCCCAAAACCCAAAGGACACCTCATGATCTCCCGAACCC 760
Db 814 GACCGTCAGTCTTCTCTTCCCTCCCAAAACCCAAAGGACACCTCATGATCTCCCGAACCC 873
QY 761 CTGAGTGCATCGGTGGTGGAGCTGAGCGACCAAGACCTGAGGTCAAGTTCAACT 820
Db 874 CTGAGTGCATCGGTGGTGGAGCTGAGCGACCAAGACCTGAGGTCAAGTTCAACT 933
QY 821 GGTACGTGGACGGCTGGAGGTGCATAATGCCAAGACAAAGCCCGGGAGGAGCAGTACA 880
Db 934 GGTACGTGGACGGCTGGAGGTGCATAATGCCAAGACAAAGCCCGGGAGGAGCAGTACA 993
QY 881 ACAGCAGTACCGTGGTGGAGCTGCTCAACCTCTGCAACAGGACTGGCTGAATGGCA 940
Db 994 ACAGCAGTACCGTGGTGGAGCTGCTCAACCTCTGCAACAGGACTGGCTGAATGGCA 1053
QY 941 AGGAGTACAGTGCAGGCTTCCAAACAGCCTCCCGACCCCATCGAGAAACCATCT 1000
Db 1054 AGGAGTACAGTGCAGGCTTCCAAACAGCCTCCCGACCCCATCGAGAAACCATCT 1113
QY 1001 CCAAGCCAAAGGCGAGCCCGAGAACCAAGGTGTACACCTTCCCGCCCATCCCGGGATG 1060
Db 1114 CCAAGCCAAAGGCGAGCCCGAGAACCAAGGTGTACACCTTCCCGCCCATCCCGGGATG 1173
QY 1061 AGCTGACCAAGAACCAAGGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1120
Db 1174 AGCTGACCAAGAACCAAGGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1233
QY 1121 TCSCCGTGGAGTGGGAGCAATGGGCGAGCGGAGAACCACTACAGAGCACCGCTCCCG 1180
Db 1234 TCSCCGTGGAGTGGGAGCAATGGGCGAGCGGAGAACCACTACAGAGCACCGCTCCCG 1293
QY 1181 TGCTGACTCCGACGGCTCTCTTCTCTTACAGCAAGCTCACCGGTGGACAGAGCAGGT 1240
Db 1294 TGCTGACTCCGACGGCTCTCTTCTCTTACAGCAAGCTCACCGGTGGACAGAGCAGGT 1353
QY 1241 GGACAGAGGGGAACGCTTCTCATGCTCCGTGATGATGAGGTCTGCAACCACTACA 1300
Db 1354 GGACAGAGGGGAACGCTTCTCATGCTCCGTGATGATGAGGTCTGCAACCACTACA 1413
QY 1301 CGCAGAGAGCCCTCTCCCTGCTCTCCGGTAAATGA 1335
Db 1414 CGCAGAGAGCCCTCTCCCTGCTCTCCGGTAAATGA 1448

RESULT 12
US-09-049-672A-21
; Sequence 21, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1655 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGUT11
; CLONE: 2747531
US-09-049-672A-21

Query Match 79.9%; Score 1066.4; DB 3; Length 1655;
Best Local Similarity 88.2%; Pred. No. 6.6e-243;
Matches 1192; Conservative 0; Mismatches 136; Indels 24; Gaps 2;

QY 2 AGTGCAGCTGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
Db 105 AGGTCAGTTGGTACAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGCAGGCT 164
QY 62 CCGTGTGACCTAGCGGATTCACCTTTCAGTGGCTACTGGATGCTCTGGGTCCGCCAGGGCTC 121
Db 165 CCGTGCACGGTTCCCGGATTCACCTCAGTGGTATTCGCTGACCTGGGTGCACAGGCTC 224
QY 122 CAGGGAAGGGCTCGAGTGGGTGCTGAAATTTAGATTGAAATCTGATTAATTATGCAACAC 181
Db 225 CTGGAACAAGGGCTTGGTGGATGGAG-----GTTAGCTCTCTGAAATGGAGGGCAG 278
QY 182 ATTATGCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAATCTAGAC 241
Db 279 TCTACGCACAGAAATTCCTGGGCGACTCACCTTCTCGAGGACACATCTGCAGACACAG 338

QY 242 TGTATCTGCAATGAACAGCTGAAACCCGAGGACACAGCGGTGTATTACTGTACA----- 297
Db 339 CCTACATGTTCTTCTGAAACAACCTAGGATCTGAGGACTCGGCCATCTATTACTGTGCAAGAC 398
QY 298 -----GATTTTCATAGCTGGGCGCAGGGAACACTAGTCACCGTCTCTCTCAG 343
Db 399 AACATTAGGATTTTCTTTCGACTTCTTGGGGCCAGGGGACAAATGCTCACCCTCTCTTCAG 458
QY 344 CTTCCACAAGGGCCCATCGGTCTTCCCTTGGCACCCCTCTCTCAAGAGCACCTCTGGGG 403
Db 459 CTTCCACAAGGGCCCATCGGTCTTCCCTTGGCACCCCTCTCTCAAGAGCACCTCTGGGG 518
QY 404 GCACAGCGGCGCTGGGCTGCTGTCTCAAGACTATCTTCCCGAACCGGTGACCGTGTCTGT 463
Db 519 GCACAGCGGCGCTGGGCTGCTGTCTCAAGACTATCTTCCCGAACCGGTGACCGTGTCTGT 578
QY 464 GGAACCTCAGCGGCGCTCACCAGCGGCTGCACACTTCCCGGCTGTCTCTACAGTCTCTCAG 523
Db 579 GGAACCTCAGCGGCGCTCACCAGCGGCTGCACACTTCCCGGCTGTCTCTACAGTCTCTCAG 638
QY 524 GACTCTACTCTCTCAGCAGCGTGTGTACCGTCTCCAGCAGCTTGGGCAACCCAGACCT 583
Db 639 GACTCTACTCTCTCAGCAGCGTGTGTACCGTCTCCAGCAGCTTGGGCAACCCAGACCT 698
QY 584 ACATCTGCAAGCTGAATCAAGCCCAAGCAACCAAGGTGGACAAGAAAGTGGAGCCCA 643
Db 699 ACATCTGCAAGCTGAATCAAGCCCAAGCAACCAAGGTGGACAAGAAAGTGGAGCCCA 758
QY 644 AATCTTGTGCAAAACTCACACATGCCCCCGGCGCCAGCACCTGAACTCTCTGGGGGGAC 703
Db 759 AATCTTGTGCAAAACTCACACATGCCCCCGGCGCCAGCACCTGAACTCTCTGGGGGGAC 818
QY 704 CGTCAGTCTTCTCTTCCCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCTG 763
Db 819 CGTCAGTCTTCTCTTCCCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCTG 878
QY 764 AGTTCACATGCTGGTGGTGGAGCGTAGGCAACGAAGACCTTGAGGTCAAGTTCAACTGGT 823
Db 879 AGTTCACATGCTGGTGGTGGAGCGTAGGCAACGAAGACCTTGAGGTCAAGTTCAACTGGT 938
QY 824 ACGTGGACGGGTGGAGGTGCATATGCGCAAGAACCCGCGGAGGAGCAGTACACACA 883
Db 939 ACGTGGACGGGTGGAGGTGCATATGCGCAAGAACCCGCGGAGGAGCAGTACACACA 998
QY 884 GCACGTACCGTGTGTGTCAGGTCTCTCACCCTCTGTCACACAGGACTGCTGAATGGCAAG 943
Db 999 GCACGTACCGTGTGTGTCAGGTCTCTCACCCTCTGTCACACAGGACTGCTGAATGGCAAG 1058
QY 944 AGTACAAAGTGAAGGTCTCCAAACAAGCCCTCCAGCCGCCCATCGAAGAAACCATCTCCA 1003
Db 1059 AGTACAAAGTGAAGGTCTCCAAACAAGCCCTCCAGCCGCCCATCGAAGAAACCATCTCCA 1118
QY 1004 AAGCAAAAGGACGCGCGAGAACCAAGGTGTACCTGCTGCCCTGCCCATCCCGGGATGAGC 1063
Db 1119 AAGCAAAAGGACGCGCGAGAACCAAGGTGTACCTGCTGCCCTGCCCATCCCGGGAGGAGA 1178
QY 1064 TGACCAAGAACCAAGGTGTACCTGCTGCCCTGCCCATCCCGGGAGGAGGAGA 1123
Db 1179 TGACCAAGAACCAAGGTGTACCTGCTGCCCTGCCCATCCCGGGAGGAGGAGA 1238
QY 1124 CCGTGGAGTGGGAGCAATGGGCGAGCGCGGAGAACAACTACAGACACACGCTCCCGGTGC 1183
Db 1239 CCGTGGAGTGGGAGCAATGGGCGAGCGCGGAGAACAACTACAGACACACGCTCCCGGTGC 1298
QY 1184 TGGACTCCGACGGTCTCTTCTCTTACAGCAAGTCTACCGTGGACAAGAGCAGGTGGC 1243
Db 1299 TGGACTCCGACGGTCTCTTCTCTTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGC 1358
QY 1244 AGCAGGGGAAGCTCTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACACGC 1303
Db 1359 AGCAGGGGAAGCTCTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACACGC 1418
QY 1304 AGAAGAGCCTCTCTCCCTGTCTCCGGGTAATGA 1335

Db 1419 AGAAGAGCCTCTCTCCCTGTCTCCCGGTAATGA 1450
RESULT 13
US-08-286-740-3
; Sequence 3, Application US/08286740
; Patent No. 5561053
; GENERAL INFORMATION:
; APPLICANT: Crowley, Craig W.
; TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
; TITLE OF INVENTION: HOST CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,740
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6557 bases
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-286-740-3

Query Match 79.7%; Score 1063.4; DB 1; Length 6557;
Best Local Similarity 88.3%; Pred. No. 5.2e-242;
Matches 1205; Conservative 0; Mismatches 121; Indels 39; Gaps 3;
QY 1 GAGGTCCAGTGTGTGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 1363 GAAGTTTCAGTGTGTGAGTCTGGCGGTGGCTGTGCAGCAGCGGGGCTCACTCCGTTG 1422
QY 61 TCTGTGCACTAGCGGATTCATTTCAC---GTGGCTACTGGATGTCTGGGTCCGCGCAG 117
Db 1423 TCTGTGCACTTCTTCTGGCTACTCCATCACCTCCGGATATAGCTGGAACTCCGTCAG 1482
QY 118 GTTCCAGGGAAGGGGCTCGAGTGGGTGGTGAATTTAGAAATCTGATAATTATGCA 177
Db 1483 GCCTCCGGGTAAAGGCTTGGAAATGGGTTC-----ATCGATTAGTATGCGGATCG 1533
QY 178 ACACATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCT 237
Db 1534 ACTAATATAAACCCTAGCGTCAAGGGCCGTATCACTATAAGTCCGACGATTCCAAAAAC 1593
QY 238 AGACTTACTCAATGAATGAACAGCTGAAACCGAGGACACAGCCGTGTATTACTGTAC- 296
Db 1594 ACATTCTACGTGAGTGAACAGCCCTGCGTGTGAGGACACCTCCGCTCTATTATTGTCT 1653
QY 297 -----AGATTTTCATAGACTGGGGCCAGGGAACACTAGTC 330

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Db 1654 CGAGGAGCACCATTATTCGGGCGCTGGCAGCTTCGGGTCAAGAACCTCTGTC 1713
QY 331 ACCGTCTCTCAGCTCCACCAAGGCCCATCGGTCTTCCCTCGGCACCTCTCCCAAG 390
Db 1714 ACCGTCTCTCGGCTCCACCAAGGCCCATCGGTCTTCCCTCGGCACCTCTCCCAAG 1773
QY 391 AGCACCTCTGGGGGACAGGGGCGCTGGGTGCTGTCAGGACTACTTCCCGAACCG 450
Db 1774 AGCACCTCTGGGGGACAGGGGCGCTGGGTGCTGTCAGGACTACTTCCCGAACCG 1833
QY 451 GTACGGGTCTGCTGGAACCTCAGGCGCTGACAGCGGCTGCACACCTTCCCGGTGTC 510
Db 1834 GTACGGGTCTGCTGGAACCTCAGGCGCTGACAGCGGCTGCACACCTTCCCGGTGTC 1893
QY 511 CTACAGTCTCTCAGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGTTCG 570
Db 1894 CTACAGTCTCTCAGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGTTCG 1953
QY 571 GGCACCCAGACCTACATCTGACAGTGAATCAAGCCGAGCAACCAAGGTGGACAAG 630
Db 1954 GGCACCCAGACCTACATCTGACAGTGAATCAAGCCGAGCAACCAAGGTGGACAAG 2013
QY 631 AAAGTGGAGCCCAAAATCTTGTGACAAAATCTCACACATGCCACCGTCCCGACCTGAA 690
Db 2014 AAAGTGGAGCCCAAAATCTTGTGACAAAATCTCACACATGCCACCGTCCCGACCTGAA 2073
QY 691 CTCGGGGGGGACCGTCACTCTTCTTCTTCCCTCCCAAAACCCAAAGACACCTCATGATC 750
Db 2074 CTCCTGGGGGGACCGTCACTCTTCTTCTTCCCTCCCAAAACCCAAAGACACCTCATGATC 2133
QY 751 TCCCGGACCCCTCAGGTGCATCGTGTGTTGGAGTGCAGTGCAGCCACCAAGACCTGAGTTC 810
Db 2134 TCCCGGACCCCTCAGGTGCATCGTGTGTTGGAGTGCAGTGCAGCCACCAAGACCTGAGTTC 2193
QY 811 AAGTTCAACTGTGTACGAGCGGTGGAGTGCATAATGCCAAGACAAAGCCGCGGGAG 870
Db 2194 AAGTTCAACTGTGTACGAGCGGTGGAGTGCATAATGCCAAGACAAAGCCGCGGGAG 2253
QY 871 GAGCAGTACAAAGCAGTACCGTGTGTTGGAGTGCATCGTCTCTGACACAGACTCGG 930
Db 2254 GAGCAGTACAAAGCAGTACCGTGTGTTGGAGTGCATCGTCTCTGACACAGACTCGG 2313
QY 931 CTGAATGGCAGAGTACAAAGTCAAGGTCTTCCCAAAAGCCCTCCAGCCCTCATCGAG 2373
Db 2314 CTGAATGGCAGAGTACAAAGTCAAGGTCTTCCCAAAAGCCCTCCAGCCCTCATCGAG 2433
QY 991 AAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCCACAGGTGTACACCTTGCCTCCCA 1050
Db 2374 AAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCCACAGGTGTACACCTTGCCTCCCA 2433
QY 1051 TCCCGGATGAGTGCACCAAGAACAGGTGAGTGCATCGTCTGTCAGAGCTTCTAT 1110
Db 2434 TCCCGGATGAGTGCACCAAGAACAGGTGAGTGCATCGTCTGTCAGAGCTTCTAT 2493
QY 1111 CCCAGGACATCCCGTGGAGTGGAGAGCAATGGGCGCGGAGAACCACTACAAGAC 1170
Db 2494 CCCAGGACATCCCGTGGAGTGGAGAGCAATGGGCGCGGAGAACCACTACAAGAC 2553
QY 1171 ACGCTCTCCGTGTGATCTCCGACCGTCTTCTTCTCTACAGCAAGCTCACCGTGGAC 1230
Db 2554 ACGCTCTCCGTGTGATCTCCGACCGTCTTCTTCTCTACAGCAAGCTCACCGTGGAC 2613
QY 1231 AAGAGCGTGGGAGCGAGCGGTCTTCTCTATGCTCGTGTATGATGAGGTCTGAC 1290
Db 2614 AAGAGCGTGGGAGCGAGCGGTCTTCTCTATGCTCGTGTATGATGAGGTCTGAC 2673
QY 1291 AACCACTACAGCAGAGAGCTCTCCCTGTCTCCGGTAAATGA 1335
Db 2674 AACCACTACAGCAGAGAGCTCTCCCTGTCTCCGGTAAATGA 2718
```

RESULT 14

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PCT-US95-09576-3
; Sequence 3, Application PC/TUS9509576
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
; HOST CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09576
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286740
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 798PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; LENGTH: 6557 bases
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US95-09576-3
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Query Match 79.7%; Score 1063.4; DB 5; Length 6557;
Best Local Similarity 88.3%; Pred. No. 5.2e-242;
Matches 1205; Conservative 0; Mismatches 121; Indels 39; Gaps 3;

QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGTGTAAGCCCGGGGGTCCCTTAGACTC 60
Db 1363 GAAGTTTCACTGGTGGAGTCTGGCGTGGCTGTGTCAGCCAGGGGGCTCACTCCGTTTG 1422
QY 61 TCCTGTGCAGCTAGCGGATTCATTCTCA---GTGGCTACTGGATGTCCTGGGTCCGCCAG 117
Db 1423 TCCTGTGCAGTTCCTGGCTACTCCATCACTCCGGATATAGCTGGAATGGATCCGTCAG 1482
QY 118 GCTCCAGGAAGAGGGCTCGAGTGGGTGCTGAAATTTAGATTGAAATCTGATAATTATGCA 177
Db 1483 GCCCGGGTAAAGGCTCGAATGGGTGC-----ATCGATTACGTATCCGGATCG 1533
QY 178 ACACATTATGCGAGTCTGTGAAGGGGAAATTCACATCTCAAGAGATGATTCAAATCT 237
Db 1534 ACTAACTATAACCCCTAGCGTCAAGGGCCGTATCACTATAAGTCGCGACGATTCCAAAC 1593
QY 238 AGACTGTATCTGCAATGAACAGCTGAAACCCGAGGACACAGCGTGTATTACTGTAC- 296
Db 1594 ACATTCTACCTGACATGAACAGCTTGGCTGTGAGGACACTGCCGTCTATTATTGTGCT 1653
QY 297 -----AGATTTTCATAGACTGGGGCCAGGGAACACTAGTGC 330
Db 1654 CGAGGAGCCACTATTTCGGCGCTGGCACTTCGCGCTGTGGGTCAAGGAACCTCTGTC 1713
QY 331 ACCGTCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCTCGGCACCTCTCCCAAG 390
Db 1714 ACCGTCTCTCGGCTCCACCAAGGGCCCATCGGTCTTCCCTCGGCACCTCTCCCAAG 1773
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QY 391 AGCACCTCTGGGGGACACAGCGGCGCTGGGCTGCTCAAGGACTACTTCCCGAACCG 450
DB 1774 AGCACCTCTGGGGGACACAGCGGCGCTGGGCTGCTCAAGGACTACTTCCCGAACCG 1833
QY 451 GTGACGCTGCTGGGACTCAGGCGGCTGACAGCGGCTGACACCTTCCCGGCTGTC 510
DB 1834 GTGACGCTGCTGGGACTCAGGCGGCTGACAGCGGCTGACACCTTCCCGGCTGTC 1893
QY 511 CTACAGTCTCAGGACTCTACTCTCCTCAGCAGCGTGTGACGCGTCCCTCCAGCAGCTG 570
DB 1894 CTACAGTCTCAGGACTCTACTCTCCTCAGCAGCGTGTGACGCGTCCCTCTAGCAGCTG 1953
QY 571 GGCACCCAGACCTACTCTGCAACGCTGAATCACAAGCCCGACACCAAGGCTGGAAG 630
DB 1954 GGCACCCAGACCTACTCTGCAACGCTGAATCACAAGCCCGACACCAAGGCTGGAAG 2013
QY 631 AAGTGAGCGCAAAATCTGTGACAAATCTCACAATGCTGACATGCCCGCTGCCAGCAGCTGAA 690
DB 2014 AAGTTGAGCGCAAAATCTGTGACAAATCTCACAATGCTGACATGCCCGCTGCCAGCAGCTGAA 2073
QY 691 CTCGCGGGGACCGCTCAGTCTTCTCTTCCCGGCAAAACCCAGGACACCTCATGATC 750
DB 2074 CTCGCGGGGACCGCTCAGTCTTCTCTTCCCGGCAAAACCCAGGACACCTCATGATC 2133
QY 751 TCCCGGACCCCTGAGGTCACATGCTGCTGCTGAGCGTGAAGCCAGGACACCTGAGGTC 810
DB 2134 TCCCGGACCCCTGAGGTCACATGCTGCTGAGCGTGAAGCCAGGACACCTGAGGTC 2193
QY 811 AAGTTCACTGCTGAGGTCAGGCGGCTGAGGTCGATGATGCAAGCAAGCGCGGAG 870
DB 2194 AAGTTCACTGCTGAGGTCAGGCGGCTGAGGTCGATGATGCAAGCAAGCGCGGAG 2253
QY 871 GAGCAGTACACAGCAGTACCTGCTGCTGAGGTCCTCAGGTCCTCAGGACGAGGTCG 930
DB 2254 GAGCAGTACACAGCAGTACCTGCTGCTGAGGTCCTCAGGTCCTCAGGACGAGGTCG 2313
QY 931 CTGAATGGCAAGGAGTACAGTCAAGGTCCTCAAGCAAGCGCTCCAGCGCCCATCGAG 990
DB 2314 CTGAATGGCAAGGAGTACAGTCAAGGTCCTCAAGCAAGCGCTCCAGCGCCCATCGAG 2373
QY 991 AAAACCATCTCCAAAGCAAGGCGAGCGGCGGAGAACCAAGGTCGATGATGCAAGGTC 1050
DB 2374 AAAACCATCTCCAAAGCAAGGCGAGCGGCGGAGAACCAAGGTCGATGATGCAAGGTC 2433
QY 1051 TCCCGGAGTCTGACAGGACGAGTCAAGGTCAGGTCAGGTCCTGCTCAAGGCTTCTAT 1110
DB 2434 TCCCGGAGTCTGACAGGAGTCAAGGTCAGGTCAGGTCAGGTCCTGCTCAAGGCTTCTAT 2493
QY 1111 CCCAGCGACATCGCGGAGTGGAGCAATGGGCGAGCGGCGGAGAACCAAGGTCGATGATGCAAGGTC 1170
DB 2494 CCCAGCGACATCGCGGAGTGGAGCAATGGGCGAGCGGCGGAGAACCAAGGTCGATGATGCAAGGTC 2553
QY 1171 ACAGCTCCCGTGTGGACTCCAGCGGCTCTTCTTCTTCTTACAGCAAGCTCAGCGTGGAC 1230
DB 2554 ACAGCTCCCGTGTGGACTCCAGCGGCTCTTCTTCTTCTTACAGCAAGCTCAGCGTGGAC 2613
QY 1231 AAGAGCAGTGGCAGGAGGAGGAGTCTTCTCATGCTCCGTCGATGATGATGAGGCTCTGAC 1290
DB 2614 AAGAGCAGTGGCAGGAGGAGGAGTCTTCTCATGCTCCGTCGATGATGATGAGGCTCTGAC 2673
QY 1291 AACCACTACAGCAGAGAGGCTCTCCCTGCTCCGCGTAAATGA 1335
DB 2674 AACCACTACAGCAGAGAGGCTCTCCCTGCTCCGCGTAAATGA 2718
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RESULT 15

US-08-030-175-7

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; Sequence 7, Application US/08030175
; Patent No. 6767996
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D.
; APPLICANT: Clark, Michael R.
```

```
; APPLICANT: Cobbold, Stephen P.
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.
; STREET: 555 13TH ST., NW Suite 701 East
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
; COMPUTER: IBM AT compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
; SOFTWARE: WordPerfect 5.0 (Dos Text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/030,175
; FILING DATE: 17-MAY-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01578
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1768-113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1458 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 36..1439
; US-08-030-175-7
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Query Match 79.4%; Score 1060; DB 4; Length 1458;

Best Local Similarity 87.9%; Pred. No. 2.1e-241;

Matches 1188; Conservative 0; Mismatches 140; Indels 24; Gaps 2;

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QY 2 AGGTGCGAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
DB 94 AGGTCCAACTGCAGGAGAGGGGTCAGGCTTGTGAGACCTAGCCAGACCTGAGGCTGA 153
QY 62 CTTGTCCAGTACGCGATTCACTTTCAGTGGCTACTGGATGTCTGGGTCCCGCAGGCTC 121
DB 154 CTTGCACCGTGTCTGGCTTCACTTCAGCAACTATGTCATGGCTGGCTGGTGAGACGAC 213
QY 122 CAGGGAAGGGCTCAGTGGTGTCTGAAATAGATTGAAATCTGATAATTATGCAACAC 181
DB 214 CTGACGAGGCTTGTGATGGATTTGGAACCACTTAG-----TCATGATGGTAGTGA 267
QY 182 ATTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGAC 241
DB 268 ACTTTCGAGACTCTGTGAAGGGGAGAGTGAATGCTGGTAGACACAGCAAGCAAGT 327
QY 242 TGTATCTGCAAAATGAACAGCCTGAAACCGAGGACACAGCGGTGTATTACTGTACA---- 297
DB 328 TCAGCCTGAGACTCAGCAGGCTGACAGCGCCGACACCGCGGTCTATTATTGTGCAAGAC 387
QY 298 -----GATTTTCATAGACTGGGGCCAGGGAAACATAGTACCGTCTCTCTCAG 343
DB 388 AAGGCACTATAGCTGTGTATACGTCACCTGGGGTCAAGGCGAGCCTCGTACAGTCTCTCAG 447
QY 344 CCTCCACCAAGGCCCATCGGTCTTCCCTTGGCCCTCTCCAGACCTCTCTGGGG 403
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